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[illegible]

Mon Sep 9 09:30:05 2002

us-09-834-291-1.rge

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 complete sequence.
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 187313)
 1 (bases 1 to 187313)

REFERENCE
 AUTHORS Blakey, S.
 TITLE Direct Submission
 JOURNAL Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
 UK.
 E-mail enquiries: humquery@sanger.ac.uk
 CR10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk

COMMENT
 On Aug 31, 2001 this sequence version replaced gi:14161146.
 requests: clonerequest@sanger.ac.uk
 During differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping above.
 only a small overlap as described as follows unless otherwise noted: all
 this sequence were finished as high quality data (i.e., phred quality >=
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all regions were covered by at least
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em: EMBL; Sg:
 SWISSPROT; Tr: TrEMBL; Wp: WormPep; Information on the WORMPep
 database can be found at: http://www.sanger.ac.uk/projects/C_elegans/wormpep
 was generated from part of bacterial clone contigs of human
 chromosome 10, constructed by the Sanger Centre Chromosome 10
 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/Map/Chr10>
 RP11-399019 is from the library RP11-11.2 constructed by the group
 of Plesier de Jong. For further details see
<http://www.pblac3.6>
 VECTOR: pBlac3.6
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 true right end of clone RP11-30415 is at 18704 in this sequence.
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 Best Local Similarity 99.7%; Pred. No. 0;

1,

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[illegible]

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 VERSION D31968.1
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 SOURCE Homo sapiens blood DNA, clone pF7.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE Wada, N., Matsumura, M., Ohba, Y., Kobayashi, N., Takizawa, T. and
 Transcription stimulation of the Fas-encoding gene by nuclear
 factor for interleukin-6 expression upon influenza virus infection
 J. Biol. Chem. 270 (30), 18007-18012 (1995)
 MEDLINE 9535401
 REFERENCE 2 (bases 1 to 2165)
 AUTHORS Nakanishi, Y.
 TITLE Direct Submission
 JOURNAL Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University,
 Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa,
 Ishikawa 920-0934, Japan (E-mail: nakanake@eds.p.kanazawa-u.ac.jp).
 Tel:076-234-4424, Fax:076-234-4480

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RESULT 7
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VERSION X81335.1
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1877)
AUTHORS Behrmann, I., Walczak, H. and Kramer, P. H.
TITLES Structure of the human APO-1 gene
JOURNAL Eur. J. Immunol. 24 (12), 3057-3062 (1994)
MEDLINE 95104292
REFERENCE 2 (bases 1 to 1877)
AUTHORS Kramer, P. H.
TITLES Direct Submission
JOURNAL Submitted (03-SEP-1994) P. H. Kramer, German Cancer Research
Center, TumorImmunology Programm, Im Neuenheimer Feld 280, 69120
Heidelberg, FRG
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DEFINITION	H sapiens Fas, Apo-1 gene (promoter and exon 1).		
ACCESSION	X82279		
VERSION	X82279.1 GI:673405		
KEYWORDS	Apo-1 gene; Fas gene.		
SOURCE	human.		
ORGANISM	Homo sapiens		
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	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1608)		
AUTHORS	Cheng, J., Liu, C., Koopman, W.J. and Mountz, J.D.		
TITLE	Characterization of human Fas gene. Exon/Intron organization and		
	promoter region		
JOURNAL	J. Immunol. 154 (3), 1239-1245 (1995)		
MEDLINE	95123075		
REFERENCE	2 (bases 1 to 1608)		
AUTHORS	Cheng, J.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-OCT-1994) J. Cheng, Univ. of Alabama at Birmingham,		
	Univ. of Alabama, 701 South 19th Street, UAB Station, LMB 473,		
	Birmingham, AL 35294-0007, USA		
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OY	1066	taagcaaaagggtatbatatgtytlttaatgggttgaattggaattggaagggagag	1125
Db	307	TAAAGCAAGGGTATTAAATGCTATTAAATGGGTTGAATCTAATTGGGAAGGAGAGAG	366
OY	1126	ttgcagaatgaggtgcagagcttgtygtgagatgccaagaagatactgaaacctttag	1185
Db	367	TTTGAGAGTGAAGTGCAGAGCTTGTTGGTGAAGTCCAAAGAAATCTGAAACCTTAAAGT	426
OY	1186	tytccagctctggaactgcataccaaattcaggtctcagtaatgatatgctatctcaacata	1245
Db	427	TGTCAGAGCTGGAAGTGTATCCAAATTGAGTTACAGTAATGATGTCAATTATCCAAACATA	486
OY	1246	ccctctgtaaaattcatgctaaactactactaagagctctcagcttccaaagcaatgty	1305
Db	487	CCTTCTGTAAATTCATGCTAAACACTTAAGACTATCTCCGTTCCAAAGCAATAGTG	546
OY	1306	actttgacaagtggttccacagagcgcagcaagaagatatacaagatttttlttaagaanaat	1365
Db	547	ACTTTATACAGTGTTTACACAGAGCAGCAAGAAATTAACAAGATTTTTTTTAAAGAAAT	606
OY	1366	ggccaggaataatgagtgatacagaagaacaggaagtaattgtgaatgttataatgctg	1425
Db	607	GCCACAGAAATATATGATACAGAGGACAGGAAGTAATGTGAATCTTAATTAATAGCTGG	666
OY	1426	ggtcatgcatgttgacttaagtgttaagcttgttccctctgagaaataaanaactaag	1485
Db	667	GGCATAGGATTTGGCTTAAAGTTGATTAGCTTTGTTTCCCTTGAGAAATTAATAACTAAG	726
OY	1486	ggggccctcccttctcagagccttatgtgcgacaactgtactcttltcataatgttaactg	1545
Db	727	GGGCCCCCTCTTTCAGAGGCCCTTATGGGCAACATCTGATTTTTCATATNGTTAACTG	786
OY	1546	tcacattccagaaggtctgtgtagcctctcatgltgacgaccaaatgtagaagccagctc	1605
Db	787	TCCATTCCAGGAACGCTCTGTGAGCCTCTCAATGTTCCACCCACAAAGTGAAGACGCCATC	846
OY	1606	aaatggcccgcaagcttctctgtgtagcttcagcaattgagcaaggtcctgttaccca	1665
Db	847	AAATGCCCCGCAAGCTTCTCTGATGACTCCAGATTTAGCCAAAGGCTCCTGTACCCA	906
OY	1666	ggcagagcctctgctctgtagcttcatctctctttaaagacctcccaacttccaggtt	1725
Db	907	GGCAGGACCTCTGGGCTCTAGCTCATCTTCTCTCAAGACCTCCCAACTTCCAGGTT	966
OY	1726	gaatacagcagaagcctttagaaggggcgagagggcggtctcaggttctcaactgaa	1785
Db	967	GAACTAACGACGAAGCCTTATGAAAGGAGGACGAGCGGCTTCGAGGTCCTTACCTGGA	1026
OY	1786	gttagcatgtagcagcgaactgtagaagcgcgcgcggagacagaatgcccatttgtgcaacga	1845
Db	1027	GTGAG-ATGCGACGCCACTGCAAGAAAGCCCGGAGACAGGAATGCCCCATTGTGAAAGAA	1885
OY	1846	cccttgaactctctctcaacctgagcttcccccctctaccgcgagcgagagccaagtgtc	1905
Db	1086	CCCTGATCCTTCTCTACCTTACCTTCTCCCTCCCTCAACCGCGGAGGACCAAGTTGG	1145
OY	1906	taataataatgtagccctccccaacccgggcttcccccagagagcttccctccactctc	1965
Db	1146	TGAATCAATGAGACCTCCCCAAACCGGGCGTTCCTCCAGACGAGGCTTCCTTCCATCTCT	1205

D	379	GTGACGAGTTTGGTGCACATGTTAAAGGAATTTGAAATTTTATAGCTTATAGTTTGG	438
O	1198	aactgcacaaactcaaggttcagtaaatgtaatcattccaaacattccttcgtaaaa	1257
D	439	AATTGATTATTAATTTAGGTTAGTATGATGCTGTTATTTTAAATATATTTTTCGTAAA	498
O	1258	tctatgctaaactactaagagatctaccgcttccaaagaatagtaactttgacagt	1317
D	499	TTTATGTTAAATTTATTTAAGAGATTTATTCGTTTAAAGTAATGTCATTTTAAATG	558
O	1318	gttccacagacacgaaagaattacaagaattttttttaaagaatttggccagaata	1377
D	559	GTTTATTTAGACTACGAAGAATTATTAAGATTTTATTTTAAAGAAATTCGTTAGGAATA	618
O	1378	atgagtaacgaagacacggaagtaattgttaatgctttaaataagctggctatgcatt	1437
D	619	ATGAGTAACGAAGGTATGAGAGTAAATTCGAATGTTAAATATGTTGGGTTATTCGATT	678
O	1438	tggcttaagtcttagctcttcttctcctcttgagaaataaaactaagggtccctccct	1497
D	679	TGGTTTAACTGTATGTTTGTGTTTTTTTGTGAAATTTAAATTTAAGCGGTTTTTTTT	738
O	1498	ttaagagccttttggcgcaacatctgtaacttttccataatgtaactgtccatccaaga	1557
D	739	TTTATGAGTTTATATGCGTAATTTGTTATTTTATATATGTTAATGTTATTTATTAAGA	798
O	1558	acgtcttgcagcctctcatctgcttgcgcgcacacatgacacacccagtcgaatgccgca	1617
D	799	ACGTTTGTGAGTTTTTATGTTGTGACTTATATAGATNGATATGTTAGTTAAATGTTTCGT	858
O	1618	agcttctctctgagctgactccacgaattagccaaagctcctgtaccagcgagaacct	1677
D	859	AGTTTTTTTGTAGTAGTATTTAGTATATTTAGTAAAGTTTTGTATTTAGTAGATTTTT	918
O	1678	gcgccttgcagcttccattctctcttcaagacacctcccaacttcccaagtttgaactacagag	1737
D	919	CGGTTTACGTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT	978
O	1738	aaagcctttagaagaagcgagaaagcgcgctctcgagctcctccctgaagtagagctgca	1797
D	979	AACTTTTATGAAAGGATGAGCGAGTCGCTTTTCAGAGTTTTTATTTGAACTGAG-ATGTTA	1037
O	1798	gcacactgcaagaacgccccgcgaagaagaatgcccatttgcacaagaacctgactcct	1857
D	1038	GTTATATGTGGAACCTTTTCGGGATAGGAATTTATTTGTGTAACGAATTTTCATTTT	1097
O	1858	ccctcaccccgactctcccccctccctaccgcgcgcagccgcgaagttgcgaatcaatga	1917
D	1098	TTTTTATTTGATTTTTTTTTTTTTTTTATTTTCGGGTAGGTTAACTCTTGCAATTAATGA	1157
O	1918	gccctcccaacccggcgcttcccaagcagagcttccctccatccctcctgcaccacggg	1977
D	1158	GTTTTTTTATTCGGGCTTTTATTTAGCGAGGTTTTTTTTTTTATTTTATTTGATTAACGG	1217
O	1978	gcttctcgtagctcgctcctctgactctgcgcgaaggtgacacacaggtgttccaagaagc	2037
D	1218	GTTTTTCGTAGTTCGTTTTTGTATTTTCGGTAAGAGTGAATATATNGGTTTAAAGCGT	1277
O	2038	tctcggagatgaggaagaaggttttaccagtagtaactgtcgtgagccttaaggcgsggac	2097
D	1278	TTTTTGGGAGTAGAGGAAGCGGTTTACGAGTGAATTTGGTTGAGTTTTTAAGGGCGGAT	1337
O	2098	tgcacaggaacacacctgagcccaagccctggctgcacagcgagagctgtcctctccccc	2157
D	1338	TGCTATCGGAATAATATTTTGAAGGTATGTTTGTTGTTTATAGCGGAGATGTTTTTTTTTC	1397
O	2158	gcggagtttgcagccgcctcagtaacgaagattggggaagccttctacactcgaagaattgc	2217
D	1398	GCCTGTTTGTGATTCGTTTATGTAACGGATGTTGGGAAATTTTTTATTTTCGAGGATG	1457
O	2218	tcaacacacatcgtggcatctggaacctctacactctgtagtaccctcctctgcgcgg	2277

Query Match	Best Local Similarity	Score	DB #	Length
Matches 698; Conservative	99.4%	Pred No. 2,1e-151;		
	0; Mismatches	4; Indels	0; Gaps	
1946	gaggtcttcctccacatctctctctgacacccggtcttcgtagctgctcctaactcg	2005		
1	GAGGCTTCCTCCATCTCTCTGACACCGGGCTTTCGTGAGCTGCTCTGATCTCG	60		
2006	cgcaagagtgacacacagtggttcaaaagccttccttgagggttgagggaaagcgtttacg	2065		
61	CGCAGAGTGTACACACAGGTCTTCAAGAGCCTTCTGGGAGTGAAGGAAACGGGTTTACG	120		
2066	agtgactgtgcttgagctctcagcctgagggcgagctgcaacgacacacccctgagccagcc	2125		
121	AGTGACTTGGCTGAGGCTTCAAGGGGCGGACATGGCAACGGAACACCTTGAGGCCAGCC	180		
2126	ctgagctgcacagcgagagctgctctctctctccgcyggttgtagaccgctcagtaagca	2185		
181	CTGGCTGCTCCAGGCGGAGAGCTCTCTCTCCCGGGTGTGTGACCCGGCTCAATACGA	240		
2186	gttgaggagactcttcaacttcgaggatctgtcacaacaacatgctggacatctgagcc	2245		
241	GTTCGGGAGACTTCTTCACTTCGAGAGATTGCTCAACAACATGCTGGGCACTCGAACCC	300		
2246	tcctaacctgttgtatccctctctctctgcccgggtgagagcttaccocgctctagtcocgg	2305		
301	TCTTACCTCTGTGTGACCTCTCTCTGCCCCGGGTGAGAGCTTACCCGCTTATGTCCTCGG	360		
2306	gataagcaaatgaggcgagcgagcgagcagctgagggatcgagggcgagcgagcgagcagc	2365		
361	GATAGGCAAAATGGGGCGGCGGAGGAGCGCTGCGGATTTGCGGGGAGCGCGCCACAGC	420		
2366	gggaacactggagagcgagcgtctgtcgcgagggcggttgagaacttgctcccgaggctgt	2425		
421	GGGCAACCTGGAGCGCGGCTGCTGCGGGGAGGGTGTGAGAACATGGCTCCCGGGGGCTGT	480		
2426	taggaacttcctcagggcccgagtgctcagaagatlgaggaacttgctttcttgagcct	2485		
481	TAGGACCTTCTCCCTGAGCCCGGGGCTGCAAAACCTGAGAGACTTGTCTTCTTGGGGCTT	540		
2486	tgaatgcaatgtgtgatacccgcttgagggcgagggcgagcgtcgagcgctcctcggagacca	2545		
541	TGATGCGAAGTGTCTGACCCCGCTGGGCAAGCGGGGAGAGCTCCCGGCTCTCTCGAGACCA	600		
2546	ctcagctcacagtttgagtggtggcgctggggcgagcaagatlgagggaggaagtcgggga	2605		
601	CTGCGCTTCCACGTTGAGGTGGGCGATGGGGGCGGAGACGAAATTGAAGCGGAAGTGTGGA	660		
2606	agccttaaggtcgtctgagggagggacccggttgaggagagga	2647		
661	AGCTTTAGGGTCTGAGGGGAGACCCCGGTGTGAGAGAGA	702		

Plasmodium pf38 contig
hfas coding sequence
Fas cDNA, Mammal
Human Fas antigen
Human Lung tumor
Human c-fms oncogene
DNA encoding Colon
EP-892047 Seq ID 4
Human colon cancer
Human Fas soluble
Human Fas soluble
Human Fas soluble
Human Fas antigen
Murine L680 genome
Murine L680 homo
Dicyclostelium plas
Human nervous syst
Human metastasis a
Human immune syste
Human polynucleoti
Nucleotide sequenc
Human reproductive
Human polynucleoti
Human actin 14 cod
Human immune syste
Human immune syste
Human immune syste
Retinoblastoma bin
Human immune syste
Human immune/haema
Murine MOC15 genom
Human immune syste
Human reproductive
Human polynucleoti
Human nervous syst

[illegible]

100

RESULT	3
ABL34418	
ID	ABL34418 standard; DNA; 1608 BP.
XX	
AC	ABL34418;
XX	
DP	26-MAR-2002 (first entry)
XX	
DE	Human immune system associated gene SEQ ID NO: 2391.
XX	
KW	Human; immune system disease; cytosine methylation; antiasthmatic;
KW	antiarteriosclerotic; antihaemic; cytostatic; neutrotropic;
KW	neutropoietic; anti-HIV; anticonvulsant; neoptopic;
KW	antirheumatic; antiarthritic; antidiabetic; ophthalmologic;
KW	acute myeloid leukaemia; cancer; eye disease; arteriosclerosis;
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; anaemia;
XX	gene; ds.
XX	
XX	Homo sapiens.
XX	

	Query Match	Best Local Similarity	29.8% 76.4% 76.4%	Score 957.4	DB 24	Length 1608	Indels 5	Gaps 3
	Matches 1215	Conservative	0	Mismatches 371				
QY	779	tatcacatccctccatccactctctttgtgtcatatagaatgcagatgtgtgcac						
DB	19	tatatattctttttattattattcttttttgcgttattagatgtgtgtgcac						
QY	839	aagctgtgcacgcccgaggtccctccatcbbgcacacagctcactcgaaggttgcgaac						
DB	79	aaggttgcagcttttagtggtttttttttagtattatggttatgttaaggtgtgtglat						
QY	899	agggcaagcctacacacacactacacagactgtgttgtaagtcagtcgaacatgtgcgaacac						
DB	139	agataagttatttaattattattataagattgtgtgttaagtcgtatgttaagaagtggaatag						
QY	959	gggtgtatgcgaagccctccagaggggtgaaccttaacctaatgttgggg-cccaacaggtcc						
DB	199	gggtgcagtcgaagctttcttggaggggttaattattagattttaggttgggtttaaatagtctt						
QY	1018	cagaagaataatctcaactctgagaggaagccctgaaggaatgaacgtgtgcttaacgaaggt						
DB	259	tugaagaataatgttaattatgttagaggaagcttgcgaaggaatgaacgtgtgcttaacgaaggt						
QY	1078	tattatgtgtatttaattatgtgttgaatactcaatttgcgaagggaggaaggttgcgaaggt						
DB	319	tattcaatgtgttcttaacttgcgttgaatttaattcttgcgaaggaaggaaggttgcgaaggt						
QY	1138	gtgcagagcttgtgtgcagatgcgaagaagatactgaacctttagtctgcagctctcg						
DB	379	gtgtagagcttctgtgcagatgcgttaaaaggaatattgaattttagtctgtgtttagtctcg						
QY	1198	aacttcacccaacttcaggtctgcagatgatgtatcgaattccaaacacactctgtgaaac						
DB	439	aattgtattttaaatttaggtcttagcaatgcagatgcatttattttaaataatatttttgcgaa						
QY	1258	ttaattcctaactacacagaagctatctacagtttccaaacacacacacacacacacacacac						
DB	499	ttratt						

[illegible]

03-FEB-2000.
16-OCT-1998; 98DE-1047779.
16-OCT-1998; 98DE-1047779.
(DEKR-) DEUT KREBSFORSCHUNGSGEZENTRUM.
Kammer P, Mueller-Schilling M, Oren M
WPI; 2000-162245/15.

Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy -
Claim 2; Fig 4; 12pp; German.

This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor intron 1 which contains a p53 binding region described in the method of the invention.

sequence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other

ery Match	8.28;	Score 262.8;	DB 21;	Length 266
est Local Similarity	99.28;			
tches 264;	Conservat.	Pred. No. 3.5e-61.		

```
conservative 0; Mismatches 2; Indels 0; Gaps 0
```

5'atccaccgacgagcagagccgggacagcgtccacccggcgactctcgagagaccacactgctgcctccacggtt 25
1 gatacccgccgggacagagccgggacagcgtccacccggcgactctcgagagaccacactgctgcctccacggtt 60			

[illegible]

RESULT	6
AAC61798	
ID	AAC61798 standard; DNA; 2551 bp
XX	

AC AAC61798;
XX
DT 06-MAR-2001 (first entry
XX

DNA encoding a human Fas (Apo-1) protein

Human, Fas; Apo-1; antisense compound; Fas ligand; Fcp-1; hepatitis Fas associated protein 1; protein tyrosine phosphatase; cancer; autoimmune disease; inflammatory disease; lymphoma; ss.

```
Location/Qualifier
221..1228
/*tag= a
/product= "Fas"
```

W0200061150-A1

19-OCT-2000.
10-APR-2000; 2000WO-US09540

12-APR-1999; 99US-0290640

(ISIS-) ISIS PHARM INC

Dean NM, Marcussen EG,

WPI: 2000-628395/60

P-PSDB; AAB19341.

Antisense oligonucleotides inhibit lung cancer

1 (Fap-1) expressio

Example 2; page 71-

The present sequence

describes antisense
region, translation

OR 3'-untranslated
ligand (FASL), or Fas

phosphatase). The an expression of Fas F

to treat autoimmune
can also be used 4

cancer or lymphoma.

Sequence 2551 BP; 826

sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other

100

Plasmid pF58 contg. human Fas cDNA.

Plasmid pF58 contg. human Fas cDNA

Query Match	Best Local Similarity	100.0%	Pred. No. 1.5e-50;	Length 2534;
Matches 226;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	2033	gacgcctctctgagtgagtgaggaagcggcttaccagtgacttgagctgagagcctcaaggagcg	2092	
Db	1	gagcgtctctctgagtgagtgaggaagcggcttaccagtgacttgagctgagagcctcaaggagcg	2092	
QY	2093	gagcactgagcaggaacacacacacccctgaagccagccctgagctgcgccagggagagctccctt	2152	
Db	61	ggcactgagcaggaacacacacacccctgaagccagccctgagctgcgccagggagagctccctt	2152	
QY	2153	ctcccgcgaggttggttgagcccgctcagtcagcgaggttgaggaagccttcttaacttcgagag	2212	
Db	121	ctcccgcgaggttggttgagcccgctcagtcagcgaggttgaggaagccttcttaacttcgagag	2212	
QY	2213	attgctcaacacacatgctcgagcattcgaccctctactcttggt	2258	
Db	181	attgctcaacacacatgctcgagcattcgaccctctactcttggt	2258	
RESULT 13				
AAV07002				
ID	AAV07002	standard; cDNA to mRNA; 2534 BP.		
XX				
AC	AAV07002;			
XX				
DT	16-JUL-1998	(first entry)		
XX				
DE	Human Fas antigen cDNA.			
XX				
KW	Human; Fas antigen; derivative; apoptosis regulation; gene therapy;			
KW	treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;			
KW	apoptosis modulation; ss.			
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	195..1202		
FT		/*tag= a		
FT	sig-peptide	195..242		
FT		/*tag= b		
FT	mat-peptide	243..1199		
FT		/*tag= c		
FT		/product= Fas_antigen		
XX				
PN	WO9742319-A1.			
XX				
PD	13-NOV-1997.			
XX				
PE	01-MAY-1997;	97WO-JP01502.		
XX				
PR	02-MAY-1996;	96JP-0135760.		
XX				
PA	(MOCH) MOCHIDA PHARM CO LTD.			
PA	(OSAB-) OSAKA BIOSCIENCE INST.			
XX				
PI	Nagata S, Nakamura N;			
XX				
DR	WPI: 1997-558981/51.			
XX				
PT	P-PSTB; AAM50289.			
XX				
PT	Fas antigen derivative containing modified extracellular region -			
PT	of viral and other diseases			
XX				
PS	Disclosure; Fig 1-2; 102bp; Japanese.			
CC				
CC	The present sequence was used in the development of novel Fas			
CC	antigen derivatives, which contain a Fas antigen extracellular			
CC	region lacking one or more amino acid residues in the region from			
CC	the amino-terminal to (but excluding) the 1st cysteine residue			

(preferably at least 29 residues are deleted).
 The derivatives are effective regulators of apoptosis and can be used (either by administration of the polypeptide, or by the use of the coding DNA in gene therapy) to treat a range of diseases, e.g. diabetes, arthritis, lupus and in particular viral diseases such as hepatitis, influenza and HIV, by modulating apoptosis of virus-infected cells.

Sequence 2534 BP; 817 A; 491 C; 499 G; 727 T; 0 other:

Query Match 7.0%; Score 224.4; DB 18; Length 2534;
 Best Local Similarity 99.0%; Pred. No. 4e-50;
 Matches 225; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2033 gacgctctggagagtgaggaagcgggtttacagagtgacttgctggaagcctcagggcg 2092
 |||||
 1 gacgctctggagagtgaggaagcgggtttacagagtgacttgctggaagcctcagggcg 60
 2093 ggcactggcaggaacacacccctgagcgcagcctggtgcccagggagctgctctt 2152
 |||||
 61 ggcactggcaggaacacacccctgagcgcagcctggtgcccagggagctgctctt 120
 2153 ctcccgcggttggtgagccgctcagtagcaggttgaggagctcttcacttcggagg 2212
 |||||
 121 ctcccgcggttggtgagccgctcagtagcaggttgaggagctcttcacttcggagg 180
 2213 atggtcacaacacatgctgagcatttgagcctcctactctggt 2258
 |||||
 181 atggtcacaacacatgctgagcatttgagcctcctactctggt 226

RESULT 14
 AAF68854/c
 ID AAF68854 standard; cDNA; 2435 BP.

XX AAF68854;

DT 12-APR-2001 (first entry)

XX Human lung tumour protein related nucleotide sequence SEQ ID NO:796.

XX Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
 KW lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
 KW cytosolic; antisense inhibition; ss.

OS Homo sapiens.

PN WO200100828-A2.

PD 04-JAN-2001.

PF 30-JUN-2000; 2000WO-US18061.

XX 30-JUN-1999; 99US-0346492.
 PR 15-OCT-1999; 99US-0419356.
 PR 17-DEC-1999; 99US-0466867.
 PR 30-DEC-1999; 99US-0476300.
 PR 06-MAR-2000; 2000US-0519642.
 PR 22-MAR-2000; 2000US-0533077.
 PR 10-APR-2000; 2000US-0546259.
 PR 27-APR-2000; 2000US-0560406.
 PR 05-JUN-2000; 2000US-0589184.

XX (CORI-) CORIXA CORP.

XX Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;
 PI Retter MW, Mannion J;

XX WPI: 2001-071488/08.

XX Lung tumor-associated proteins and the nucleic acids that encode them,
 PT useful for preventing, diagnosing and treating lung cancer

XX Claim 4; Page 415-416; 436pp; English.

PS The present invention describes immunogenic portions of lung tumour-
 XX associated proteins (I) and the nucleic acids (NAS) that encode them.
 CC (I) have cytostatic activity and can be used in gene therapy, antisense
 CC inhibition and in vaccines. The NAS and the lung tumour-associated
 CC proteins they encode may be used in the prevention, treatment and
 CC diagnosis of diseases associated with their inappropriate expression,
 CC especially lung cancers. For example, the NAS may be administered to
 CC treat diseases by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of the protein by expressing inactive proteins
 CC or to supplement the patient's own production of (I). Additionally, the
 CC NAS may be used to produce the lung-tumour associated protein, according
 CC to standard recombinant DNA methodology. Conversely, antisense NA
 CC molecules may be administered to down regulate protein expression by
 CC binding with the cells own genes and preventing their expression. The NA
 CC and complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar NA sequences in
 CC samples, and hence which patients may be in need of treatment of antibodies
 CC cancer. The (I) may be used as antigens in the production of antibodies
 CC and in assays to identify modulators (agonists and antagonists) of the
 CC expression and activity of the protein. AAF68083 to AAF68878 and
 CC AAB76848 to AAB76878 represent human lung tumour protein related
 CC nucleotide and protein sequences which are used in the exemplification
 CC of the present invention.

Sequence 2435 BP; 620 A; 599 C; 614 G; 601 T; 1 other;

Query Match 1.9%; Score 60; DB 22; Length 2435;
 Best Local Similarity 69.8%; Pred. No. 2.1e-05;
 Matches 81; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 676 tttctccctctcttttaccatttttataatgaactttcatttggaatggtt 735
 |||||
 DB 2434 tttttttttttttttttttttttaaatttaaaacatttttttgaaatgac 2375

QY 736 taggattccaanaattgcagagataacagagaatgccataccatcc 791
 |||||
 DB 2374 ttagatttaccagaaagattgcagagatgacaaagatttctgtatccctcacc 2319

RESULT 15
 AAV20441
 ID AAV20441 standard; DNA; 35100 BP.

XX AAV20441;

DT 17-JUN-1998 (first entry)

XX Human c-fms oncogene.

XX Human; oncogene; proto-oncogene; neoplastic disease; anticancer;
 KW cancer; antisense oligonucleotide; c-fms; ds.

OS Homo sapiens.

PN US5734039-A.

PD 31-MAR-1998.

PF 15-SEP-1994; 94US-0306691.

PR 15-SEP-1994; 94US-0306691.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Calabretta B, Skorski T;

XX WPI: 1998-229882/20.

XX Anticancer composition comprising two anti-sense oligo:nucleotide(s)

PT - targeting cytoplasmic and nuclear oncogene(s)
 XX
 PS Claim 1; Column 59-90; 92pp; English.
 XX

CC The present sequence represents an oncogene from the present invention.
 CC The present invention describes a composition which comprises two
 CC antisense oligonucleotides. The first oligonucleotide is specific for a
 CC cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1,
 CC c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and
 CC c-yes. The second oligonucleotide is specific for a nuclear oncogene or
 CC proto-oncogene selected from myc, jun, c-ets, c-fos, c-myc, B-myc,
 CC c-rel, c-vav, c-ski, c-spl, cyclin D1, PML/RAR alpha, AML1/MTG8,
 CC E2A/Prl and AL1-1/AF-4. The composition is used for treating cancer.
 CC The combination of antisense oligonucleotides has synergistically
 CC enhanced ability to inhibit growth of cancer cells.
 XX
 SQ Sequence 35100 BP; 8474 A; 8597 C; 9682 G; 8347 T; 0 other;

Query Match 1.9% Score 59.8; DB 19; Length 35100;
 Best Local Similarity 55.6% Pred. No. 0.00012;
 Matches 115; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
 QY 534 gaagatccacataatgtgagtgctgtatataatcacactcaagagatactgatttgt 593
 DB 3806 gaggctgcagtgagctgagatcatgacactgacccacagcctagcgacagagaagact 593
 QY 594 caattgtcccttccctcttcttctctctctctccctccctccctccctccctccctcc 3865
 DB 3866 caatctcccttccctcttcttctctctctctccctccctccctccctccctccctcc 653
 QY 654 tcccttccctccctccacaccccttcttctcttcttcttcttcttcttcttcttcttcc 3925
 DB 3926 ttccttccctccctccctccctcccttcttcttcttcttcttcttcttcttcttctt 713
 QY 714 actttcaatttggaaatagatttga 740
 DB 3986 ttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 3985
 3986 ttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 4012

Search completed: September 7, 2002, 18:39:36
 Job time: 29870 sec


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/lab host="DH10B"
/notes="Vector: Bluescript SK; Site_1: EcoRI; Site_2: XhoI
: This library was constructed by Kelian Tang, Robert
Cole, and L. David Sibley at Washington University. cDNAs
were synthesized from poly(A)+ RNA by oligod(T) priming,
size-selected and directionally cloned into the Uni-ZAP XR
lambda vector (Stratagene). The primary library was mass
excised as phagemids and rescued in SOLR cells. The
transformed library was recovered from the SOLR cells and
, Inc.) for sequencing. WARNING: This library may contain
a small percentage contaminants from human fibroblast
cells."
BASE COUNT      86 a 191 c 140 g 89 t
ORIGIN

```

```

Query Match      100.0%; Score 125; DB 10; Length 506;
Best Local Similarity 100.0%; Pred. No. 1e-19;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

OY 1 gatccgcgtgagcagcgagcagctccgcgctctcggagaccactgagctcagctt 60
Db 177 GATCCCGCTGGGCGAGCGGGCGGCGCTCGGCGCTCTCGAGACACTGCGCTCCACGCTT 118
OY 61 gaggtggcgctggggggcgagcaggaattgagcggaagctctgggaagctttaggtcgc 120
Db 117 GAGGTGGCGCTGGGGGCGGCGGACGAGCAATTAAGCGAAGCTCGGAGACCTTAGGCTCGC 58
OY 121 tggag 125
Db 57 TGGAG 53

```

```

RESULT 2
LOCUS AV695647 617 bp mRNA linear EST 16-JAN-2002
DEFINITION AV695647 GKC Homo sapiens cDNA clone GKCCD11 5', mRNA sequence.
ACCESSION AV695647
VERSION AV695647.1 GI:10297510
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE 1 (bases 1 to 617)
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Shen, K., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Hu, G., Gu, J., Chen, Z., and Han, Z., Xu, S., Gu, W., Huang, W., Zhao, X.,
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

```

```

TITLE
JOURNAL Chinese National Human Genome Center at Shanghai
MEDLINE 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
COMMENT Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

```

```

FEATURES
SOURCE
Location/Qualifiers
1..617
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GKCCD11"
/clone_lib="GKC"
/tissue-type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/notes="Vector: Bluescript sk(-); Site_1: EcoRI; Site_2:

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BASE COUNT      122 a 210 c 179 g 104 t 2 others
ORIGIN

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Query Match      100.0%; Score 125; DB 9; Length 617;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 gatccgcgtgagcagcgagcagctccgcgctctcggagaccactgagctcagctt 60
Db 140 GATCCCGCTGGGCGAGCGGGCGGCGCTCGGCGCTCTCGAGACACTGCGCTCCACGCTT 81
OY 61 gaggtggcgctggggggcgagcaggaattgagcggaagctctgggaagctttaggtcgc 120
Db 80 GAGGTGGCGCTGGGGGCGGCGGACGAGCAATTAAGCGAAGCTCGGAGACCTTAGGCTCGC 21
OY 121 tggag 125
Db 20 TGGAG 16

```

```

RESULT 3
LOCUS AL540709 899 bp mRNA linear EST 16-FEB-2001
DEFINITION AL540709 LTL_FL002.PL1 Homo sapiens cDNA clone CS0DE002YN18 5 prime
, mRNA sequence.
ACCESSION AL540709
VERSION AL540709.1 GI:12871113
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE 1 (bases 1 to 899)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

```

```

FEATURES
SOURCE
Location/Qualifiers
1..899
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DE002YN18"
/clone_lib="LTL FL002_PL1"
/lab_host="DH10B"
/notes="Organ: Placenta; Vector: pCMVSPORT 6; 1st strand
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by life
technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
http://fulllength.invitrogen.com URL :

```

```

BASE COUNT      192 a 288 c 245 g 170 t 4 others
ORIGIN

```

```

Query Match      100.0%; Score 125; DB 9; Length 899;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 gatccgcgtgagcagcgagcagctccgcgctctcggagaccactgagctcagctt 60
Db 190 GATCCCGCTGGGCGAGCGGGCGGCGCTCGGCGCTCTCGAGACACTGCGCTCCACGCTT 131
OY 61 gaggtggcgctggggggcgagcaggaattgagcggaagctctgggaagctttaggtcgc 120

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EST 25-SEP-2001

LOCUS	60
DEFINITION	mR
ACCESSION	BI

VERSION
KEYWORDS
SOURCE
ORGANISM

data; Craniata; Vertebrata; Euteleostomi;
Pisces; Clupeidae; Clupeinae; Clupeinae;
Hominidae; Homo.

REFERENCE AUTHORS TITLE	1 N N N

Health.gov/
Mammalian Gene Collection (MGC)

ET

Life Technologies, Inc.
Life Technologies, Inc.
The I.M.A.G.E. Consortium (LINT)
Genomics, Inc.

AG.E. Consortium/LINL at:
column: 17

FEATURES
source

```

ifiers
mo sapiens"
on:9606"

```

110B" pooled colon, kidney, stomach; Vector:
110C" pooled colon, kidney, stomach; R

to male colon; 46 yo male kidney, and pool
yo male and 70 yo female. Library is
and directionally cloned (EcoRV site
insert size 1.4 kb,

range 1.3 kb. Library is constructed by full-length clones and was constructed by Research Genetics tracking code (nitrogen). " is a NIH-MGC Library."

BASE COUNT
ORIGIN

200 5
131 8. NA 10: Length 793;

Query ma
Best Loca
Matches

```

Pred.No. 0.2e 10; Indels 0; Gaps
0; Mismatches 2;
aaatccgcgcgtcctcgcgagaccactgcgtccacgtt 60

```

db 557

AGCTCCGGCGCTCCTCGGAGACCACTGCCTCAGAAC-
aaagaattgaagcggaaagtctgsgaagcttaagggtcg 120
tgcacccatgcaaacacacacacacacacacacacacac

Db	497
QY	121

ACGHN1 101110021

Db 43 /

RESULT

1:00am EST 30-JA

LOCUS
DEFINITION

90 Homo sapiens cDNA clone IMAGE.100000000

VERSION
KEYWORDS
SOURCE

1

```

CDNA Library Arrayed by: The I.M.A.G.E. Consortium, Inc.
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.lnl.gov
Plate: L1AM10237 row: 1 column: 24
High quality sequence start: 9
High quality sequence stop: 727.
Location/Qualifiers
1..1140

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Best Local Similarity	97.6%;	Pred.	No.	2.4e-16;			
Matches	123;	Conservative					

[illegible]

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
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AV692383	359 bp	AV692383	GKC	Homo sapiens	CDNA clone GKC05	5', mRNA sequence.
AV692383						
AV692383.1	GI:10294246					
EST.						
human.						
Homo sapiens						

REFERENCE	AUTHORS
1 (bases 1 to 359)	Primates; Catarrhini; Hominae; Homo.
Xu, X., Huang, T.	Primates; Catarrhini; Hominae; Homo.

TITLE	Author
Insight into hepatocellular carcinoma	Huang, W., Zhao, X., Chen, Z. and Han, Z.

JOURNAL
Proc. Natl. Acad. Sci. U.S.A.
of corresponding noncancerous liver
hepatocellular carcinoma

15089-15094 (2001)

Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: zengqiang@genomics.cn

BASE COUNT	ORIGIN	57 a	148 c	98 g	55 t	1 others
BASE COUNT	ORIGIN	57 a	148 c	98 g	55 t	1 others

Query Match	87.2%;	Score 109;	DB 9;	Length 359;
Best Local Similarity	100.0%;	Pred. No.	5.2e-16;	
Matches 109;	Conservative			

[illegible]

RESULT	8		
BI463384			
LOCUS	BI463384	800 bp	mRNA
DEFINITION	603304413f1 NTH_MGC_97		linear
DESCRIPTION	mRNA sequence.		
ACCESSION	BI463384		
VERSION	BI463384.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		

REFERENCE
AUTHORS (bases 1 to 800)
TITLE NIH-MGC <http://mgc.ncl.nih.gov/>
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Stenmark

CDNA Library Preparation: Tanokuchi, M.D., Ph.D., Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Plate: LLAM1681 row: j column: 03
High quality sequence strip: 731.
location/Qualifiers
1. 800

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/db_xref="taxon:9606"
/clone="IMAGE:5270114"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescript (modified"

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Description

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3	125	100.0	702	9	HSA279012	AJ279012	Homo sapi
4	125	100.0	720	6	AX026090	AX026090	Sequence
5	125	100.0	3212	6	AX026089	AX026089	Sequence
6	123.4	98.7	702	9	HSA279011	AJ279011	Homo sapi
7	121.8	97.4	702	9	HSA279013	AJ279013	Homo sapi
8	121.8	97.4	187313	9	AL157394	AJ157394	Homo sapi
9	109.4	87.5	2155	9	HUMFAS	AJ157394	Homo sapi
10	36.8	29.4	733	8	AF272338	DJ1968	Homo sapi
11	36.6	29.3	1259	9	HUM51CP	AF272328	Phoebe fo
12	36.6	29.3	4657	6	AX332217	L24444	Human DNA r
13	36.6	29.3	4657	6	AX332217	AX332217	Sequence
14	36.6	29.3	4743	9	HUM51C	L36818	Human (clon
15	36.6	29.3	134635	9	HSY14385	Y14385	Homo sapien
16	36.6	29.3	204118	9	AP000593	AF000593	Homo sapi
17	36.6	29.3	204118	9	AP000812	AF000812	Homo sapi
18	34.4	27.5	73629	2	AC097603	AC097603	Rattus no
19	34	27.2	3694	1	AC101616	AC101616	Mus muscu
20	34	27.2	136131	2	SCC6ARB1P	AC101616	Mus muscu
21	33.8	27.0	10883	9	AC097289	AC101616	Mus muscu
22	33.8	27.0	139468	8	AB019433	AC101616	Mus muscu
23	33.8	27.0	143653	8	AC090441	AC101616	Mus muscu
24	33.8	27.0	164818	2	AC074099	AC101616	Mus muscu
25	33.8	27.0	165363	2	AC073847	AC101616	Mus muscu
26	33	26.4	1613	1	AC103058	AC101616	Mus muscu
27	33	26.4	3582	9	HSFEREC1	AC103058	Mus muscu
28	32.8	26.2	2027	8	AF165179	AC103058	Mus muscu
29	32.8	26.2	2036	8	AF165180	AC103058	Mus muscu
30	32.8	26.2	2036	8	AF165180	AC103058	Mus muscu
31	32.8	26.2	3656	6	AX017614	AC103058	Mus muscu
32	32.8	26.2	3768	9	HSMB0294	AC103058	Mus muscu
33	32.8	26.2	4412	8	AF151783	AC103058	Mus muscu
34	32.8	26.2	4412	8	AF050128	AC103058	Mus muscu
35	32.8	26.2	6771	8	HS091543	AC103058	Mus muscu
36	32.8	26.2	9824	2	AP001756	AC103058	Mus muscu
37	32.8	26.2	110717	2	AP003951	AC103058	Mus muscu
38	32.8	26.2	167405	2	AP002483	AC103058	Mus muscu
39	32.8	26.2	185975	2	AC104581	AC103058	Mus muscu
40	32.6	26.1	5719	10	AF373559	AC103058	Mus muscu
41	32.6	26.1	143805	9	HS091543	AC103058	Mus muscu
42	32.6	26.1	190632	2	AC105644	AC103058	Mus muscu
43	32.6	26.1	204412	2	AC021446	AC103058	Mus muscu
44	32.4	25.9	4807	1	AF100457	AC103058	Mus muscu
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RESULT	1				
LOCUS	AX026120	266 bp	DNA	linear	PAT 16-SEP-2000
DEFINITION	Sequence	32	from patent	DE198477779.	
ACCESSION	AX026120				
VERSION	AX026120.1	GI:10187551			
KEYWORDS					
SOURCE					
ORGANISM	human.				
	Euro sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 266)				
AUTHORS	Mueller-Schilling,M., Krammer,P. and Oren,M.				
TITLE	Novel receptor data useful for identifying apoptosis-modulating				
	substances potentially useful for cancer chemotherapy				
JOURNAL	Patent: DE 19847779-C 32 03-FEB-2000;				
	DEUTSCHES KREBSFORSCH (DE)				
FEATURES	location/Qualifiers				
SOURCE	1..266				
	1..266db="Homo sapiens"				

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            /db_xref="taxon:9606"  
BASE COUNT 49 a      72 c      110 g      35 t  
ORIGIN
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gene
exon
5'UTR
CDS

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314..>702

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ORIGIN

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Matches 123;	Conservative	0;	Mismatches	2.
1 nt mismatches				2.

Db 555 GACCCCTCTGGGACGGGCGGCGACGCTCCGGGCTCTCTGGAGACCACTGGCGTCACGTT 60
 QY 61 gaagtagggcgctgggggagcgagcagaatctgaagcggaaagctctggaaagctttgggctcgg 614
 Db 615 GAGGTGGCGATGGGGGGCGGACAGCAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCCG 614
 QY 121 tggag 125
 Db 675 TCGAG 679

	8	
AL157394		
LOCUS		
DEFINITION	Human DNA sequence from clone Rpl1-399019 on chromosome 10,	
ACCESSION	AL157394	
VERSION	ALI57394.15	GI:15384622
KEYWORDS		
HTG		
SOURCE	human	

REFERENCE	
AUTHORS	I. Dales; Eutheria; Primates; Carnalia; Vertebrata; Euteleostomi;
TITLE	Dales I to 187313)
JOURNAL	Blacky S Direct Submission Submitted 12-2-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA. Requests: clone-email enquiries: dmunquely@sanger.ac.uk Clone During Aug 31, 2001 this sequence version replaced g1:1461146. Where differences are found these are together with a note.
COMMENT	

Regions were either finished as follows (see Fig. 1) or sequenced with Sanger chemistry or covered by high quality or sequenced with an alternate one plasmid subclone and repeats; all regions had sequencing problems, such as assembly subclone or more than one M13 subclone; and at least two abbreviations was confirmed by restriction digest. The following table lists the source primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SwissProt; Tr, TREMBL; Wp, WormPeP; Information on the WormPeP database can be found at <http://www.sanger.ac.uk/projects/C-elegans/wormpep>. This sequence was generated from part of bacterial clone construct C09G11.6 Chromosome 10, constructed from bacterial clone construct C09G11.6.

http://www.sanger.ac.uk/HGP/Chr10
of Pieter de Jong. For further details see

[illegible]

...TACCGGCGGAGCCGCAAGGATYGAAGCGGA 193

REFERENCE
AUTHORS
TITLE

mammalia; Eutheria; Eumalacostraca; Craniata; Vertebrata; Euteleostomi; Primates; Carnivora; Hominoidea; Hominidae; Homo.

1 (bases 1 to 1269)

Moses, R. E.

CDS

Query Match	29.3%;	Score 36.6;	DB 9;	Length 1269;
Best Local Similarity	58.9%;			
Matches 63;	Conservation			

RESULT 12	AX332217	4657 bp	DNA	linear	PAT 09-JAN-2002
LOCUS	AX332217	2726 from	Patent WO0194629.		
DEFINITION					

REFERENCE
AUTHORS

I (sites)
Young P F
Zacharia; primates; Catarrhini; Hominoidea; Homo.
Verbeke; Euteleostomi;
Homidae; Homo.

source

Query Match	29.38;	Score 36.6;	DB 6;	Length 4657;
Best Local Similarity	58.98;			
Matches	63;	Conservative		

Db
4322 GGTGGGCGCGAGCTCCTTGAAGC 109

Procedural

KEYWORDS 51C protein.
SOURCE human

ORGANISM HC

TITLE	Author(s)
Whitney, M.A., Grompe, M., Friedberg, A.S. and Moses, R.E.	Cloning and characterization of a human CDMA (transmembrane) homology with insect
Carlo, H., Merkens, L.S., Tittle, T.V., Jakobs, P.M.,	

JOURNAL
OF
MEDICAL
PHYSIOLOGY
96079124
homology with inositol triphosphate phosphatases
29 (1), 285-287 (1995)
EATON, R. E. sharing of a human cDNA (INPPL) with inositol triphosphate phosphatases

Source

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source      Location/Qualifiers
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    /doc="3.766

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KALQADMSSTPAAPDQSSPPKTRLLQOONPEFGDELSLVLKSLKDLFSLGLOKKA
GRLVLRQADSEDMWTFTHRIKQLIKSNQVKKLGVLRKDKRQKQKFLSYDVGSA

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us-09-834-291-2_copy_1_125.rge

Page 8

Query Match	29.3%	Score 36.6;	DB 9;	Length 124635;
Best Local Similarity	58.9%;	Pred. No. 34;		
Matches 63;	Conservative	0;	Mismatches 44;	Indels 0;

	Best Match	Best Local Similarity	Score	DB	Length
Qy	3	29.3%	36.6	9	124635
Db	27573	58.9%	Pred No. 34		
Qy	63	Conservative	0	Mismatches	44
Db	27633	Indels	0	Gaps	0

Search completed: September 7, 2002, 18:26:54
Job time: 29113 sec

Mon Sep 9 09:30:39 2002

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model
September 7, 2002, 18:30:49 ; Search time 12179.2 seconds
(without alignments) updates/sec
4857.402 Million cell

US-09-834-291-4

2827 1 tggagactctcagaataatg.....tggctatcaagaagacgctg 2827

Title:

2827 1 tggagactctcagaataatg.....tggctatcaagaagacgctg 2827

Perfect score:

IDENTITY NUC

Sequence:

Gapop 10.0, Gapext 1.0

Scoring table:

1797656 seqs, 10463268293 residues

3595312

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq

Minimum Match 0%

Maximum Match 100%

Post-processing: Listing first 45 summaries

Database:

GenBank: 1: gb Da: 2: gb Hg: 3: gb In: 4: gb Om: 5: gb Ov: 6: gb Pat: 7: gb Ph: 8: gb Pr: 9: gb St: 10: gb St: 11: gb St: 12: gb Sy: 13: gb Un: 14: gb Vt: 15: em Da: 16: em Fun: 17: em Hum: 18: em In: 19: em Mu: 20: em Om: 21: em Or: 22: em Ov: 23: em Pat: 24: em Ph: 25: em Pl: 26: em Ro: 27: em St: 28: em Un: 29: em Vt: 30: em Htg Hum: 31: em Htg Inv: 32: em Htg Other: 33: em Htg Inv

pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score distribution.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

us-09-834-291-4.rge

1 2827 100.0 2827 6 AX026092
2 2380 84.2 2380 6 AX026091
3 2365.6 83.7 187313 6 AL157394
4 2346.6 83.0 3212 6 AX026089
5 2162 76.5 2344 9 HSDP955FR
6 1714.4 60.2 1877 9 HSDP955FR
7 1702.4 60.2 1608 6 HSDP955FR
8 1372.8 48.6 1608 6 HSDP955FR
9 879.4 30.3 1608 6 HSDP955FR
10 856.8 30.3 1608 6 HSDP955FR
11 611.8 21.6 398 11 G27038
12 259 9.2 2719 9 BC012479
13 245 8.7 702 9 HSA279012
14 216 7.6 702 9 HSA279012
15 216 7.6 702 9 HSA279012
16 188.8 6.7 1728 4 BMU24240
17 161 5.7 266 6 HSA011034
18 161 5.7 266 6 HSA011034
19 161 5.5 2551 9 HSAPO1
20 153 5.5 2551 9 HSAPO1
21 153 5.5 2551 9 HSAPO1
22 129 4.6 2471 6 HSAPO1
23 129 4.6 2471 6 HSAPO1
24 129 4.6 2534 6 HSAPO1
25 129 4.6 2534 6 HSAPO1
26 129 4.6 2534 6 HSAPO1
27 129 4.6 2534 6 HSAPO1
28 129 4.6 2534 6 HSAPO1
29 129 4.6 2534 6 HSAPO1
30 79.4 2.8 167564 2 AF267170
31 78.6 2.8 167564 2 AF267170
32 78.6 2.8 167564 2 AF267170
33 73.8 2.6 170261 2 AC008542
34 73.8 2.6 170261 2 AC008542
35 73.8 2.6 170261 2 AC008542
36 73.8 2.6 170261 2 AC008542
37 70.2 2.5 629271 2 AC009961
38 69.8 2.5 629271 2 AC009961
39 69.8 2.5 629271 2 AC009961
40 69.8 2.5 629271 2 AC009961
41 68.8 2.4 110602 2 AL358592
42 68.8 2.4 110602 2 AL358592
43 68.8 2.4 110602 2 AL358592
44 68.8 2.4 110602 2 AL358592
45 67.4 2.4 182553 2 AL449266
67.4 2.4 182553 2 AL449266

ALIGNMENTS

RESULT 1
AX026092 2827 bp DNA
LOCUS Sequence
DEFINITION 4 from patent DE19847779.
ACCESSION AX026092.1 GI:10187523
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Chordata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 2827)
Mammalia; Euteleostomi; Primates; Catarrhini; Homiidae; Homo.
AUTHORS
Kramer, P. and Oren, M.
TITLE
Novel receptor and useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
PATENT: DE 19847779-C 4 03-FEB-2000;
JOURNAL
DEUTSCHES KREBSFORSCH (DE)
location/Qualifiers
FEATURES
source
BASE COUNT
ORIGIN
728 a 676 c 657 g 766 t

Query Match		100.0%	Score 2827	DB 6	Length 2827
Best Local Similarity		100.0%	Pred. No. 0		
Matches 2827		Conservative 0	Mismatches 0		
				Indels 0	Gaps 0
OY	1	tgaagagctctggaatactgctggttaataataataaactcttgagagtgccaaactgtc			
DB	1	tgaagagctctggaatactgctggttaataataataaactcttgagagtgccaaactgtc			
OY	61	ttcccccagaacacccagcaatcattgagtgctcattcaatagattcttcaagaagttcca			
DB	61	ttcccccagaacacccagcaatcattgagtgctcattcaatagattcttcaagaagttcca			
OY	121	aagcgaagaagtttgagggaacagatataataatccaccccttgaattgcatlac			
DB	121	aagcgaagaagtttgagggaacagatataataatccaccccttgaattgcatlac			
OY	181	taagagccctgagaagtttgatttaagaagaatttcaaatcaagaagtaaccgaagatttc			
DB	181	taagagccctgagaagtttgatttaagaagaatttcaaatcaagaagtaaccgaagatttc			
OY	241	ctgaagttatttgaccatgaagaacatagctctcccaacaagaacatattccatctcctt			
DB	241	ctgaagttatttgaccatgaagaacatagctctcccaacaagaacatattccatctcctt			
OY	301	gaacttgaggaatattgacgtacgtggtagaggtagagggaagggatagacataga			
DB	301	gaacttgaggaatattgacgtacgtggtagaggtagagggaagggatagacataga			
OY	361	aagagcagagacccctggagggaacagaatactcaagtttaactccagctctgcatctatca			
DB	361	aagagcagagacccctggagggaacagaatactcaagtttaactccagctctgcatctatca			
OY	421	actaaacactcttgccaaatgtctgaagctcttctgctcaatcttcttatttga			
DB	421	actaaacactcttgccaaatgtctgaagctcttctgctcaatcttcttatttga			
OY	481	taagtttaaatcaactcaactcactgaggtggttaagatttaagtaagtaagtaagtaag			
DB	481	taagtttaaatcaactcaactcactgaggtggttaagatttaagtaagtaagtaagtaag			
OY	541	cacatattgaggtggtggtggttcaactcaactcaagaagaactgatttgcataattgc			
DB	541	cacatattgaggtggtggtggttcaactcaactcaagaagaactgatttgcataattgc			
OY	601	ccttcaccccttctctctctccctccctccctccctccctccctccctccctccctcc			
DB	601	ccttcaccccttctctctctccctccctccctccctccctccctccctccctccctcc			
OY	661	cttcacccacaccccttct			
DB	661	cttcacccacaccccttct			
OY	721	atttggaataagtttgaatttcaaaaaatttcagagataatacaaggaatgcacata			
DB	721	atttggaataagtttgaatttcaaaaaatttcagagataatacaaggaatgcacata			
OY	781	taacatccctccatccact			
DB	781	taacatccctccatccact			
OY	841	ggtctgagcccccaggggtctctctctctctctctctctctctctctctctctctct			
DB	841	ggtctgagcccccaggggtctctctctctctctctctctctctctctctctctctct			
OY	901	acaagccttcaacaactcaagaactggtgtagagtagaagtagaagtagaagtagaag			
DB	901	acaagccttcaacaactcaagaactggtgtagagtagaagtagaagtagaagtagaag			
OY	961	gtgagtagaagaccctcagagggtagaacttagatttgaggcccaagaaggtctcca			
DB	961	gtgagtagaagaccctcagagggtagaacttagatttgaggcccaagaaggtctcca			
OY	1021	gaagaaatgtcactgagaggaagcctgaaggaatgaacagtgaggttaaggaaggtta			
DB	1021	gaagaaatgtcactgagaggaagcctgaaggaatgaacagtgaggttaaggaaggtta			
OY	1081	ttaaagtttataatgaggttgatctaatcttggaaggaagaggtctgcagagtaggt			
DB	1081	ttaaagtttataatgaggttgatctaatcttggaaggaagaggtctgcagagtaggt			
OY	1141	gaagagcttgtagagcagtagcgaagaagtaacttgaaccttgagtgctcagcttgaa			
DB	1141	gaagagcttgtagagcagtagcgaagaagtaacttgaaccttgagtgctcagcttgaa			
OY	1201	ctgaccccaattcaggttgctcagtaatgagtagcattatccaaactcctctgaa			
DB	1201	ctgaccccaattcaggttgctcagtaatgagtagcattatccaaactcctctgaa			
OY	1261	catgcttaacttaaggaagctatcaccgttccaaagcaatagtgacttgaacagtg			
DB	1261	catgcttaacttaaggaagctatcaccgttccaaagcaatagtgacttgaacagtg			
OY	1321	tcacccagagcaggaagaatttaagaatttctttaaagaataatctgaggaagta			
DB	1321	tcacccagagcaggaagaatttaagaatttctttaaagaataatctgaggaagta			
OY	1381	gagtaacgaaggaagaagaattatgtgaatgttataatagcttgagggtcagatctg			
DB	1381	gagtaacgaaggaagaagaattatgtgaatgttataatagcttgagggtcagatctg			
OY	1441	gcttaagttgtagcttct			
DB	1441	gcttaagttgtagcttct			
OY	1501	cagagccctatgagcgaac			
DB	1501	cagagccctatgagcgaac			
OY	1561	gtctgtagacccctcaatgtctgagcgaacacacacacacacacacacacacacacac			
DB	1561	gtctgtagacccctcaatgtctgagcgaacacacacacacacacacacacacacacac			
OY	1621	tcttctctctgtagtactcagcaatgaagcagctctgtagcagctctgtagcagctct			
DB	1621	tcttctctctgtagtactcagcaatgaagcagctctgtagcagctctgtagcagctct			
OY	1681	gctctgagctcacttct			
DB	1681	gctctgagctcacttct			
OY	1741	gctttagaagagcaggaagccggtctcagaggtcctcagctctgagcttgaagtgagca			
DB	1741	gctttagaagagcaggaagccggtctcagaggtcctcagctctgagcttgaagtgagca			
OY	1801	cactgaggaagcccccggaggaagaatgagcatttgtagcaagaaccttgactctc			
DB	1801	cactgaggaagcccccggaggaagaatgagcatttgtagcaagaaccttgactctc			
OY	1861	taacccctgactctccctccctccctccctccctccctccctccctccctccctccct			
DB	1861	taacccctgactctccctccctccctccctccctccctccctccctccctccctccct			
OY	1921	cctcccaacccggggtctcccaagcagaggtctcctcccaactcctctgaacaaagtag			
DB	1921	cctcccaacccggggtctcccaagcagaggtctcctcccaactcctctgaacaaagtag			
OY	1981	ctgagagtagaggaagcgggttgaagtagcagtagcagtagcagtagcagtagcagtag			
DB	1981	ctgagagtagaggaagcgggttgaagtagcagtagcagtagcagtagcagtagcagtag			
OY	2041	ctggagtagaggaagcgggttgaagtagcagtagcagtagcagtagcagtagcagtag			
DB	2041	ctggagtagaggaagcgggttgaagtagcagtagcagtagcagtagcagtagcagtag			

Qy	1408	gaatggttaaalatalagcttgggagctatgagatttggcttaagtttgttaagcttggtttctc	1467
Db	961	GAATGTTTAATATAGCTGGGGCTATGCGATTTGGCTTAACTGTACTTTGTTTCTC	1020
Qy	1468	ttagaataataaacaataaggagccctcccttctcaagacctatggcgaaactctgtac	1527
Db	1021	TTTGAGAAATATAAAACCTAAGGGGCCCTCCCTTTTCAAGCCCTATGGCGCAACTCTGTAC	1080
Qy	1528	tttttcatttggttaactctgtccattccaaagacgtcttggagctctcaatgtttgagcca	1587
Db	1081	TTTTTCATATGGGTAACTGATCCATTCCAGGAACGCTGTGACCTCTCATGTTCGAGCCA	1140
Qy	1588	caaatggaacagccccagccaatggccccgaagttctctcttgagtgagctccagaatta	1647
Db	1141	CAAAATGACAGACCCAGCAATGCCCGCAAGCTTTCTCTGAGTGACTCTCAGCAATTA	1200
Qy	1648	gccaagagctcctgttaccagagcagacctctgcgctctgagctccattctcctcaagac	1707
Db	1201	GCCAAAGGCTCTGTACCCAGGAGGACCTCTGGCGCTGTGAGCTTCATTCTCTTCAAGAC	1260
Qy	1708	ctccccaactctccagagtttgaactaaagagaagaccttggaaaaggcagaagcgagct	1767
Db	1261	CTCCCAACTCTCCAGCTTGAATACAGAGAACCTTTTGAAGAAAGGACAGAGCGCGCT	1320
Qy	1768	ctcgaggtctcaactctgaagttagacatggcaaccaactctgaaaagccccggagaagaa	1827
Db	1321	CTCGAGGTCTTACCCTGAAGTAGATGCCACCACTGAGGAAAGCCCGGACAGAGAA	1380
Qy	1828	tgccatttgtcaacagcaacctgtactctctctcctcaacctgtactctccctctacc	1887
Db	1381	TGCCATTTTGTGAACGAACCTTGACTCTTCTCACACCTGACTCTCCCTCCCTACAC	1440
Qy	1888	cgcgcgagcgcaagtttgtctgaatcaatlgagacctcccaaccggagcggtctcccaagc	1947
Db	1441	CGCGCGCAGGCCAAGTTGTGAAATCAATGAGAGCCCTCCCAACCCGGGCGTTCCCAAGCG	1500
Qy	1948	aggcttctccctccatctcctctgacccacccggagcttttctgtagctcgctctgtatccgc	2007
Db	1501	AGGCTTCTCTTCCATCTCCTCTGACACCGGGCTTTTGTGAGACTCTGTCTGATCTCGC	1560
Qy	2008	gcaagaagtacacacagagtggttcaaaagaagctcttggggagtgaggaagcggttaaga	2067
Db	1561	GCAAGAGTACACACAGGTGTTCAAAAGCGCTTCTGGGGAGTAGAGGAAGCGGTTTACAA	1620
Qy	2068	gtgacttggctggagacctcaaggggcgggcgcaactgtgacgaggaacaacctgagccaagcc	2127
Db	1621	GTGACTTGGCTGGAGCCCTCAAGGGGGGACACTTGGACGGAACAACCTTGAGGGCAGCCG	1680
Qy	2128	tgggtgccagcgagagctgcctctctcccgcggaactacgtacagaagctcgagaagtaact	2187
Db	1681	TGGGTGCCAGGCGGAGCTGCTCTTCTTCCCGGCAATGTACAGAGCTCGAAGAACTACT	1740
Qy	2188	agtggccacgctggcgcgctgacatttaagtttaagttcgtctggagggggagccccggttgg	2247
Db	1741	AGTGGCCACAGTGGGGCCCTGCACTTAAAGCTTAAAGGTCTGTGAGGGGGACCCCGGTTGG	1800
Qy	2248	agaagggagacggaactcctctgacaagccccctgacaagcccaagcccaaaagtcgcgctccggcg	2307
Db	1801	AGAGAGGAGCGGAACCTCTGTGACAAGCCCTGTACAAGCCAAAGGCTCCGCTCGGGG	1860
Qy	2308	cggtgtgggtgagtgcgcgcgcccccgggggcggggagagagacctgacgcttcaagac	2367
Db	1861	CGGCTGGGTGAGTCCGGCGCCGCCCGGGGGGAGAGACGCTGACGCTTCAGAAC	1920
Qy	2368	agatatgtctcaatttcttggcagttctcagaagtagaataaagtctgacacggaagcagt	2427
Db	1921	AGATATTTGCTCATTTTCTGGCAAGTTCTCAACAGTAGAATAAATCAAGCAACGACGT	1980
Qy	2428	ggttaagccggagagctcggaaagaacgaccccttcttctctgaaaaagtctatagcgca	2487
Db	1981	GGTTAAGCCGGAGGCTCTCGAAGAACGGCACCTTTCTTCTCGAAAAAGTTATATGGGG	2040
Qy	2488	gctgaatgagctcttggagggctgtttaccglttttatttgcacacagaagaagaact	2547

	Db	2041	GCTGATGAGCCTTTCGAGCGCTGTATTACCGTTTATTATGTCACACAGAAAGGAACACT	2100
	Oy	2548	gcctggtcccttcoccggaattcctcctttaagacgttaagtcgcctgcctgagtgtt	2607
	Db	2101	GCCTTGTCCTCCCTTCGGGAATCTCTCTTTAAGACGTAAAGTCGCGCTGAGTGGTTT	2160
	Oy	2608	catttgatlttgtttctbcgccctcctctctctctcttcttgaccttctaagcttagc	2667
	Db	2161	CATTGCTTTGTGTTTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2220
	Oy	2668	ccatgtgatcttctgcttgcttgctcctgcctcgtcgggttggtgctctcgttccaacgcag	2727
	Db	2221	CGATGCTGATTTCTGCTTGTCTCCGCTGCGGCTTGCGTGTAAGTCTGCCACGCAACG	2280
	Oy	2728	aaccggcgccctatatlttgcccagaacttggagcagcctgttttgaagaagctcctgct	2787
	Db	2281	AACC CGCGCCCTATTATTATTTGGCCAAAACCTTGACACAGCGCTGTGTAAGAAGTCCCTGCT	2340
	Oy	2788	cagaatgcacagcttgcagatgagctgaatcaacaagaagcgtg	2827
	Db	2341	CAGAAATGCCAGCTTGCAGATGCGTAATCAAGAAGACGTG	2380
RESULT	3			
LOCUS	AL157394			
DEFINITION	Human DNA sequence from clone Rpl1-39019 on chromosome 10,			
ACCESSION	AL157394			
VERSION	ALI57394.15			
KEYWORDS	HTG.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	Blakey,S.			
JOURNAL	Direct Submission			
	Submitted (22-AUG-2001) \			

FEATURES

[illegible]

Db 144909	GCCTTGCTCCCTTCGGGAAATCTCTTTAAGACTTAAAGTCGCTCCGAACTGGTTT	144968
Qy 2608	catttcttctgtttcttccttcgccttccttccttccttccttccttccttccttccttc	
Db 144969	CATTCTGTTTGTGTTTCTTGCCCTTCTTCTCTTTGGCCCTTTTACCTTGACATC	145028
Qy 2668	caatgttgattcttccttccttccttccttccttccttccttccttccttccttccttc	
Db 145029	CCATGCTGATTTCTCTGTTGTCCTCTGCTGGGTTGTGTACTCTTTCCACCCTCAAG	145088
Qy 2728	aaccgcgcgcctcattattgcccagaagaacttgcagcgcctgtttgaaagaatccctgc	2787
Db 145089	AACCCGCGCCCTATTATTGGCCAAAGAAATCTGAGACCCCTTTTGGAAAGTCCCTCCCT	145148
Qy 2788	cagaatctccagcttcagatctgcataatcaagaagacgtg	2827
Db 145149	CAGAAATCCAGCTTGACAGATGCTAATCAAGAGACGCTG	145188

[illegible]

[illegible]

BASE COUNT	Number=1	
508 a	555 c	555 g
ORIGIN		547 t

QY	Sequence	Mismatches	Indels	Gaps
447	aagcttttgcatactttttatrttaaac	1	0	0

[illegible]

Qy	1287	accggttccaagaacatagtagtaccttgtaacagtggttaccagaagccagaagaagatatacaag	1346
Db	841	accggttccaagaacatagtagtaccttgtaacagtggttaccagaagccagaagaagatatacaag	1346
Qy	1347	attttttttaagaagaatctggccagggaataatagatgaacgaagaagaagaataattg	900
Db	901	attttttttaagaagaatctggccagggaataatagatgaacgaagaagaagaagaataattg	900
Qy	1407	tgaatgttaataatagctcggggctatlgagattggcttaagttagtcttggtttccct	960
Db	961	tgaatgttttaataatagctcggggctatlgagattggcttaagttagtcttggtttccct	1465
Qy	1467	cttgaagaataaanaactaaaggggccccccttttcagagccctatlgcgcaaatctgta	1020
Db	1021	cttgaagaataaanaactaaaggggccccccttttcagagccctatlgcgcaaatctgta	1526
Qy	1527	cttttcaatagtgttaacttccattccagaagaacgctctgtgagccctatgttgcaacc	1080
Db	1081	ctttttcatatgtgttaacttccattccagaagaacgctctgtgagccctatgttgcaacc	1586
Qy	1587	acaagctgagcagcagcccaagtcataatgcgccgaagctttctctgtgagtacccagaact	1140
Db	1141	acaagctgagcagcagcccaagtcataatgcgccgaagctttctctgtgagtacccagaact	1646
Qy	1647	agccaagctccctgtacccaagcaggaactctgcctctgaagctccatcttcctttaaga	1200
Db	1201	agccaagctccctgtacccaagcaggaactctgcctctgaagctccatcttcctttaaga	1706
Qy	1707	cctcccacaacttcccaagttgaactacagagaagcctcttagaagaaggcagagccgggc	1260
Db	1261	cctcccacaacttcccaagttgaactacagagaagcctcttagaagaaggcagagccgggc	1766
Qy	1767	tctgaagctcccaactcgtgaagtgagcctgacgacactcagaagcagcccgaggaacga	1320
Db	1321	tctgaagctcccaactcgtgaagtgagcctgacgacactcagaagcagcccgaggaacga	1826
Qy	1827	atgccaattgtgcaacgaacccctgtactcttccctcaaccctgaactctcccccctccac	1380
Db	1381	atgccaattgtgcaacgaacccctgtactcttccctcaaccctgaactctcccccctccac	1886
Qy	1887	ccgcgcgcagcgaagtgctgaatcaatlgagccctcccccacaacccgggctttcccaagc	1440
Db	1441	ccgcgcgcgcagcgaagtgctgaatcaatlgagccctcccccacaacccgggctttcccaagc	1946
Qy	1947	gaggttccctcccaactccctcctgacacacaggaggttttgtagctgctctgcatctgc	1500
Db	1501	gaggttccctcccaactccctcctgacacacaggaggttttgtagctgctctgcatctgc	2006
Qy	2007	cgcgaagatlgacacacagagtggttcaagaagcgtctctggggagtggaagggaagggttaag	1560
Db	1561	cgcgaagatlgacacacagagtggttcaagaagcgtctctggggagtggaagggaagggttaag	2066
Qy	2067	agtgaactgtgctgagcctcaaggcggcgagcactggaaggaacacacccctgaagccagcc	1620
Db	1621	agtgaactgtgctgagcctcaaggcggcgagcactggaaggaacacacccctgaagccagcc	2126
Qy	2127	ctgagctgcacagcggagagctgctcttcccgcgag	2162
Db	1681	ctgagctgcacagcggagagctgctcttcccgcgag	1716

RESULT	7				
HSAPT1					
LOCUS	HSAPT1	1877 bp	DNA	linear	PRI 08-JUN-1995
DEFINITION	H.sapiens APT gene, exon 1.				
ACCESSION	X81335				
VERSION	X81335.1	GI:537410			
KEYWORDS	AP0-1 gene; apt gene.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
REFERENCE	1 (bases 1 to 1877)				

/usedin-X81335:hsRNA-

Q

TGGAGGCGAAGAACCC

QY	1167	gaatcctgaaaccccttagtgglygtlccagctcgtggaactgatacctaattcgaagttcagtaat	1226
Db	720	GAATACGTGAACCTTTAGTGTGTCCAGTCTGGAACTGCATCCAAATTCAGTTCAGTAAT	779
QY	1227	gatgcattatccaacaacatactctctgtaaaaatcattatgactaaactaacctaacgactcttc	1286
Db	780	GATGCATTTATTCAAACCTACCTTCTGTAAAAATTCATAGCTAAACTACTCTAAGACCTATCT	839
QY	1287	accgtttccaagaaataagtagtactttgaacagtgcttcacagagcacagaagaattacaag	1346
Db	840	ACCGTTCCAAAGCAATAGTACTTTGAACAGTGTACCCAGACACAGAAAGATTTCAG	899
QY	1347	attttttttaagaagaattggcccgagaaataatgtaacgaagaagacaagaagtaattg	1406
Db	900	ATTTTTTTTTAAAGAAATTTGGCCAGAAATATATGATACGAAGACAGCAAGTAATTG	959
QY	1407	tgaattttaaataatagctgggactatgagatitgagatitgagatitgagatitgagatitg	1466
Db	960	TGAATCTTTAATATATAGCTGGGCTATGCAATTTGGCTTAAGTTTATGCTTTGTTTCT	1019
QY	1467	cttgagaaataaaactaaggaggccctcccttttaaggccctatgagccctatgagcaacatcta	1526
Db	1020	CTTGGAAATTAATAAACTAAAGGGGCCCTCCTTTTGAGAGCCCTATGGCGCAACATCTGA	1079
QY	1527	cttttcataatgataactgttcaatcttcacaggaagcgtctgtagactctcattgttgagcc	1586
Db	1080	CTTTTTCATATGTTAACTGTATCTGTCTCCAGAAAGCTGTGAGCCTCTCATATTGTCAGCC	1139
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REFERENCE
1 (sites)
Olek, A., Piepenbrock, C. and Berlin, N.:
Diseases associated with the immune system
in humans. 2003.

Olek, A., Prependo, J. M., & Berman, J. L. (2003).
Diagnosis of diseases associated with
2392 03-JAN-2002; 2000038-A

Patent: WO 02009260
Epidemiology AG (DE)
Qualifiers

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11-11-11	77.1%				

Best Local Similarity	0;	Mismatches
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932 TCCATTCCAAAGCTGTATAAACCCTCATATTACACCA

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D.D. 044

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished
Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center of Medicine
Stanford University School of Palo Alto, CA 94025, USA
Stanford University School of Medicine
4005 Miranda Ave #800
Tel.: (650) 320-5801
Fax: (650) 320-5801
Email: A: olivier@ccr.stanford.edu
B: alexander@stanford.edu
Primer A: AGCCCGACGAGGAGCA
Primer B: AACCCGACGAGGAGCA
Size: 150
PCR Profile:
Initial Incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol:
Template: 25 ng each 1 uM
Primer: each 200 uM
dNTPs: 0.05 units/uL
Taq polymerase: 10 uL
Total vol: 2.5 mM
Buffer: MgCl₂: 50 mM
KCl: 20 mM
Tris-HCl: 8.3 pH:

Prepared with primer pairs provided by Sandoz, derived from H86126
-- Washington University/Merck EST sequence.
1..398

FEATURES
source

Mon Sep 9 09:30:39 2002

Search completed: September 7, 2002, 18:35:34
Job time: 29633 sec

us-09-834-291-4.rge

Mon Sep 9 09:30:41 2002

us-09-834-291-4.rml

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model
September 7, 2002, 18:26:08 : Search time 212.3 Seconds
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Title: US-09-834-291-4
Perfect score: 2827
Sequence: 1 tgaagactcaggaatg.....tggcattcaagaagagctg 2827

Scoring table: IDENTITY_NUC
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Searched: 38353-segs, 122816752 residues 767066

Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
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2	129	4.6	2471	1 US-08-444-231-18	Sequence 18, Appl
3	129	4.6	2471	1 US-08-152-443A-18	Sequence 18, Appl
4	129	4.6	2534	2 US-08-219-237B-1	Sequence 1, Appl
5	129	4.6	2534	4 US-08-468-560C-1	Sequence 16, Appl
6	129	4.6	2534	4 US-09-180-100-16	Sequence 14, Appl
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8	67.4	2.4	7218	1 US-08-836-022A-10	Sequence 3, Appl
9	63.6	2.2	19307	3 US-09-427-048A-10	Sequence 3, Appl
10	63.6	2.2	19307	3 US-08-836-022A-3	Sequence 2, Appl
11	62.6	2.2	9972	3 US-09-427-048A-3	Sequence 2, Appl
12	62.6	2.2	4476	3 US-08-801-344-2	Sequence 2, Appl
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17	51.6	1.8	556	4 US-08-332-766A-8	Sequence 18, Appl
18	50.8	1.8	370	2 US-08-623-906A-18	Sequence 7, Appl
19	49.8	1.8	5751	4 US-09-417-455-7	Sequence 7, Appl
20	49.8	1.8	5751	4 US-09-348-584A-9	Sequence 9, Appl
21	49.2	1.7	361	4 US-08-713-557B-35	Sequence 35, Appl
22	48.4	1.7	50	2 US-08-458-434A-6	Sequence 6, Appl
23	48.4	1.7	15144	1 US-08-480-784-24	Sequence 24, Appl
24	48.4	1.7	421	1 US-08-483-553-24	Sequence 24, Appl
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29	48	1.7	421	1 US-08-488-011B-24	Sequence 24, Appl
30	48	1.7	421	1 US-08-850-727-24	Sequence 24, Appl
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33	48	1.7	421	5 PCT-US95-10220-24	Sequence 2, Appl
34	47.8	1.7	5852	1 US-07-867-106-2	Sequence 27, Appl
35	47.6	1.7	1679	2 US-08-332-766A-27	Sequence 11, Appl
36	47.4	1.7	1679	4 US-08-365-486A-11	Sequence 11, Appl
37	47.4	1.7	12141	4 US-08-880-342-11	Sequence 10, Appl
38	47.4	1.7	80246	4 US-09-078-294-4	Sequence 4, Appl
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43	46.8	1.7	446	2 US-08-332-766A-10	Sequence 19, Appl
44	46.6	1.6	444	4 US-09-018-584A-19	Sequence 19, Appl
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ALIGNMENTS

RESULT 1
US-09-290-640-1 Application US/09290640
Sequence 1, Application US/09290640
Patent No. 6204055
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290, 640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2551
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (221)..(1228)
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 267
ISSUE: 15
PAGES: 10709-10715
DATE: 1992-05-25
DATABASE ACCESSION NUMBER: X63717/Genbank
DATABASE ENTRY DATE: 1996-07-19
US-09-290-640-1

Query Match 5.5%: Score 155; DB 4; Length 2551;
Best Local Similarity 100.0%; Pred. No. 1e-33; 0; Indels 0; Gaps 0;
Matches 155; Conservative 0; Mismatches

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RESULT 2
US-08-444-231-18

Sequence 18, Application US/08444231
Patent No. 5652210

GENERAL INFORMATION:

APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES: 22
ADDRESS: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,231
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/152,443
FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 195..1136
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243
US-08-444-231-18

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US-08-152-443A-18
Sequence 18, Application US/08152443A
Patent No. 5653070
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES: 22
ADDRESS: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,443A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/152,443A
FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 195..1136
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243
US-08-152-443A-18

Query Match

Best Local Similarity 4.6%; Score 129; DB 1; Length 2471;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GGCACGTGGCAGCAACACCCCTGAGGCCAGCCCTGCTGCCAGCGGAGAGCTGCTCTT 120
QY 2154 ctccgcgcg 2162
DB 121 CTCCGCGCG 129

RESULT 4

US-08-219-237B-1
Sequence 1, Application US/09219237B
Patent No. 5874546
GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:

US-08-219-237B-1

Mon Sep 9 09:30:41 2002

us-09-834-291-4.rml

ADDRESSEE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 516762
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
TOPOLOGY: linear
ORIGINAL SOURCE: CDNA to mRNA
ORGANISM: Homo sapiens
IMMEDIATE SOURCE: LIBRARY: PCEV4
CLONE: clone pfs8

FEATURE: CDS
NAME/KEY: 195..1202
LOCATION: 195..1202
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: sig_peptide
NAME/KEY: 195..242
LOCATION: 195..242
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: mat_peptide
NAME/KEY: 243..1199
LOCATION: 243..1199
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: polyA_site
NAME/KEY: 1831..1836
LOCATION: 1831..1836
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: sig_peptide
NAME/KEY: 2352..2357
LOCATION: 2352..2357
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FEATURE: mat_peptide
NAME/KEY: 243..1199
LOCATION: 243..1199
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: polyA_site
NAME/KEY: 2518..2523
LOCATION: 2518..2523
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
IDENTIFICATION METHOD: to an established consensus
US-08-219-237B-1

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Best Local Similarity 100.0%; Pred. No. 2; 3e-26; Indels 0; Gaps 0;
Matches 129; Conservative 0; Mismatches 0;
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DB 121 CTCCGCGG 129

RESULT 5
US-08-468-560C-1
Sequence 1, Application US/08468560C
Patent No. 6270998
GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
INVENTOR: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESS: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,560C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20-4393P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
TOPOLOGY: linear
ORIGINAL SOURCE: CDNA to mRNA
ORGANISM: Homo sapiens
FEATURE: CDS
NAME/KEY: 195..1202
LOCATION: 195..1202
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: sig_peptide
NAME/KEY: 195..242
LOCATION: 195..242
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: mat_peptide
NAME/KEY: 243..1199
LOCATION: 243..1199
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: polyA_site
NAME/KEY: 1831..1836
LOCATION: 1831..1836
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: sig_peptide
NAME/KEY: 2352..2357
LOCATION: 2352..2357
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: mat_peptide
NAME/KEY: 243..1199
LOCATION: 243..1199
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: polyA_site
NAME/KEY: 2518..2532
LOCATION: 2518..2532


```

GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)834-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-f1s
US-08-232-463-14

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Best Local Similarity 8.0%; Pred. No. 1.2e-08;
Matches 35; Conservative 228; Mismatches 174; Indels 0; Gaps 0;
QY 807 ttgtgtctattagatgctcagagtggtgacacagctgcacgcccagggcttcctca 866
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QY 867 tggcactacagctactcgaaggtgacacagacaaagcctatcacaccatacaagct 926
DB 1382 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1323
QY 927 ggtgtaagtcagtcagacagacacacagagtgatgacagccctcagagaggttaa 986
DB 1322 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1263
QY 987 cctaaccgatctgagggcccaacacagctccagaagaagtgcacactgagaggaagc 1046
DB 1262 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1203
QY 1047 ctgaagatgaacagcgggctacgaaggtatataatgtatataatggtgtaac 1106
DB 1202 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1143
QY 1107 taattggagagagagaggttcagacagtgatgacagagctggtgagacatgccaag 1166
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QY 1167 gaatactgaacctttagtgtgctcagtcgnaactgcatccaattcaagttcagta 1226
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QY 1227 gatgcatcattccaac 1243
DB 1022 GTGAGCGTATGCGCAAC 1006

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RESULT 9
US-08-836-022A-10
Sequence 10, Application US/08836022A
Patent No. 6001557
GENERAL INFORMATION:
APPLICANT: Trustees of the University of Pennsylvania
APPLICANT: Wilson, James M.
APPLICANT: Fisher, Krishna J.
APPLICANT: Chen, Shu-Jen
APPLICANT: Weltman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,022A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,381
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVPM.008PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-5818
TELEFAX: 215-540-9200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
US-08-836-022A-10

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Query Match 2.2%; Score 63.6; DB 3; Length 19307;
Best Local Similarity 65.5%; Pred. No. 2.7e-07;
Matches 93; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 2114 cctgagcagcacccttgctgcacagcgaggtcctctcccgcgagacatgtacaga 2173
DB 16048 CGCGCGCGCTCAGCTGCGCCATCGATACGCTACGCGGACCGCGCATGTACGA 16107
QY 2174 gctgagagagactagtgacacagtgagcagtgacacctaagcttgggtcgctgag 2233
DB 16108 GCTGAGAGAGTACTGTGCGCACGTTAGCTTAACTTGGCACTGGCGTCTGT 16167
QY 2234 gggaccccggttgagagagga 2255
DB 16168 TTACAAACGTCGTGACTGGAA 16189

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RESULT 10
US-09-427-048A-10

Sequence 10, Application US/09427048A
Patent No. 6203975

GENERAL INFORMATION:

APPLICANT: Trustees of the University of Pennsylvania

Wilson, James M.

Fisher, Krishna J.

Chen, Shu-Jen

Meltzman, Matthew

TITLE OF INVENTION: Improved Adenovirus Virus and

METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P O Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/427,048A

FILING DATE: 21-Oct-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/836,022

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: GNVPN.008PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 19307 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-427-048A-10

Query Match 2.2%; Score 63.6; DB 4; Length 19307;
Best Local Similarity 65.5%; Pred. No. 2.7e-07;
Matches 93; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 2114 cctgaagcagccctgctgcccagcggagctgctcttcctcccgagacatgtacaga 2173
DB 16048 CCGGCGCGCTGAGCTGGCGCATGCGATGCGTGCAGCCGCGGACATGTACAGA 16107
QY 2174 gctcgaagaagtaagtagtgcacagctggccgtgaccccttaagcttaaggtcgtgagag 2233
DB 16108 GCTCGAGAAGTACTAGTGCACAGTGGCCGCTGACCTTAAGCTTGGGCACTGGCGGTGT 16167
QY 2234 gggaccgcgttgagagagaga 2255
DB 16168 TTTACACGTCGTGACTGGAA 16189

RESULT 11
US-08-836-022A-3/C
Sequence 3, Application US/08836022A
Patent No. 6001557

GENERAL INFORMATION:

APPLICANT: Trustees of the University of Pennsylvania

Wilson, James M.

Fisher, Krishna J.

Chen, Shu-Jen

Meltzman, Matthew

TITLE OF INVENTION: Improved Adenovirus Virus and

METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P O Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,022A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/331,381

FILING DATE: 28-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: GNVPN.008PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 9972 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: CDNA

US-08-836-022A-3

Query Match 2.2%; Score 62.6; DB 3; Length 9972;
Best Local Similarity 65.2%; Pred. No. 3.4e-07;
Matches 92; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 2115 ctagagcagccctgctgcccagcggagctgctcttcctccggagacatgtacagag 2174
DB 2980 CGGCGCGCTGAGCTGGCGCATGCGATGCGTGCAGCCGCGGACATGTACAGA 2921
QY 2175 ctcgaagaagtaagtagtgcacagctggccgtgaccccttaagcttaaggtcgtgagag 2234
DB 2920 CTCGAGAAGTACTAGTGCACAGTGGCCGCTGACCTTAAGCTTGGGCACTGGCGGTGT 2861
QY 2235 ggaaccgcgttgagagagaga 2255
DB 2860 TTACACGTCGTGACTGGAA 2840

RESULT 12
US-09-427-048A-3/C
Sequence 3, Application US/09427048A
Patent No. 6203975

GENERAL INFORMATION:

APPLICANT: Trustees of the University of Pennsylvania

Wilson, James M.

Fisher, Krishna J.

Chen, Shu-Jen

Meltzman, Matthew

TITLE OF INVENTION: Improved Adenovirus Virus and

METHODS OF USE THEREOF

Mon Sep 9 09:30:41 2002

us-09-834-291-4.rni

Page 7

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/427,048A
FILING DATE: 21-Oct-1999
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/836,022
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVFN, 008PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9972 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-427-048A-3

Query Match
Best Local Similarity 65.2%; Score 62.6; DB 4; Length 9972;
Matches 92; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 2115 ctgagagccagccctgctgcccagcgagagctgctcttcctccgagagacgtacagag 2174
DB 2980 CGGCCCGCTGCGACCTGCGCCCATCGATACGCGCTACGTCGCGCGCCGCGACATGTACAGAG 2921
QY 2175 ctcgagaagtaactagtgccacgttgagcgctgacacttaagcttaagtgctgagagag 2234
DB 2920 CTCGAGAGTACTAGTGGCCGCGCGCTGACCTTAAGCTTGGCACTGGCGCTGTT 2861
QY 2235 ggaaccgggttgagagagga 2255
DB 2860 TTACAACGTGTGACTGGAA 2840

RESULT 13
US-08-801-344-2
Sequence 2, Application US/08801344
Patent No. 6087140
GENERAL INFORMATION:
APPLICANT: Cameron, Douglas C.
APPLICANT: Shaw, Anita J.
APPLICANT: Altaras, Nedim E.
TITLE OF INVENTION: MICROBIAL PRODUCTION OF 1,2-PROPANEDIOL
TITLE OF INVENTION: FROM SUGAR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Demilt Ross & Stevens S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WI
COUNTRY: U.S.A.
ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,344
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER: 09820.037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Vector pSE380
US-08-801-344-2

Query Match
Best Local Similarity 75.0%; Score 62.4; DB 3; Length 4476;
Matches 78; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 2115 ctgagagccagccctgctgcccagcgagagctgctcttcctccgagagacgtacagag 2174
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QY 2175 ctcgagaagtaactagtgccacgttgagcgctgacacttaagctt 2218
DB 583 CTCGAGAGTACTAGTGGCCGCGCGCTGACCTTAAGCTT 626

RESULT 14
US-09-498-599-2
Sequence 2, Application US/09498599
Patent No. 630352
GENERAL INFORMATION:
APPLICANT: Cameron, Douglas C.
APPLICANT: Shaw, Anita J.
APPLICANT: Altaras, Nedim E.
TITLE OF INVENTION: MICROBIAL PRODUCTION OF 1,2-PROPANEDIOL FROM SUGAR
TITLE OF INVENTION: 1,2-PROPANEDIOL FROM SUGAR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Demilt Ross & Stevens S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WI
COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,599
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER: 09820.037
TELECOMMUNICATION INFORMATION:

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using sw model
September 7, 2002, 18:41:53 | Search time 1139.19 seconds
Run on: (without alignments)
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Title:	US-09-834-291-4	
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Searched:
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Maximum Match 100%
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319 tattaatggttacttaataacattttt ||||| ||||| ||||| ||||| ||||| |||||

1139 gtgcagagcttggtgtagcagtccaaagcaataactat
||||| ||||| ||||| ||||| ||||| ||||| |||||
378

379 gtgtaaagtttgtagcagatgttlaagaagaatatgtaattttatctt 1198
1199 aactcaatctatcttcttcttcttcttcttcttcttcttcttcttctt

[illegible]

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499 ttatgttaaatatttcaagagtatttcgctttaagaacttgacagt 1318
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619 atgagtaacgaaggatagaagtaattgtgaatatctttaaatactggcgcatgcgatt 1438

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5' - G A A C C A A G T A A G G T T T T G T A C T T C A G T A G G A T T T T 3' 918

useful] for the treatment, prevention, and diagnosis of colon

Claim 1; Page 010 021

sequence 839 bp, 211 bp

Query match	Score	Pred. No.	Indels	Gaps
94.78%	5.1e-42	0	0	

1955 cttccatcctctgaccaaccgggcttctcgagaccos
78

10 atgcacacacgacgtccgacccgggcttctcgtgagctcgcclccclcgacccccc-2

2015 tgacacacagggtgltccaaagagc 138

2075 qqctggagcctcagggcggcactggcacggaaacacacccccc-3'

Dd 139 ggcgggcccgaagg 2162

D_b 199 ccagucgacccccc-

AAZ88700 standard; DNA; 266 BP.

11-MAY-2000 (first entry)

Human CD95 receptor interaction; apoptosis; apoptosis-modulation; DE

XX
KM
XX

CANCER

AA	Location/Qualifiers
FH	Key
	160 179

**EI
YY**

XX
XX
03 FEB-2000

XX 10 00 11 00 12 00 13 00 14 00 15 00 16 00 17 00 18 00 19 00 20 00 21 00 22 00 23 00 24 00 25 00 26 00 27 00 28 00 29 00 30 00 31 00 32 00 33 00 34 00 35 00 36 00 37 00 38 00 39 00 40 00 41 00 42 00 43 00 44 00 45 00 46 00 47 00 48 00 49 00 50 00 51 00 52 00 53 00 54 00 55 00 56 00 57 00 58 00 59 00 60 00 61 00 62 00 63 00 64 00 65 00 66 00 67 00 68 00 69 00 70 00 71 00 72 00 73 00 74 00 75 00 76 00 77 00 78 00 79 00 80 00 81 00 82 00 83 00 84 00 85 00 86 00 87 00 88 00 89 00 90 00 91 00 92 00 93 00 94 00 95 00 96 00 97 00 98 00 99 00 100 00 101 00 102 00 103 00 104 00 105 00 106 00 107 00 108 00 109 00 110 00 111 00 112 00 113 00 114 00 115 00 116 00 117 00 118 00 119 00 120 00 121 00 122 00 123 00 124 00 125 00 126 00 127 00 128 00 129 00 130 00 131 00 132 00 133 00 134 00 135 00 136 00 137 00 138 00 139 00 140 00 141 00 142 00 143 00 144 00 145 00 146 00 147 00 148 00 149 00 150 00 151 00 152 00 153 00 154 00 155 00 156 00 157 00 158 00 159 00 160 00 161 00 162 00 163 00 164 00 165 00 166 00 167 00 168 00 169 00 170 00 171 00 172 00 173 00 174 00 175 00 176 00 177 00 178 00 179 00 180 00 181 00 182 00 183 00 184 00 185 00 186 00 187 00 188 00 189 00 190 00 191 00 192 00 193 00 194 00 195 00 196 00 197 00 198 00 199 00 200 00 201 00 202 00 203 00 204 00 205 00 206 00 207 00 208 00 209 00 210 00 211 00 212 00 213 00 214 00 215 00 216 00 217 00 218 00 219 00 220 00 221 00 222 00 223 00 224 00 225 00 226 00 227 00 228 00 229 00 230 00 231 00 232 00 233 00 234 00 235 00 236 00 237 00 238 00 239 00 240 00 241 00 242 00 243 00 244 00 245 00 246 00 247 00 248 00 249 00 250 00 251 00 252 00 253 00 254 00 255 00 256 00 257 00 258 00 259 00 260 00 261 00 262 00 263 00 264 00 265 00 266 00 267 00 268 00 269 00 270 00 271 00 272 00 273 00 274 00 275 00 276 00 277 00 278 00 279 00 280 00 281 00 282 00 283 00 284 00 285 00 286 00 287 00 288 00 289 00 290 00 291 00 292 00 293 00 294 00 295 00 296 00 297 00 298 00 299 00 300 00 301 00 302 00 303 00 304 00 305 00 306 00 307 00 308 00 309 00 310 00 311 00 312 00 313 00 314 00 315 00 316 00 317 00 318 00 319 00 320 00 321 00 322 00 323 00 324 00 325 00 326 00 327 00 328 00 329 00 330 00 331 00 332 00 333 00 334 00 335 00 336 00 337 00 338 00 339 00 340 00 341 00 342 00 343 00 344 00 345 00 346 00 347 00 348 00 349 00 350 00 351 00 352 00 353 00 354 00 355 00 356 00 357 00 358 00 359 00 360 00 361 00 362 00 363 00 364 00 365 00 366 00 367 00 368 00 369 00 370 00 371 00 372 00 373 00 374 00 375 00 376 00 377 00 378 00 379 00 380 00 381 00 382 00 383 00 384 00 385 00 386 00 387 00 388 00 389 00 390 00 391 00 392 00 393 00 394 00 395 00 396 00 397 00 398 00 399 00 400 00 401 00 402 00 403 00 404 00 405 00 406 00 407 00 408 00 409 00 410 00 411 00 412 00 413 00 414 00 415 00 416 00 417 00 418 00 419 00 420 00 421 00 422 00 423 00 424 00 425 00 426 00 427 00 428 00 429 00 430 00 431 00 432 00 433 00 434 00 435 00 436 00 437 00 438 00 439 00 440 00 441 00 442 00 443 00 444 00 445 00 446 00 447 00 448 00 449 00 450 00 451 00 452 00 453 00 454 00 455 00 456 00 457 00 458 00 459 00 460 00 461 00 462 00 463 00 464 00 465 00 466 00 467 00 468 00 469 00 470 00 471 00 472 00 473 00 474 00 475 00 476 00 477 00 478 00 479 00 480 00 481 00 482 00 483 00 484 00 485 00 486 00 487 00 488 00 489 00 490 00 491 00 492 00 493 00 494 00 495 00 496 00 497 00 498 00 499 00 500 00 501 00 502 00 503 00 504 00 505 00 506 00 507 00 508 00 509 00 510 00 511 00 512 00 513 00 514 00 515 00 516 00 517 00 518 00 519 00 520 00 521 00 522 00 523 00 524 00 525 00 526 00 527 00 528 00 529 00 530 00 531 00 532 00 533 00 534 00 535 00 536 00 537 00 538 00 539 00 540 00 541 00 542 00 543 00 544 00 545 00 546 00 547 00 548 00 549 00 550 00 551 00 552 00 553 00 554 00 555 00 556 00 557 00 558 00 559 00 560 00 561 00 562 00 563 00 564 00 565 00 566 00 567 00 568 00 569 00 570 00 571 00 572 00 573 00 574 00 575 00 576 00 577 00 578 00 579 00 580 00 581 00 582 00 583 00 584 00 585 00 586 00 587 00 588 00 589 00 590 00 591 00 592 00 593 00 594 00 595 00 596 00 597 00 598 00 599 00 600 00 601 00 602 00 603 00 604 00 605 00 606 00 607

•

XX WPI: 1995-200120/26.
 DR P-PSDB; AAR76238.
 XX New nucleic acid encoding Fas protein without its trans-membrane region
 PT - and related vectors, transformed cells, transgenic animals, protein and
 PT antibodies, useful for control of Fas mediated apoptosis
 XX
 XX Claim 3; Fig.3-1 to 3-4; 38pp; English.
 PS
 XX mRNA was obtd. from human lymphocytes and PCR was used to make
 CC cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane
 CC region) mRNA. The PCR product was ligated into pBluescript and the
 CC recombinant plasmid was used to transfect E. coli DH5-alpha cells.
 CC Insert sequence of pBluescript-Fas-delta-TM is given in AAQ93879.
 XX
 SQ Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;

Query Match 4.6%; Score 129; DB 16; Length 2471;
 Best Local Similarity 100.0%; Pred. No. 9e-25; 0; Indels 0; Gaps 0;
 Matches 129; Conservative 0; Mismatches 0;

QY 2034 gagcctctgaggagtgaggagcggtttacgagtgacttgctgagcctcagggcg 2093
 1 gagcctctgaggagtgaggagcggtttacgagtgacttgctgagcctcagggcg 60
 DB 2094 ggcactggcagcagacacacccctgagccagcctgctgcccagcgagctcctt 2153
 61 ggcactggcagcagacacacccctgagccagcctgctgcccagcgagctcctt 120
 QY 2154 ctcccgcg 2162
 121 ctcccgcg 129

DB 121 ctcccgcg 129

RESULT 8
 AAX24878
 ID AAX24878 standard; DNA; 2471 BP.

AC AAX24878;
 XX 21-JUN-1999 (first entry)

XX Soluble Fas receptor DNA.

DE Fas receptor; Fas ligand; FasL; proinflammatory; immunosuppressive;
 XX graft versus host disease; autoimmune disease; psoriasis;
 KW rheumatoid arthritis; systemic lupus erythematosus; gene therapy;
 KW ss.

XX Mammalia.

XX Key Location/Qualifiers

FT CDS 195..1139
 FT /tag= a
 FT /transl_except= (pos:519..521, aa:Gly)

FT sig_peptide 195..242
 FT /tag= b

FT mat_peptide 243..1136
 FT /tag= c

FT polyA_signal 2349..2354
 FT /tag= d

FT polyA_signal 2455..2460
 FT /tag= e

XX MO9903999-A1.

XX 28-JAN-1999.

XX 16-JUL-1998; 98WO-US14771.

XX 17-JUL-1997; 97US-0052829.

XX (UNMI) UNIV MICHIGAN.
 PA Chen J, Nabel GJ;
 PI WPI: 1999-132243/11.
 XX P-PSDB; AAW98070.
 DR
 XX Inhibition of proinflammatory responses - using an agent which
 PT modulates FasL stimulation, used for treating graft versus host
 PT disease or autoimmune disease
 XX
 XX Disclosure; Fig 4B; 71pp; English.

This present sequence is a DNA clone encoding soluble Fas receptor (see AAW98070). The invention provides a method for inhibiting a proinflammatory response in a cell mixture by administering an immunosuppressive agent which inhibits the proinflammatory activity of Fas ligand (FasL). In some embodiments, FasL is coadministered with the immunosuppressive agent, and the cell mixture comprises neutrophil cells. The method can be practised in vitro, ex vivo or in vivo. Suitable immunosuppressive agents include antisense molecules that inhibit endogenous FasL expression, soluble Fas receptors, ribozymes that inhibit the endogenous expression of FasL, drugs that inhibit FasL signalling, agents that induce the endogenous expression of transforming growth factor (TGF)-beta, and polynucleotides coding for an immunosuppressive agent such as FasL with an undesired FasL-mediated proinflammatory response, e.g. graft versus host disease, or an autoimmune disease such as systemic lupus erythematosus, rheumatoid arthritis and psoriasis. The invention also provides a method for identifying agents which modulate FasL stimulation of a proinflammatory response.

Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;

Query Match 4.6%; Score 129; DB 20; Length 2471;
 Best Local Similarity 100.0%; Pred. No. 9e-25; 0; Indels 0; Gaps 0;
 Matches 129; Conservative 0; Mismatches 0;

QY 2034 gagcctctgaggagtgaggagcggtttacgagtgacttgctgagcctcagggcg 2093
 1 gagcctctgaggagtgaggagcggtttacgagtgacttgctgagcctcagggcg 60
 DB 2094 ggcactggcagcagacacacccctgagccagcctgctgcccagcgagctcctt 2153
 61 ggcactggcagcagacacacccctgagccagcctgctgcccagcgagctcctt 120

QY 2154 ctcccgcg 2162
 121 ctcccgcg 129

DB 121 ctcccgcg 129

RESULT 9

AAQ29959
 ID AAQ29959 standard; cDNA to mRNA; 2334 BP.

XX AAQ29959;

AC 12-MAR-1993 (first entry)

XX Human cell surface antigen.

XX Fas antigen; apoptosis; pF58; NGFR/TNFR family; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT sig_peptide 195..242
 FT /tag= a

FT mat_peptide 243..1199
 FT /tag= b

XX

XX

SEQUENCE 14
ID AAT27558 standard; cDNA: 19307 BP.
AAT27558;
07-AUG-1996 (first entry)
Shuttle vector pAdDel.CMVdys.
KM Adenovirus type 5; Ad5' vector; gene therapy; gene transfer;
helper virus; dystrophin; muscular dystrophy; ds; cyclic.
OS Synthetic.
PM M09613597-A2.
PD 09-MAY-1996.
PF 27-OCT-1995; 95MO-US14017.
PR 28-OCT-1994; 94US-0331381.
PA (TYPE-) UNIV PENNSYLVANIA.
XX Chen S, Fisher KJ, Weltzman M, Wilson JM;
PI WPI; 1996-251463/25.
XX Recombinant adenovirus produced from shuttle vector and helper virus
PT - has crippled packaging function, useful for delivering
PS transgene(s) to target cells
Example 9; Fig 12A-12P; 149pp; English.
CC Shuttle vector pAdDel.CMVdys (AAT27558) comprises the adenovirus
CC cis elements needed for replication and virion encapsidation but
CC is deleted of all viral genes. It carries a mouse dystrophin
CC minigene under control of the CMV promoter. It is used with a helper
CC infection but which has disabled packaging function. Recombinant
CC adenovirus is produced that is characterized by high filter titer
CC delivery to host cells and the ability to stably integrate the
CC transgene into the host cell chromosome. Such a vector can be used
CC to transfer the dystrophin gene for use in muscular dystrophy gene
XX therapy.
XX Sequence 19307 BP. AATC

Matches	93;	Similarity	65.58;	Score	63.6;	DB	17;	Length	19307;
			Conservative		Pred. No.	3.8e-06;			Mismatches
OV	2114								

[illegible]

32 190.2 6.7 466 17 US-09-333-909-2214
33 190.2 6.7 466 31 US-09-817-500-2214
34 188.4 6.7 532 29 US-09-726-788-5938
35 188 6.7 565 25 US-09-652-124-2645
36 182.6 6.5 473 16 US-09-334-611-3879
37 182.6 6.5 473 34 US-09-904-809-3879
38 182.6 6.5 473 34 US-09-925-564-39624
39 182.6 6.5 473 34 US-09-534-843-23549
40 179.6 6.4 453 29 US-09-726-788-5938
41 178.8 6.3 462 12 US-09-716-475-4710
42 178.8 6.3 462 12 US-08-869-540-581
43 166.4 5.9 263 40 US-09-834-291-32
44 166.4 5.9 266 32
45 161 5.7

ALIGNMENTS

Sequence 2214, Ap
Sequence 2214, Ap
Sequence 5938, Ap
Sequence 2645, Ap
Sequence 3879, Ap
Sequence 39624, Ap
Sequence 3879, Ap
Sequence 23549, A
Sequence 4710, Ap
Sequence 3862, Ap
Sequence 581, App
Sequence 32, Appl

US-09-834-291-4
Sequence 4 Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
TITLE OF INVENTION: P53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 198 47 779.1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 2827
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-834-291-4

Query Match Best Local Similarity 100.0%; Score 2827; DB 32; Length 2827;
Matches 2827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 tgaggaactctcaggaatgctgtaataataaataaacccttagagatcccaactgt 60
QY 61 ttccccaagaacacagcatcattaggttcaatcaatagattcttcaagaattcca 120
DB 61 ttccccaagaacacagcatcattaggttcaatcaatagattcttcaagaattcca 120
QY 121 aaggaagaaggttggaacagctatataataatcccaacccttgaacatggaatc 120
DB 121 aaggaagaaggttggaacagctatataataatcccaacccttgaacatggaatc 120
QY 181 taaggcccttggaaggtttgatttaagaagaagtttcaaatgaagtaaccagaattt 240
DB 181 taaggcccttggaaggtttgatttaagaagaagtttcaaatgaagtaaccagaattt 240
QY 241 ctaagatatttgacatgaacataatgctccccaagaacacataatctctatctt 300
DB 241 ctaagatatttgacatgaacataatgctccccaagaacacataatctctatctt 300
QY 301 gaacttgagatattagagcagctagctggaaggttaggggaagggatgacata 360
DB 301 gaacttgagatattagagcagctagctggaaggttaggggaagggatgacata 360
QY 361 aaggaagaaggttggaacagctatataataatcccaacccttgaacatggaatc 420
DB 361 aaggaagaaggttggaacagctatataataatcccaacccttgaacatggaatc 420

361 aaggaagaaggttggaacagctatataataatcccaacccttgaacatggaatc 540
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[illegible]

[illegible]

Page 5

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	1020		
Db	8894	acaagcctatacaacacatcaacagatcgctggtgaatgtgaatgtgaacatgtaaacacag	8953
	9013		
OY	961	gtgatcggaagcccttagagaggtgaactcaacatttgagggcccaaacagctccca	1020
	1080		
Db	8954	gtgatcggaagcccttagagaggtgaactcaacatttgagggcccaaacagctccca	9013
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OY	1021	gaagaataatgtaactctgagaggaagccctgaagaatgtaacagtgagcttaagccaaggtta	1140
	9133		
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	1200		
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QY	841	gctcgtcagcccgaggtctctctcatatgcatacaagctcactcgaaggttgaaacag	900
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QY	901	acaagcctatacaacccctcaagagctcgttgatgagcagtgacagtgacaaacacag	960
Db	8894	acaagcctatacaacccctcaagagctcgttgatgagcagtgacagtgacaaacacag	8953
QY	961	gtgagcgaagccctcagagaggttaacctatgatttgagggcccaaacagctcca	1020
Db	8954	gtgagcgaagccctcagagaggttaacctatgatttgagggcccaaacagctcca	9013
QY	1021	gaagaaatgctcaactcagagagagcctcgaagagatacaacagtcaggtcaagaggtta	1080
Db	9014	gaagaaatgctcaactcagagagagcctcgaagagatacaacagtcaggtcaagaggtta	9073
QY	1081	ttatgtgttataatggtgttaactatccttggaagggagagaggttgagaggtgaggt	1140
Db	9074	ttatgtgttataatggtgttaactatccttggaagggagagaggttgagaggtgaggt	9133
QY	1141	gcagagcttggtgagcagatgcacaaagaaatactgaacctttagtcgtccagtctgaa	1200
Db	9134	gcagagcttggtgagcagatgcacaaagaaatactgaacctttagtcgtccagtctgaa	9193
QY	1201	ctgcatacaactcaggttcaatgataatgtatcatalcccaaacatccttcgtaaat	1260
Db	9194	ctgcatacaactcaggttcaatgataatgtatcatalcccaaacatccttcgtaaat	9253
QY	1261	catgctaaacctcaagagctatcaccgtcccaagcaatagtgatcttgaaacgtt	1320
Db	9254	catgctaaacctcaagagctatcaccgtcccaagcaatagtgatcttgaaacgtt	9313
QY	1321	tcacccagagccagaaagaattacaaagtctttctttaaagaatacttgccaggaataat	1380
Db	9314	tcacccagagccagaaagaattacaaagtctttctttaaagaatacttgccaggaataat	9373
QY	1381	gaatlaacgaagcagagaaatgttgatgttataatagctcgggagcatalgattg	1440
Db	9374	gaatlaacgaagcagagaaatgttgatgttataatagctcgggagcatalgattg	9433
QY	1441	gcttaaatgttgatgcttcttctcctctggaataataaactaaggggccctcccttc	1500
Db	9434	gcttaaatgttgatgcttcttctcctctggaataataaactaaggggccctcccttc	9493
QY	1501	cagaagcctatgagcacaatccttcttcaatgatttlaactgtccattccaggaac	1560
Db	9494	cagaagcctatgagcacaatccttcttcaatgatttlaactgtccattccaggaac	9553
QY	1561	gtctcgtagcctctcatgttcagccacaacatggaacgcccagctcaaatgcccgaag	1620
Db	9554	gtctcgtagcctctcatgttcagccacaacatggaacgcccagctcaaatgcccgaag	9613
QY	1621	tccttctcgtatgactcccaagcaattagcgaagcttcctgtaccagagcagagccttcg	1680
Db	9614	tccttctcgtatgactcccaagcaattagcgaagcttcctgtaccagagcagagccttcg	9673
QY	1681	gctctagagctcattcctccttaagaacctcccaacttcccaaggttgaactcagcagaa	1740
Db	9674	gctctagagctcattcctccttaagaacctcccaacttcccaaggttgaactcagcagaa	9733
QY	1741	gctcttgaagaagcagagagcggtctcgaagtctccacactgaagtgaacagccagc	1800
Db	9734	gctcttgaagaagcagagagcggtctcgaagtctccacactgaagtgaacagccagc	9793
QY	1801	caatgcagagagcccccggagacgaatgccaattgttgaaagaaaccttgaccttcc	1860
Db	9794	caatgcagagagcccccggagacgaatgccaattgttgaaagaaaccttgaccttcc	9853
QY	1861	tcacccgtactctcccccctccacccgcgcagcgaagttgtcgtaatcaatggagc	1920
Db	9854	tcacccgtactctcccccctccacccgcgcagcgaagttgtcgtaatcaatggagc	9913

[illegible]

QY	447	aagctttttggtacattttttattttaagaagttaatacaaccatctact	506
Db	1	aagctttttggtacattttttattttaagaagttaatacaaccatctact	60
QY	507	gggtctaataagataagatlaaagtaaggaagatccacataatgtgagttgctgtatata	566
Db	61	gggtctaataagataagatlaaagtaaggaagatccacataatgtgagttgctgtatata	120
QY	567	ttcacactcaagagataatgattttgttcaattgttcccttttctctctcc	626
Db	121	ttcacactcaagagataatgattttgttcaattgttcccttttctctctcc	180
QY	627	tccctccatctccttcccttactctctctctccctccctcccaacccttttccctcct	686
Db	181	tccctccatctccttcccttactctctctctccctccctcccaacccttttccctcct	746
QY	687	tctttttaacatttttatttaataagacttctcaatttttggaatagtttaagatttcaa	300
Db	241	tctttttaacatttttatttaataagacttctcaatttttggaatagtttaagatttcaa	360
QY	747	aaaatttgcagagataatacagaagaatgcccacatacaactctctctatcccaacttctt	806
Db	301	aaaatttgcagagataatacagaagaatgcccacatacaactctctctatcccaacttctt	866
QY	807	tgtgttctcattagatgctcagagtggttgcacaagaagcttgccaaagcccaaggcttcccta	420
Db	361	tgtgttctcattagatgctcagagtggttgcacaagaagcttgccaaagcccaaggcttcccta	480
QY	867	tggcactcaacagttactactcaagagtgagacaagagacagcctatacaacactcaagaact	926
Db	421	tggcactcaacagttactactcaagagtgagacaagagacagcctatacaacactcaagaact	986
QY	927	gggtgtaagtgcacgtcacagatgcacaacacacaggggtgtaatgaaagccttcaggggggttaa	540
Db	481	gggtgtaagtgcacgtcacagatgcacaacacacaggggtgtaatgaaagccttcaggggggttaa	1046
QY	987	ccttaacctagatcttgagggcccaacacagctccagaagaagaatgctcaactgtgagagaagc	600
Db	541	ccttaacctagatcttgagggcccaacacagctccagaagaagaatgctcaactgtgagagaagc	660
QY	1047	ctgaagagatgaaacgttggtcctaagacaaagggttattcaatgtgttatttaatgtgttgaatc	1106
Db	601	ctgaagagatgaaacgttggtcctaagacaaagggttattcaatgtgttatttaatgtgttgaatc	1166
QY	1107	taatttggagaaggagagaggtttgcagagtgaggtgcagagcttgggtgcacgtgcagaaag	720
Db	661	taatttggagaaggagagaggtttgcagagtgaggtgcagagcttgggtgcacgtgcagaaag	1226
QY	1167	gaatactgaaacctttagtgcagctctggaactgcatccaattcaattcaagttcaagtaat	780
Db	721	gaatactgaaacctttagtgcagctctggaactgcatccaattcaattcaagttcaagtaat	1286
QY	1227	gattgcatatccaacacatacctctcgttlaaattcaatgcttaactcaactcaagagctact	840
Db	781	gattgcatatccaacacatacctctcgttlaaattcaatgcttaactcaactcaagagctact	1346
QY	1287	accgttccaagcaataatgacatttgaacagtggttcaaccagagcagcaagaagattacaag	900
Db	841	accgttccaagcaataatgacatttgaacagtggttcaaccagagcagcaagaagattacaag	1406
QY	1347	attttttttaagaagaaattgaccagaagaataatgataacgaagacagaagtaattg	960
Db	901	attttttttaagaagaaattgaccagaagaataatgataacgaagacagaagtaattg	1466
QY	1407	tgaatgtttaataatgcttggggctatgcgatttggcttaagtgttgcgtttgtttcct	1020
Db	961	tgaatgtttaataatgcttggggctatgcgatttggcttaagtgttgcgtttgtttcct	1526
QY	1467	cttgagaataaanaactaaaggggcctccttttcaagagcctataggggacaacatctgta	1080
Db	1021	cttgagaataaanaactaaaggggcctccttttcaagagcctataggggacaacatctgta	1146

QY 1527 cttttcatactgtaactgtcattccaggaagctgtgagccctcactggttgagcc 1586
 Db 1081 cttttcatactgtaactgtcattccaggaagctgtgagccctcactggttgagcc 1140
 QY 1587 acaactgagagccaggaatgaatgagccagagctgttctctgagtgactcagcaalt 1646
 Db 1141 acaactgagagccaggaatgaatgagccagagctgttctctgagtgactcagcaalt 1200
 QY 1647 agccaagctctgtacccaagcagagctgtgagccctcactggttgagccctcagcaalt 1706
 Db 1201 agccaagctctgtacccaagcagagctgtgagccctcactggttgagccctcagcaalt 1260
 QY 1707 cctccccaactcccaagctgtgaactgaagcagagcccttgaagagcagagcagcagc 1766
 Db 1261 cctccccaactcccaagctgtgaactgaagcagagcccttgaagagcagagcagcagc 1320
 QY 1767 tctcgagctcctcaactgaagtgagcagcagcagcagcagcagcagcagcagcagc 1826
 Db 1321 tctcgagctcctcaactgaagtgagcagcagcagcagcagcagcagcagcagcagc 1380
 QY 1827 atgccaattgtgcaagcagcagcagcagcagcagcagcagcagcagcagcagc 1886
 Db 1381 atgccaattgtgcaagcagcagcagcagcagcagcagcagcagcagcagcagc 1440
 QY 1887 ccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1946
 Db 1441 ccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1500
 QY 1947 gaggctcctccatcctcctgagcagcagcagcagcagcagcagcagcagcagc 2006
 Db 1501 gaggctcctccatcctcctgagcagcagcagcagcagcagcagcagcagcagc 1560
 QY 2007 cgcgaagtgacacacagcagcagcagcagcagcagcagcagcagcagcagcagc 2066
 Db 1561 cgcgaagtgacacacagcagcagcagcagcagcagcagcagcagcagcagcagc 1620
 QY 2067 agtgactgtgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 2126
 Db 1621 agtgactgtgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 2160
 QY 2127 ctgagctgacagcagcagcagcagcagcagcagcagcagcagcagcagc 1680
 Db 1681 ctgagctgacagcagcagcagcagcagcagcagcagcagcagcagcagc 1716

RESULT 7
 US-08-377-522-1
 Sequence 1, Application US/08377522
 GENERAL INFORMATION:
 APPLICANT: Mountz, John D.
 APPLICANT: Liu, Changdan
 APPLICANT: Cheng, Jianhua
 APPLICANT: Koopman, William J.
 TITLE OF INVENTION: Human Fas Gene Promoter Region
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESS: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: Texas
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/377, 522
 FILING DATE: 20-Jan-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:

NAME: Serlich, Gary J.
 REGISTRATION NUMBER: 34,430
 REFERENCE/DOCKET NUMBER: 00AB:034/SBR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1608 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1467..1496
 US-08-377-522-1

Query Match 48.6%; Score 1372.8; DB 7; Length 1608;
 Best Local Similarity 99.4%; Pred. No. 2,4e-287;
 Matches 1388; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
 QY 767 agagaatgcccataatcacatccctcctatcccaactcttctgtctatagatgctca 826
 Db 7 ACAGAGTGGCTTATACATCTCTTATCCACTCTTTGTGTGCTATGATGCTCA 66
 QY 827 gagtgtgtgacaaagctgtgagcagcagcagcagcagcagcagcagcagcagc 886
 Db 67 GAGTGTGTGACAAAGCTGTGACAGCCAGGAGGCTTCCATGCTGACCTAAAGTCTACTGA 126
 QY 887 aagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 946
 Db 127 AAGTGTGACAAAGCTGTGACAGCCAGGAGGCTTCCATGCTGACCTAAAGTCTACTGA 186
 QY 947 atgcaaaacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1006
 Db 187 ATGCAAAACACAGGCTGTGATGAAGCCCTCAGGAGGCTTAACTTAACTTAACTTAA 246
 QY 1007 ccaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1066
 Db 247 CCAACAGGCTCCAGAAAGTCAACTGACAGAGGAGCTTAAAGTCAAGTCAAGTCAAG 306
 QY 1067 taagcaagagcttataatgtgtatataatgtgtatataatgtgtatataatgtgt 1126
 Db 307 TAGCAAGAGGCTTATTAATGTTATGTTATGTTATGTTATGTTATGTTATGTTATG 366
 QY 1127 ttgcagagtgaggtgagcagcagcagcagcagcagcagcagcagcagcagcagc 1186
 Db 367 TTGCAGAGTGAGGTGAGCAGCTGTGTGACAGTGCAGAAAGAACTGAACCTTTAGT 426
 QY 1187 tgtcagctgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1246
 Db 427 TGTCAGCTGTGAGCTGTGACAGCTGTGTGACAGTGCAGAAAGAACTGAACCTTTAGT 486
 QY 1247 cctctgtataatcattgctaaactaactaagagctatccagcttccaaagcaatagtg 1306
 Db 487 CCTCTGTATAATTCATAGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 546
 QY 1307 acttgaacagtgltacacagcagcagcagcagcagcagcagcagcagcagcagcagc 1366
 Db 547 ACTTGAACAGTGTTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 606
 QY 1367 ggcgaagaaatagatgaagcagcagcagcagcagcagcagcagcagcagcagcagc 1426
 Db 607 GGCAGGAATATATGATGAACGAAAGACAGAGATTTGGAATGTTATATATAGCTGG 666
 QY 1427 ggcatacgattgtgctaaagtgtgagctgttctcctctgagaaataaataaactga 1486
 Db 667 GGCATAGGATTTGGCTTAAGTTGTAGCTTTGTTCTCTTGAAGAAATAAATAACTAAG 726
 QY 1487 ggcgcctccttccagagccctatgagcagacacatcgtacttcttcatatggttaactg 1546

```

1  MEDIUM TYPE: 3.5 inch floppy
2  COMPUTER: Apple Macintosh
3  OPERATING SYSTEM: Macintosh
4  SOFTWARE: Microsoft Word for Macintosh
5  CURRENT APPLICATION WORD
6  APPLICATION APPLICATION DATA:
7  FILLING DATE: January 20, 1995
8  CLASSIFICATION: 435
9  PRIOR APPLICATION: DATA
10 APPLICATION NUMBER:
11 FILLING DATE:
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Benjamin Aaron Adler, Ph.D., J.D.
14 REGISTRATION NUMBER: 35,423
15 REFERENCE/DOCKET NUMBER: D5919
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: (713) 777-2321
18 TELEFAX: (713) 777-6908
19 INFORMATION FOR SEQ ID NO: 1:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 1608 bp
22 TYPE: nucleic acid
23 STRANDEDNESS: double-stranded
24 TOPOLOGY: linear
25 MOLECULE TYPE:
26 DESCRIPTION: genomic DNA
27 HYPOTHETICAL: no
28 ANTI-SENSE: no
29 FRAGMENT TYPE:
30 ORIGINAL SOURCE:
31 ORGANISM: human
32 TISSUE TYPE: placental
33 IMMEDIATE SOURCE:
34 LIBRARY: (F1X11, EMBL-SP6/T7
35 CLONE: F1X1, F1X2, F1X3; EMBL1, EMBL2, EMBL3
36 POSITION IN GENOME:
37 FEATURE:
38 PUBLICATION INFORMATION:
39 US-08-377-522D-1

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	Query Match	48.6%	Score 1372.8;	DB 7;	Length 1608;
	Best Local Similarity	99.4%	Pred. No. 2.4e-287;		
	Matches 1388;	Conservative	0;	Mismatches 7;	Gaps 1;
QY	767	agaagaatgccatataccatccctccattaccattctttctgtctatatagatgca			
Db	7	AAGAGAGATGCCCTATACCATCTCTCTTATCCCACTTTTGTGCTATTGATGCTCA			
QY	827	gaagtgtgacaaagccttggaagcccaaggtcttcctcaatgacataacgttactga			
Db	67	GAGGTGTGACAAAGCGTTGGCAGCCGACGGGCTTCTCATGAGCATCAACTTACTGA			
QY	887	aaggtggaagaagacaagcctatcaaacctcaagaagtgtgttaagtgcagtgcag			
Db	127	AAGTGGAAAGAGACAAACCTATCAACACTTACAAGACTGTGTGTAAGTCAGTGACAG			
QY	947	atgcaaaacaagagtgatcgtggaagccctccagaggttaacctaaactagaattgagggc			
Db	187	ATGCAAAACACAGGGGTGATGSAAGCCCTCAGGAGGCTTAACTTAACCTAGATTGAGGCC			
QY	1007	ccaagaagctccagaagaanaaatgtcaacttgaagaggaagccttgaagaatgaacaatgaggc			
Db	247	CCAACAGGCTCCAGAAATAATGTCAACTAGAGGAGAAAGCCTAAGAGATGAAACAGTGGGC			
QY	1067	taagaagaaggtctatcaatgtctattcaatgggtttaaacttaatttggaagggagagaag			
Db	307	TAAAGAAAGGGTTATTATATGTATTAAATGGTTTAAATCTAATTTGGAGAGGAGAGAGG			
QY	1127	ttgcagagtgaagtgcagagccttggtggagacagatgccaaaggaataactgaaccttaagt			
Db	367	TTGCAGAGTGAAGTGACAGACCTTGTGGTGGACGATGCCAAAGAAATCTACTGAACCTTTACTG			


```

1  APPLICANT: Morris, MacDonald
2  /
3  APPLICANT: Lal, Preeti
4  /
5  TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
6  /
7  TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
8  /
9  TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
10 /
11 FILE REFERENCE: GX-0019-1 P
12 /
13 CURRENT APPLICATION NUMBER: US/60/324,185
14 /
15 CURRENT FILING DATE: 2001-09-21
16 /
17 NUMBER OF SEQ. ID NOS.: 35862
18 /
19 SOFTWARE: PERL Program
20 /
21 SEQ ID NO 29531
22 /
23 LENGTH: 3814
24 /
25 TYPE: DNA
26 /
27 ORGANISM: Homo sapiens
28 /
29 FEATURE:
30 /
31 NAME/KEY: misc_feature
32 /
33 OTHER INFORMATION: incyte ID NO: 415714.1
34 /
35 US-60-324-185-29531

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Query Match	25.0%;	Score 706;	DB 71;	Length 3814;
Best Local Similarity	99.9%;	Pred. No. 2.3e-142;	Mismatches 0;	Indels 1;
Matches 717;	Conservative	0;	142;	Gaps 1
QY 1446 agtgttagcttgttcttctcttgggaataaataagggccctcccttccag 1505	1	agtgttagcttgttcttctcttgggaataaataagggccctcccttccag 60		
DB 1506 cccatagggcaacatctgttacttttcatatgttatactgttccatccagaagctgt 1565		1 agtgttagcttgttcttctcttgggaataaataagggccctcccttccag 60		
QY 1506 cccatagggcaacatctgttacttttcatatgttatactgttccatccagaagctgt 1625		61 cccatagggcaacatctgttacttttcatatgttatactgttccatccagaagctgt 120		
DB 1566 tgaagctctcatgttgcagccacaacatgtgacagccaggtcaaatgtcccgcaagtctt 1685		121 tgaagctctcatgttgcagccacaacatgtgacagccaggtcaaatgtcccgcaagtctt 180		
QY 1626 cctctagtgatccagcaattagccaaggtctctgttaccagaagcagactgtgctct 1745		1626 cctctagtgatccagcaattagccaaggtctctgttaccagaagcagactgtgctct 240		
DB 181 cctctagtgatccagcaattagccaaggtctctgttaccagaagcagactgtgctct 300		181 cctctagtgatccagcaattagccaaggtctctgttaccagaagcagactgtgctct 300		
QY 1686 gagctccatcttctctcaagaacctcccaactccaggttgaactacagcagaagcctt 1805		241 gagctccatcttctctcaagaacctcccaactccaggttgaactacagcagaagcctt 360		
DB 1746 tagaagaaggcaggaagcggcgtctctgaagtccttcaacctgaagtgaagatgccaagctgt 1865		301 tagaagaaggcaggaagcggcgtctctgaagtccttcaacctgaagtgaagatgccaagctgt 420		
QY 1806 caggaagaagcccgaggaagaatgtcccatgtgtcaacggaacctgtctccctccaac 1925		361 caggaagaagcccgaggaagaatgtcccatgtgtcaacggaacctgtctccctccaac 480		
DB 361 caggaagaagcccgaggaagaatgtcccatgtgtcaacggaacctgtctccctccaac 480		421 ctgacttctccctccctccatcccgcgacagcaggtctccatctcttgaccccgggcttttc 1985		
QY 1926 ccaaacccggcggtcccccagcgaggtctctccatctctcttgaccccgggcttttc 540		481 ccaaacccggcggtcccccagcgaggtctctccatctctcttgaccccgggcttttc 2045		
DB 481 ccaaacccggcggtcccccagcgaggtctctccatctctcttgaccccgggcttttc 2045		1986 gttagctcgtctctgaatctcgccagagatgtgacacaggtgttcaagaagcttttgg 600		
QY 2046 gattgagggagagcgtttacagatgactgtgtgtggagcctccaaggcgggcacttgacac- 2104		541 gttagctcgtctctgaatctcgccagagatgtgacacaggtgttcaagaagcgttttgg 660		
DB 601 gattgagggagagcgtttacagatgactgtgtgtggagcctccaaggcgggcacttgacac 2162		601 gattgagggagagcgtttacagatgactgtgtgtggagcctccaaggcgggcacttgacac 718		
QY 2105 ggaacacacccctgagcgcaagcctctgtctgcccagcgggagctgtccttctcccgcg 718		661 ggaacacacccctgagcgcaagcctctgtctgcccagcgggagctgtccttctcccgcg 718		
DB 661 ggaacacacccctgagcgcaagcctctgtctgcccagcgggagctgtccttctcccgcg 718				

Query Match 21.6%; Score 611.8; DB 32;
Best Local Similarity 99.7%; Length 720;
Matches 613; Conservative 0.14

every match	15.0%	Score 424.2;	DB 18;	Length 449;
Best Local Similarity	99.3%;	Pred. No. 1.7e-81;		
Matches 426; Conservative	0;	Mismatches 7		

RESULT 13
US-09-524-038-674/C
: Sequence 674

GENERAL INFORMATION:
 APPLICATION: 09/4, Application US/09524038
 APPLICANT: Dymanac, Radoje T.
 APPLICANT: Labat, Ivan
 APPLICANT: Stache-crain, Birgit
 APPLICANT: Dickson, Mark C.
 APPLICANT: Jones, Lee W.
 TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
 FROM VARIOUS LIBRARIES
 FILE REFERENCE: 780CIP
 CURRENT APPLICATION NUMBER: US/09/524,038
 CURRENT FILING DATE: 2000-03-13
 EARLIER APPLICATION NUMBER: 09/404,284
 EARLIER FILING DATE: 1999-09-21

NUMBER OF SEQ. ID NOS: 4670
 SOFTWARE: Hy-patent.pl Version 3.1
 SEQ ID NO 674
 LENGTH: 449
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-524-038-674

Query Match 15.08; Score 424.2; DB 19; Length 449;

Best Local Similarity 99.3%; Pred. No. 1.7e-81; Mismatches 3; Indels 0; Gaps 0;

Matches 426; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1680 cgccttgagccttccttccttcagaccccccactcccaaggttgaaatcacagca 1739
 |||
 Db 449 GGTTCGAGCTCCTCCTTCCTTCAGACCTCCCAACTCCAGGTTGAATACAGACA 390
 |||
 Db 1740 agccttgaag 1799
 |||
 Db 389 AGCCTTGAAGAAAGGCGAGAGAGCGGCTCTCGAGTCTCAGCTGAGTGAAGACATGCCAG 330
 |||
 Db 1800 ccactgag 1859
 |||
 Db 329 CCACCTGACAGAAAGCGCCCGGACAGAAATGCCATTTGTGCAACGAACCTGACTCTTC 270
 |||
 Db 1860 ctacacctgactctccctccctccctccctccctccctccctccctccctccctccct 1919
 |||
 Db 269 CTCACCCCTGACTTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 210
 |||
 Db 1920 cccctcccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1979
 |||
 Db 209 CCTCCCAAGCCGCGGCGTCCCTCCAGAGAGCTTCTCCATCTCTCCAGCAGCGGG 150
 |||
 Db 1980 ctttcgtgagctcgtctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 2039
 |||
 Db 149 CTTTGTGAGCTCGTCTCTGATCTGCGCAGAGATGACACAGGTGTCAAGAGGCT 90
 |||
 Db 2040 tctggag 2099
 |||
 Db 89 TCTGGGAGTGAAGAAAGCCGTTTACAGTACCTTGGCTGAGGCGGCGGACT 30
 |||
 Db 2100 ggcacggaa 2108
 |||
 Db 29 GGCACGGCA 21

RESULT 14

US-09-306-350A-14682/c
 ; Sequence 14682, Application US/09306350A

GENERAL INFORMATION:
 ; APPLICANT: Dickson, Mark C.

APPLICANT: Drmanac, Radoje T.

APPLICANT: Jones, Lee W.

APPLICANT: Labat, Ivan

TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained

FILE REFERENCE: 20411-776

CURRENT FILING DATE: 1999-05-07

NUMBER OF SEQ ID NOS: 41304

SOFTWARE: pl_CT_1 Version 1.1

SEQ ID NO 14682

LENGTH: 458

TYPE: DNA

ORGANISM: Homo sapiens

US-09-306-350A-14682

Query Match 11.3%; Score 319.6; DB 17; Length 458;

Best Local Similarity 96.3%; Pred. No. 9.1e-59;

Matches 391; Conservative 0; Mismatches 9; Indels 6; Gaps 6;

Db 961 gtgatgaaagccctcaag 1020
 |||
 Db 457 GTGATGAAAGCCCTCAGAGAGGTTAAGCTTAAGATTGA-GGCCCAAGAGGCTTCA 399
 |||
 Db 1021 gaagaaatgtcaactgag 1080
 |||
 Db 398 GAAGAAATGTCAACTGAG 340
 |||
 Db 1081 ttaatgttttaattgag 1140
 |||
 Db 339 TTAATGTGTTAATGAGGTTAATGAGGTTAATGAGGTTAATGAGGTTAATGAGGTT 281
 |||
 Db 1141 gaagagcttgatgag 1200
 |||
 Db 280 GAGAGGCTTGTGGGAG 222
 |||
 Db 1201 ctgacatcaaatcag 1260
 |||
 Db 221 CTGACATCCAAATTCAGGTTCAAGTATGATGATGATGATGATGATGATGATGATGAT 163
 |||
 Db 1261 catgtcaactaactaag 1320
 |||
 Db 162 CAGCTAACTAGTAAGAGCTATCTACCGTTCCAAAGCAATAG-GACTTTGAACAGTGT 104
 |||
 Db 1321 tcacag 1366
 |||
 Db 103 TCACAG 58
 |||

RESULT 15

US-09-909-629-14682/c
 ; Sequence 14682, Application US/09909629

GENERAL INFORMATION:
 ; APPLICANT: Dickson, Mark C.

APPLICANT: Drmanac, Radoje T.

APPLICANT: Jones, Lee W.

APPLICANT: Labat, Ivan

TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained

FILE REFERENCE: 20411-776

CURRENT FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: 09/306,350

PRIOR FILING DATE: 1999-05-07

NUMBER OF SEQ ID NOS: 41304

SOFTWARE: pl_CT_1 Version 1.1

SEQ ID NO 14682

LENGTH: 458

TYPE: DNA

ORGANISM: Homo sapiens

US-09-909-629-14682

Query Match 11.3%; Score 319.6; DB 34; Length 458;

Best Local Similarity 96.3%; Pred. No. 9.1e-59;

Matches 391; Conservative 0; Mismatches 9; Indels 6; Gaps 6;

Db 961 gtgatgaaagccctcaag 1020
 |||
 Db 457 GTGATGAAAGCCCTCAGAGAGGTTAAGCTTAAGATTGA-GGCCCAAGAGGCTTCA 399
 |||
 Db 1021 gaagaaatgtcaactgag 1080
 |||
 Db 398 GAAGAAATGTCAACTGAG 340
 |||
 Db 1081 ttaatgttttaattgag 1140
 |||
 Db 339 TTAATGTGTTAATGAGGTTAATGAGGTTAATGAGGTTAATGAGGTTAATGAGGTT 281
 |||
 Db 1141 gaagagcttgatgag 1200
 |||
 Db 280 GAGAGGCTTGTGGGAG 222
 |||

QY 1201 ctgcattccaaattcagggttcagtaataatgcatatccaaacataccttctgtaaat 1260
 |||||
 Db 221 CTGCATCCCAATTCAGGTTCACTAATGICATTAATCCAAACA-ACCTTCTGTAAAT 163
 |||||
 QY 1261 catgctaacttacccttaagaagctatctacggttccaaagcaatagtgactttgaacagtgt 1320
 |||||
 Db 162 CATGCTAAACTACGTAAGAGCTATCTACGTTCCAAAGCAATAG-GACTTTGAACAGTGT 104
 |||||
 QY 1321 tcaccagagcagcaagaattacaagaattttttaagaagaatt 1366
 |||||
 Db 103 TCACCAAGAGCACCAGAAATTAACAAGATTTTCTCTGCGCGAT 58
 |||||

Search completed: September 7, 2002, 22:35:39
 Job time: 44033 sec

Db 8294 gaacttgagataatttgacgtacgtggttagagggttagggggttagtgcataaga 8353
OY 361 aagagcgagacgttgaggagaagaata tctaaagttaattccctgactgctatttatta 420
Db 8354 aagagcgagacgttgaggagaagaata tctaaagttaattccctgactgctatttatta 8413
OY 421 actaacacatcttgccaattgttgtaagcttttttggctacattttttatttgaag 480
Db 8414 actaacacatcttgccaattgttgtaagcttttttggctacattttttatttgaag 8473
OY 481 taagttaataatcacatcactcactcgtggtatcaatgaatgaatgaatgaatgc 540
Db 8474 taagttaataatcacatcactcactcgtggtatcaatgaatgaatgaatgaatgc 8533
OY 541 cacatatgtgagttgttggtttataatcaacactcaagagatactgatttgcattgt 600
Db 8534 cacatatgtgagttgttggtttataatcaacactcaagagatactgatttgcattgt 8593
OY 601 ccttccctctttttc 660
Db 8594 ccttccctctttttc 8653
OY 661 ctccctcacaccccttc 720
Db 8654 ctccctcacaccccttc 8713
OY 721 atttggataatgtttaggatttcaaaaaattgcagagataatcaagaatgtccata 780
Db 8714 atttggataatgtttaggatttcaaaaaattgcagagataatcaagaatgtccata 8773
OY 781 taacatctcctc 840
Db 8774 taacatctcctc 8833
OY 841 ggtctgagacgcccagaggtctctctcactcactcactcactcactcactcactcactc 900
Db 8834 ggtctgagacgcccagaggtctctctcactcactcactcactcactcactcactcactc 8893
OY 901 acaagacactcaacacactcaagaactgtgtgtaagtgcagtgcagatactgcaaacacag 960
Db 8894 acaagacactcaacacactcaagaactgtgtgtaagtgcagtgcagatactgcaaacacag 8953
OY 961 gtatgtgaagacccctcactcactcactcactcactcactcactcactcactcactc 1020
Db 8954 gtatgtgaagacccctcactcactcactcactcactcactcactcactcactcactc 9013
OY 1021 gaaagaatgtcactcactcactcactcactcactcactcactcactcactcactc 1080
Db 9014 gaaagaatgtcactcactcactcactcactcactcactcactcactcactcactc 9073
OY 1081 ttaatgtttaaatttggttgtaacttaattgggaagggaagggttgccagatgaggt 1140
Db 9074 ttaatgtttaaatttggttgtaacttaattgggaagggaagggttgccagatgaggt 9133
OY 1141 gcagagcttggtgagcgtgcgaaggaatactgaacactttagtgtgcagttcgtgaa 1200
Db 9134 gcagagcttggtgagcgtgcgaaggaatactgaacactttagtgtgcagttcgtgaa 9193
OY 1201 ctgacccaatcaaggttcaagtaatgtcatatccaaactacacttcttgaataatt 1260
Db 9194 ctgacccaatcaaggttcaagtaatgtcatatccaaactacacttcttgaataatt 9233
OY 1261 catgtcaaacactcaagactctacgttccaaagcaatagtgacttgaacagtg 1320
Db 9254 catgtcaaacactcaagactctacgttccaaagcaatagtgacttgaacagtg 9313
OY 1321 tcaacgagagcagaagaatataagaatttttttaagaagaattggcaggaataat 1380
Db 9314 tcaacgagagcagaagaatataagaatttttttaagaagaattggcaggaataat 9373
OY 1381 gagtaacgagagcagaagaatataagaatttttaataatagctgggactgacttg 1440
Db 1440 gagtaacgagagcagaagaatataagaatttttttaataatagctgggactgacttg 1440

Db 9374 gagaacagaagacagagaatgtgtaattgttaataatataatgctgggactgacttg 9433
OY 1441 gcttaagtgttaactgttttctctctctctctctctctctctctctctctctctctct 1500
Db 9434 gcttaagtgttaactgttttctctctctctctctctctctctctctctctctctctct 9493
OY 1501 cagagccctatgagcagaactctgtaatttcaatgtaattgtaattgtaattgtaattg 1560
Db 9494 cagagccctatgagcagaactctgtaatttcaatgtaattgtaattgtaattgtaattg 9553
OY 1561 gctgtgaactctcaatgtgtgcagcccaacatggaagcccaatggaagcccaatggaag 1620
Db 9554 gctgtgaactctcaatgtgtgcagcccaacatggaagcccaatggaagcccaatggaag 9613
OY 1621 tcttctctgagtgactcagaactatagccaaggtcctgttaccagcagaagcctctgc 1680
Db 9614 tcttctctgagtgactcagaactatagccaaggtcctgttaccagcagaagcctctgc 9673
OY 1681 gcttgaactcactc 1740
Db 9674 gcttgaactcactc 9733
OY 1741 gcttgaagaaggagagagcagcgtctcagaggtcctcactcactcactcactcactc 1800
Db 9734 gcttgaagaaggagagagcagcgtctcagaggtcctcactcactcactcactcactc 9793
OY 1801 cactcagaagacgcccagcagaggaatgccaattgtgcaacgaacactgactcctcc 1860
Db 9794 cactcagaagacgcccagcagaggaatgccaattgtgcaacgaacactgactcctcc 9853
OY 1861 tcaacctgaactctcccccctcactcactcactcactcactcactcactcactcactc 1920
Db 9854 tcaacctgaactctcccccctcactcactcactcactcactcactcactcactcactc 9913
OY 1921 cctccccaaccccgagcgttcccccagcagagcttccctccactcactcactcactcactc 1980
Db 9914 cctccccaaccccgagcgttcccccagcagagcttccctccactcactcactcactcactc 9973
OY 1981 tttctgtgagctgctctcactcactcactcactcactcactcactcactcactcactc 2040
Db 9974 tttctgtgagctgctctcactcactcactcactcactcactcactcactcactcactc 10033
OY 2041 ctgggagtgagagagcaggttcaagagtgactgctcagcactcagcactcagcactcagc 2100
Db 10034 ctgggagtgagagagcaggttcaagagtgactgctcagcactcagcactcagcactcagc 10093
OY 2101 gaaaggaacacacccctgagcagcagcctgtgctgccaagcagcagcagcagcagc 2160
Db 10094 gaaaggaacacacccctgagcagcagcctgtgctgccaagcagcagcagcagcagc 10153
OY 2161 g-----gacatgtacagagctcagagtaact----- 2187
Db 10154 ggggttggtgagacccgtcactcagaggttggtgagagctcttccactcagagatgtc 10213
OY 2188 ----- 2187
Db 10214 aacaacacatgctgcatctgacatccctcactcactcactcactcactcactcactc 2187
OY 2188 ----- 2187
Db 10274 gaggcttaacccgccttactgctccgggagatagcaaaagtggggcgggcggagcgtgc 10333
OY 2210 ----- 2209
Db 10334 gggatgctgagcagcagcgcagcagcagcagcagcagcagcagcagcagcagcagc 10393
OY 2210 ----- 2209
Db 10394 gttggagactggtctccggggtgctgttaggacttccctcagcagcagcagcagcagc 2209
OY 2210 ----- 2209
Db 10454 ctggagagactgcttctcttggccttgatgcgaagtgtcgtatcccgctgaggagcggg 10513


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; SEQ ID NO 477
; LENGTH: 772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (593)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (594)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (704)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-211-364-477

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Query Match
Best Local Similarity 99.6%; Score 237.4; DB 6; Length 772;
Matches 238; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1924 ccccaaccggcggtcccccagaggtctctccatctctctgaccacgggctt 1983
Db 9 cgcacaaccggcggtcccccagaggtctctccatctctctgaccacgggctt 1983
QY 1984 tcgtgagctcgtctctgagtcgagtcgagtcgagtcgagtcgagtcgagtcg 2043
Db 69 tcgtgagctcgtctctgagtcgagtcgagtcgagtcgagtcgagtcgagtcg 128
QY 2044 gggagtgagggagggaggtttacagtgagtcgagtcgagtcgagtcgagtcg 2103
Db 129 gggagtgagggagggaggtttacagtgagtcgagtcgagtcgagtcgagtcg 2103
QY 2104 cggaaacacccctgagggcagccctgctgctgctgctgctgctgctgctg 188
Db 189 cggaaacacccctgagggcagccctgctgctgctgctgctgctgctgctgctg 247

```

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RESULT 4
US-10-143-906-21
; Sequence 21, Application US/10143906
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P127001N
; CURRENT APPLICATION NUMBER: US/10/143,906
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (594)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (593)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (704)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-143-906-21

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Query Match
Best Local Similarity 99.6%; Score 237.4; DB 7; Length 772;
Matches 238; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Matches 238; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1924 ccccaaccggcggtcccccagaggtctctccatctctctgaccacgggctt 1983
Db 9 cgcacaaccggcggtcccccagaggtctctccatctctctgaccacgggctt 1983
QY 1984 tcgtgagctcgtctctgagtcgagtcgagtcgagtcgagtcgagtcgagtcg 2043
Db 69 tcgtgagctcgtctctgagtcgagtcgagtcgagtcgagtcgagtcgagtcg 128
QY 2044 gggagtgagggagggaggtttacagtgagtcgagtcgagtcgagtcgagtcg 2103
Db 129 gggagtgagggagggaggtttacagtgagtcgagtcgagtcgagtcgagtcg 2103
QY 2104 cggaaacacccctgagggcagccctgctgctgctgctgctgctgctgctg 188
Db 189 cggaaacacccctgagggcagccctgctgctgctgctgctgctgctgctgctg 247

```

```

RESULT 5
PCT-US02-10824-85
; Sequence 85, Application PC/TUS0210824
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Prostate Cancer Expression Profiles
; FILE REFERENCE: 9U 206 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/10824
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/281,732
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/281,731
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 85
; LENGTH: 2551
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-10824-85

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Query Match
Best Local Similarity 100.0%; Score 155; DB 1; Length 2551;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 2008 gaaagtgagacacacaggtgttcaagaagcgtctcgggagtgagggaggttaca 2067
Db 1 gaaagtgagacacacaggtgttcaagaagcgtctcgggagtgagggaggttaca 2067
QY 2068 gtgacttgctgagcctcagggcgggcgagtcgagtcgagtcgagtcgagtcg 2127
Db 61 gtgacttgctgagcctcagggcgggcgagtcgagtcgagtcgagtcgagtcg 2127
QY 2128 tggctgccagggcgagtcgctctctcctcccg 2162
Db 121 tggctgccagggcgagtcgctctctcctcccg 155

```

```

RESULT 6
PCT-US02-25766-9394
; Sequence 9394, Application PC/TUS0225766
; GENERAL INFORMATION:
; APPLICANT: GENE LOGIC, INC.
; APPLICANT: MUNGER, William E
; APPLICANT: FAULK, Ronald
; APPLICANT: SUN, Hongwei
; APPLICANT: SASAI, Hitoshi
; APPLICANT: WAGA, Iwao
; APPLICANT: YAMAMOTO, Jun
; TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
; FILE REFERENCE: 44921-5068-WO
; CURRENT APPLICATION NUMBER: PCT/US02/25766
; CURRENT FILING DATE: 2002-08-14

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PRIOR APPLICATION NUMBER: US 60/311,837
 PRIOR FILING DATE: 2001-08-14
 NUMBER OF SEQ ID NOS: 13946
 SOFTWARE: Patentln Ver. 2.1
 SEQ ID NO 9394
 LENGTH: 2551
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Genbank Accession No. X63717
 PCT-US02-25766-9394

Query Match 5.5%; Score 155; DB 1; Length 2551;
 Best Local Similarity 100.0%; Pred. No. 3.1e-23;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2008 gcaagagtgacacacaggtgttcaagaagcgttcttgaggagtgaggagcggtttacga 2067
 1 gcaagagtgacacacaggtgttcaagaagcgttcttgaggagtgaggagcggtttacga 60
 QY 2068 gtgacttgctggagagcctcgaaggcgagcactgagcaggaacacacccctgaagcgagccc 2127
 61 gtgacttgctggagagcctcgaaggcgagcactgagcaggaacacacccctgaagcgagccc 120
 DB 2128 tggctgccagcgagcgagctgctcttctccgcgg 2162
 121 tggctgccagcgagcgagctgctcttctccgcgg 155

RESULT 7
 US-10-035-832-1263
 Sequence 1263, Application US/10035832
 GENERAL INFORMATION:
 APPLICANT: Morris, David
 APPLICANT: Engelhard, Eric
 TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
 FILE REFERENCE: A-71249/RMS/DCF
 CURRENT FILING DATE: 2002-07-22
 PRIOR APPLICATION NUMBER: US 09/747,377
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: US 09/798,586
 PRIOR FILING DATE: 2001-03-02
 NUMBER OF SEQ ID NOS: 1613
 SOFTWARE: Patentln Version 3.1
 SEQ ID NO 1263
 LENGTH: 2551
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-035-832-1263

Query Match 5.5%; Score 155; DB 6; Length 2551;
 Best Local Similarity 100.0%; Pred. No. 3.1e-23;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2008 gcaagagtgacacacaggtgttcaagaagcgttcttgaggagtgaggagcggtttacga 2067
 1 gcaagagtgacacacaggtgttcaagaagcgttcttgaggagtgaggagcggtttacga 60
 QY 2068 gtgacttgctggagagcctcgaaggcgagcactgagcaggaacacacccctgaagcgagccc 2127
 61 gtgacttgctggagagcctcgaaggcgagcactgagcaggaacacacccctgaagcgagccc 120
 DB 2128 tggctgccagcgagcgagctgctcttctccgcgg 2162
 121 tggctgccagcgagcgagctgctcttctccgcgg 155

RESULT 8
 US-10-007-926A-143
 Sequence 143, Application US/10007926A

GENERAL INFORMATION:
 APPLICANT: BERTUCCI, FRANCOIS
 APPLICANT: HOULGATTE, REMI
 APPLICANT: BIRNBAUM, DANIEL
 APPLICANT: NGUYEN, CATHERINE
 APPLICANT: VIENS, PATRICE
 APPLICANT: FERT, VINCENT
 TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
 FILE REFERENCE: 1546-R-00
 CURRENT APPLICATION NUMBER: US/10/007,926A
 CURRENT FILING DATE: 2001-12-07
 PRIOR APPLICATION NUMBER: 60/254,090
 PRIOR FILING DATE: 2000-12-08
 NUMBER OF SEQ ID NOS: 468
 SOFTWARE: Patentln Ver. 2.1
 SEQ ID NO 143
 LENGTH: 2551
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: tumor necrosis factor receptor superfamily,
 US-10-007-926A-143

Query Match 5.5%; Score 155; DB 7; Length 2551;
 Best Local Similarity 100.0%; Pred. No. 3.1e-23;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2008 gcaagagtgacacacaggtgttcaagaagcgttcttgaggagtgaggagcggtttacga 2067
 1 gcaagagtgacacacaggtgttcaagaagcgttcttgaggagtgaggagcggtttacga 60
 QY 2068 gtgacttgctggagagcctcgaaggcgagcactgagcaggaacacacccctgaagcgagccc 2127
 61 gtgacttgctggagagcctcgaaggcgagcactgagcaggaacacacccctgaagcgagccc 120
 DB 2128 tggctgccagcgagcgagctgctcttctccgcgg 2162
 121 tggctgccagcgagcgagctgctcttctccgcgg 155

RESULT 9
 US-09-053-375B-233
 Sequence 233, Application US/0905375B
 GENERAL INFORMATION:
 APPLICANT: Chenchik, Alex
 APPLICANT: Bibilashvili, Robert
 TITLE OF INVENTION: Nucleic Acid Arrays
 FILE REFERENCE: CLON-006
 CURRENT APPLICATION NUMBER: US/09/053,375B
 CURRENT FILING DATE: 1998-08-31
 NUMBER OF SEQ ID NOS: 1543
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 233
 LENGTH: 2534
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-053-375B-233

Query Match 4.6%; Score 129; DB 5; Length 2534;
 Best Local Similarity 100.0%; Pred. No. 1.1e-17;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2034 gacgctcttgaggagtgaggagcggtttacgaagtgacttgcttgagcctcgaagggcg 2093
 1 gacgctcttgaggagtgaggagcggtttacgaagtgacttgcttgagcctcgaagggcg 60
 QY 2094 ggcacttgacacggaacacacccctgaagcgagccttgctgcccagcgagcggtctctt 2153
 61 ggcacttgacacggaacacacccctgaagcgagccttgctgcccagcgagcggtctctt 120

QY 2154 ctccgcgcg 2162
Db 121 ctccgcgcg 129

RESULT 10

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US-10-035-832-1259
; Sequence 1259, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1259
; LENGTH: 55996
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (29253)..(29272)
; OTHER INFORMATION: "n" at positions 29253 thru 29272 can be any base
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (31023)..(31239)
; OTHER INFORMATION: "n" at positions 31023 thru 31239 can be any base
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (42691)..(42710)
; OTHER INFORMATION: "n" at positions 42691 thru 42710 can be any base
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (46987)..(47006)
; OTHER INFORMATION: "n" at positions 46987 thru 47006 can be any base
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (48271)..(48290)
; OTHER INFORMATION: "n" at positions 48271 thru 48290 can be any base
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (50692)..(50711)
; OTHER INFORMATION: "n" at positions 50692 thru 50711 can be any base
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (53136)..(53155)
; OTHER INFORMATION: "n" at positions 53136 thru 53155 can be any base
; NAME/KEY: misc-feature
; LOCATION: (55549)..(55568)
; OTHER INFORMATION: "n" at positions 55549 thru 55568 can be any base
US-10-035-832-1259
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Query Match 2.4%; Score 68.2; DB 6; Length 55996;
Best Local Similarity 63.6%; Pred. No. 0.00028;
Matches 152; Conservative 0; Mismatches 83; Indels 4; Gaps 3;

QY 1272 actaagagctatctacgttccaagcaatgacttgacttgaacagtgcttcaaca--gag 1329
Db 7739 actaagtgctactcttcttcaaaagaaagacttgacttgacttcaactag 7798
QY 1330 cagcaagaattcaagatttttttaagaagaatctggcgaagaataatgagtaacga 1389
Db 7799 cagtaagaagataagaatttttttaacgaagaatctgctcaggaataatccgtaacaa 7858

QY 1390 aggaaggaagtaattgtgaatttaataagctgggcatgagattggcctaagt 1449
Db 7859 aag-gaagaaagataatgctt-aacacagcagtgaggttcccttcaacgaat 7916
QY 1450 gtagcttgcttcccttggagaataaactcaagggccctcccttcaagacc 1508
Db 7917 agacttctcttttggatagattatcctgcatgctccctcaactcttccacc 7975

RESULT 11

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US-10-027-632-145670/c
; Sequence 145670, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145670
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-145670
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Query Match 2.2%; Score 60.8; DB 7; Length 816;
Best Local Similarity 69.2%; Pred. No. 0.0033;
Matches 83; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 697 ttttttatttaagacttcttcatcttggaatagttttagatttcaaaattgca 756
Db 307 tcttttttttaataatgctttttttagaacatttttgcctctacgaattattgca 248
QY 757 gagataacagagatgccatataccatccctccatccacttcttctgtctat 816
Db 247 AGCATGCTACAGAAATTCACATCTGCACACCGTTCCCTGTTTAAACATTTAT 188

RESULT 12

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US-10-113-872-796/c
; Sequence 796, Application US/10113872
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C19
; CURRENT APPLICATION NUMBER: US/10/113,872
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: FastSeq for Windows Version 4.0
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us-09-834-291-4.rtf

Page 8

Search completed: September 8, 2002, 01:14:46
Job time: 37364 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 14:51:47 ; Search time 8462.63 Seconds
(without alignments)
4508.751 Million cell updates/sec

Title: US-09-834-291-4
Perfect score: 2827
Sequence: 1 tggagactctcagaatgataatg.....tgcctatcaaaagagacgtg 2827

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vitl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465.4	16.5	467	9	AA704610 z1j19h02.s
2	438.4	15.5	793	10	BT763679 603049567
3	298.4	10.5	603	9	AA058563 z1f53b04.s
4	294.4	10.4	577	9	AA056275 z1f53b03.s
5	286.4	10.1	442	9	AA011028 z1f49e11.s
6	286.4	10.1	547	9	AA047220 z1f49e11.s
7	285.4	10.1	447	9	AA057418 z1f59h03.s
8	276.4	9.8	467	9	AA020992 z1f59h03.s
9	270	9.6	376	10	AA020992 z1f59h03.s
10	259	9.2	388	10	H86126
11	254.4	9.0	287	9	AA018441
12	253.6	9.0	381	10	H86544
13	197	7.0	419	10	R85827
14	185.2	6.6	696	9	AV715411
15	181.8	5.7	429	9	BI838027
16	161	5.2	1339	10	AM239285
17	145.6				BG288747

18	124.2	4.4	300	9	AN100132
19	117	4.1	932	9	AL542093
20	105.4	3.7	1052	10	BM455788
21	96	3.4	283	10	BM090262
22	85	3.0	899	9	AL540709
23	80.4	2.8	1101	12	CNS00396
24	72	2.5	506	10	BG659530
25	67	2.4	1101	12	CNS00396
26	65	2.3	286	10	BI029879
27	64.6	2.3	343	10	BI045052
28	64.6	2.3	343	10	BI045083
29	64	2.3	169	10	BG998195
30	64	2.3	205	10	BG997854
31	64	2.3	267	10	BG961378
32	63.8	2.2	306	9	AA668797
33	63.6	2.2	316	10	BI004597
34	63.6	2.2	549	9	AA521324
35	63.6	2.2	583	9	AA521406
36	63.6	2.2	280	10	BG998167
37	63.4	2.2	1101	12	CNS0182P
38	63.2	2.2	275	10	BI005814
39	63	2.2	276	10	BG015436
40	63	2.2	279	10	BG978282
41	63	2.2	287	10	BF759346
42	63	2.2	319	10	BI028532
43	63	2.2	1201	12	CNS0165X
44	63	2.2	987	12	CNS01671
45	62.8	2.2			

ALIGNMENTS

RESULT 1
AA704610 467 bp mRNA linear EST 24-DEC-1997
z1j19h02.s1 Soares fetal_liver.spleen_JNF15.S1 Homo sapiens cDNA
DEFINITION
LOCUS
ACCESSION
AA704610.1 GI:2714528
VERSION
AA704610.1
KEYWORDS
SOURCE
Homo sapiens
ORGANISM
human.
REFERENCE
1 (bases 1 to 467)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenger, K., Steptoe, M., Tan, F., Theisling, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 459.

FEATURES

source
1. 467
/organism="Homo sapiens"
/db_xref="GDB:138712"
/db_xref="taxon:9606"
/clone="IMAGE:450771"
/clone_lib="Soares_fetal_liver_spleen_JNF15.S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and spleen; Vector: pT73D (Pharmacia)

Query Match	10.1%;	Score 286.4;	DB 9;	Length 442
Best Local Similarity	99.08;	Pred. No. 1.1e-41;		

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/organism="Homo sapiens"
/db_xref="GDB:128857"
/db_xref="taxon:9606"
/clone="IMAGE:380300"
/clone_lib="Scares retina N2b4HR"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pRT33 (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

```

strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCGAAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 131 a 128 c 125 g 158 t 5 others
 ORIGIN
 Query Match 10.1%; Score 286.4; DB 9; Length 547;
 Best Local Similarity 99.3%; Pred. No. 1.1e-41; Indels 1; Gaps 1;
 Matches 298; Conservative 0; Mismatches 1;

QY 2528 gtccacagaaagaaacgtcctgtctccctccgggaattctctttaagactga 2587
 1 gtccacagaaagaaacgtcctgtctccctccgggaattctctttaagactga 60
 QY 2588 agtcgctgctagtggttctatctgtttcttctccctctctctctctt 2647
 61 agtcgctgctagtggttctatctgtttcttctccctctctctctctt 120
 DB 2648 cccttctctagctgacccctcctcctcctcctcctcctcctcctc 2707
 121 cctctctctagctgacccctcctcctcctcctcctcctcctcctc 2767
 QY 2708 tactcgtctccacgcagcagaaacccggcgctattttgccaagaacttgagcagc 2767
 181 tactcgtctccacgcagcagaaacccggcgctattttgccaagaacttgagcagc 240
 DB 2768 gtttgaagaatcctcgtcagaaatgcagcttgc-agatgctatcaagaagacgt 2826
 241 gtttgaagaatcctcgtcagaaatgcagcttgc-agatgctatcaagaagacgt 300

RESULT 7 447 bp mRNA linear EST 18-SEP-1996
 AA057418
 LOCUS z559h03.s1 Soares retina N2b4HR Homo sapiens cDNA clone
 DEFINITION IMAGE:381269 3', mRNA sequence.

ACCESSION AA057418.1 GI:1550059
 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 447)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)

TITLE JOURNAL
 COMMENT Contact: Wilson R.
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through INL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40M3 fwd. from Amersham
 High quality sequence stop: 339.
 Location/Qualifiers

FEATURES
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 /db_xref="GDB:1289526"

/db_xref="taxon:9606"
 /clone="IMAGE:381269"
 /clone_1b="Soares retina N2b4HR"
 /sex="male"
 /tissue_type="retina"
 /dev_stage="55 year old"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: eye; Vector: pRT73 (pharmacia) with a modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCGAAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 95 a 109 c 107 g 133 t 3 others
 ORIGIN
 Query Match 10.1%; Score 285.4; DB 9; Length 447;
 Best Local Similarity 98.7%; Pred. No. 1.7e-41; Indels 3; Gaps 1;
 Matches 297; Conservative 0; Mismatches 3;

QY 2528 gtccacagaaagaaacgtcctgtctccctccgggaattctctttaagactga 2587
 1 gtccacagaaagaaacgtcctgtctccctccgggaattctctttaagactga 60
 QY 2588 agtcgctgctagtggttctatctgtttcttctccctctctctctctt 2647
 61 agtcgctgctagtggttctatctgtttcttctccctctctctctctt 120
 DB 2648 cccttctctagctgacccctcctcctcctcctcctcctcctcctc 2706
 121 ccttctctagctgacccctcctcctcctcctcctcctcctcctc 2766
 QY 2707 gtactgctccacgcagcagaaacccggcgctattttgccaagaacttgagcagc 2766
 181 gtactgctccacgcagcagaaacccggcgctattttgccaagaacttgagcagc 240
 DB 2767 gtttgaagaatcctcgtcagaaatgcagcttgc-agatgctatcaagaagacgt 2826
 241 gtttgaagaatcctcgtcagaaatgcagcttgc-agatgctatcaagaagacgt 300

RESULT 8 467 bp mRNA linear EST 30-JAN-1997
 AA020992
 LOCUS z65f07.s1 Soares retina N2b4HR Homo sapiens cDNA clone
 DEFINITION IMAGE:363877 3' similar to contains Alu repetitive element; mRNA sequence.

ACCESSION AA020992.1 GI:1484745
 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 467)
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Marra, M., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.

male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH-MGC Library."

BASE COUNT 253 a 181 c 194 g 200 t

ORIGIN

Query Match Best Local Similarity 6.4%; Score 181.8; DB 10; Length 828; Matches 198; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2406 aataagtcagcaccgaagcagtggttaagccgagggctcggagaacgacaccccttct 2465
 Db 1 AATAAGTCAGCACCGAAGCAGTGTAAAGCCGAGGGCTCGGAGAGACGGACACCTTTCT 60
 QY 2466 ttcctgaaaaagtatatatggggctggaatgaagctctcggagcttgtaacgatttta 2525
 Db 61 TTCTCGAAAAAAGTTAAATGGGGCTGAATGAGCTTCTGGAGGCTGTGTACCGTTTATA 120
 QY 2526 ttgtcacacgaagaagaacatgctgtctccttcgggaattctctttaagactg 2585
 Db 121 TTGTCACACAGAAAGAAAGAACTGCTGTCTCCCTTCGGAATTCCTTTAAGACTG 180
 QY 2586 taagtcgctgcctgaagtggttcaatttgcttcttcgccc 2630
 Db 181 TTCTTACGCTGTGTGCTAGATTATGTCACAAAGGTAAATGCC 225

Search completed: September 7, 2002, 14:51:57
 Job time: 16216 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:26:54 ; Search time 12179.2 Seconds
(Without alignments)
4089.359 Million cell updates/sec

Title: US-09-834-291-3
Perfect score: 2380
Sequence: 1 agcttttttggtacattt.....tgctatcaagagacgctg 2380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Length DB ID

Description

1	2380	100.0	2380	6	AX026091	AX026091 Sequence
2	2380	100.0	2827	6	AX026092	AX026092 Sequence
3	1921.8	80.7	187313	9	AL157394	AL157394 Human DNA
4	1899.6	79.8	3212	6	AX026089	AX026089 Sequence
5	1715	72.1	2344	9	HSCD955FR	X87625 H.sapiens C
6	1713.4	72.0	2165	9	HUMFAS	D31968 Human DNA f
7	1701.4	71.5	1877	9	HSAPT1	X81335 H.sapiens A
8	1372.8	57.7	1608	6	AX347321	X82279 H.sapiens F
9	879.4	36.9	1608	6	AX347320	AX347320 Sequence
10	856.8	36.0	1608	6	AX347320	AX347320 Sequence
11	611.8	25.7	720	6	AX026090	AX026090 Sequence
12	259	10.9	398	11	G27038	G27038 SHGC-30908
13	245	10.3	2719	9	BC012479	BC012479 Homo sapi
14	216	9.1	702	9	HSN279011	AJ279011 Homo sapi
15	216	9.1	702	9	HSN279012	AJ279012 Homo sapi
16	216	9.1	702	9	HSN279013	AJ279013 Homo sapi
17	188.8	7.9	1728	4	BRU24240	U24240 Bos taurus
18	161	6.8	266	6	AX026120	AX026120 Sequence
19	161	6.8	266	6	HSN011034	AJ011034 Homo sapi
20	155	6.5	2551	6	AR143111	AR143111 Sequence
21	155	6.5	2551	6	HSAP01	X63717 H.sapiens m
22	129	5.4	2471	6	I58632	I58632 Sequence 18
23	129	5.4	2471	6	I63530	I63530 Sequence 18
24	129	5.4	2534	6	A87646	A87646 Sequence 4
25	129	5.4	2534	6	AR163572	AR163572 Sequence
26	129	5.4	2534	6	AR173438	AR173438 Sequence
27	129	5.4	2534	6	E05110	E05110 cDNA encodi
28	129	5.4	2534	6	HUMFASNT	M67454 Human Fas a
29	129	5.4	2534	23	E09121	E09121 cDNA encodi
30	78.6	3.3	167564	2	AF267170	AF267170 Homo sapi
31	78.6	3.3	167919	2	AC090193	AC090193 Homo sapi
32	73.8	3.1	143584	2	AC008404	AC008404 Homo sapi
33	73.8	3.1	170261	2	AC008542	AC008542 Homo sapi
34	73.8	3.1	17387	9	AC090063	AC090063 Homo sapi
35	73.8	3.1	189076	2	AC023788	AC023788 Homo sapi
36	71.8	3.0	7218	6	I66494	I66494 Sequence 14
37	69.8	2.9	62999	2	AC087594	AC087594 Homo sapi
38	69.8	2.9	216571	9	AC009961	AC009961 Homo sapi
39	69.6	2.9	194183	2	AC026010	AC026010 Homo sapi
40	68.8	2.9	81117	9	AC016898	AC016898 Homo sapi
41	67.4	2.8	7218	6	I66494	I66494 Sequence 14
42	66.6	2.8	273413	2	AC079314	AC079314 Homo sapi
43	65.6	2.8	148069	9	AC006428	AC006428 Homo sapi
44	65.6	2.8	163951	2	AC091976	AC091976 Homo sapi
45	65	2.7	71112	2	AC102285	AC102285 Mus muscu

ALIGNMENTS

RESULT 1
AX026091 2380 bp DNA linear PAT 16-SEP-2000
LOCUS AX026091 Sequence 3 from Patent DE19847779.
DEFINITION AX026091
ACCESSION AX026091
VERSION AX026091.1 GI:10187522
KEYWORDS

SOURCE

ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

REFERENCE
1 (bases 1 to 2380)
Mueller-Schilling M., Krammer P. and Oren M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 3 03-FEB-2000;

JOURNAL

DEUTSCHES KREBSFORSCH (DE)
Location/Qualifiers
1. .2380
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 579 a 595 c 568 g 638 t
ORIGIN

Query Match 100.0%; Score 2380; DB 6; Length 2380;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 GCGTAAATAGATAGATATTAAGTAAGTAAGAGATCCACATATGTGAGTTGCTGGCTATATAT 120
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 Db 121 TCACACTCAAGAGATAGTGTATTTGTCTAATTTGCTTCCCTTTTCTCTCTCTCT 180
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 Db 181 CCTTCACATTCCT 240
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 Db 481 GTGCTAAGTGCAGTGAACAGATGCAAAACAGAGGTGATGAGAAAGCCCTCAGAGGGTAAAC 540
 QY 541 ctaaccagaatttgaagggcccaaacaggtctccagaagaanaatgtaacttgaaagaagcc 600
 Db 541 CTAACTCAGATTTGAGGGCCCAACAGGCTCCAGAGAAATGTCACTGAGAGAGAGCC 600
 QY 601 tgaaggaatgaacagtggtggaagaaggtatataatgtttatataatggttgaatct 660
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 QY 661 aattgggaagggagagaaggttgcagaagtgaagtgacagagcttggtggaagtgccaaagg 720
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 QY 1921 agatatgtctatatttctggcaggtctcgaagcgtaggaatlaagtcagacgaagcagt 1980
 Db 1921 AGATATGTCTATTTTTCGGAGTTCTCAGAGTGAAGAAATTAATGACGAGCAAGCAAGT 1980
 QY 1981 gtttaagccggaaggtctcgaagaagtgacacttcttctcgaagaagttatattgaggg 2040
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 QY 2041 gctgaaatgagcttctgagagcttggttaccgttttctatgttcaacagagaagaagaact 2100
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[illegible]

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OY	421	ggcactaac	agctct	ctctct	aaag	gttg	aaacaga	gaacg	ctctac	acactca	aagctg	480	
Db	868	ggcactaac	agctct	ctctct	aaag	gttg	aaacaga	gaacg	ctctac	acactca	aagctg	480	
OY	481	gtgtgaag	tgtag	ctacag	atg	caaa	caag	gtgtga	tgaaag	ccctca	agaggttaac	540	
Db	928	gtgtgaag	tgtag	ctacag	atg	caaa	caag	gtgtga	tgaaag	ccctca	agaggttaac	540	
OY	541	ctaacc	tagat	ttgag	ggccca	aacg	gctcc	gaag	aaatg	tcac	ttgag	ggagacc	600
Db	988	ctaacct	agattg	agggcc	cccaaac	agcctc	ccga	aaamaa	ttctca	acttg	agaggaagcc	1047	
OY	601	tgaagatga	acag	ttgg	gtc	taag	caaa	aggtt	ta	ta	gtgtat	ta	660
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Db	1108	aattggga	gaagggag	aggttgc	agag	tgtag	gtgc	agag	ttgtg	tgacatgc	720		
OY	721	aatatga	aaac	ctttag	ttgtc	tcag	ctc	tgna	actg	atcc	aaat	taag	780
Db	1168	aatatga	aaac	ctttag	ttgtc	tcag	ctc	tgna	actg	atcc	aaat	taag	780
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OY	961	gaatgt	ttat	at	atag	cttgg	gtg	atg	atg	atg	atg	atg	1020
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OY	1021	ttgaga	ataa	aa	actta	ag	ggcc	ctcc	ctt	ca	gag	cc	1080
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OY	1081	ttttcata	tg	ttta	ctt	atg	cttcc	ag	aa	gctt	g	ag	1140
Db	1528	ttttcata	tg	ttta	ctt	atg	cttcc	ag	aa	gctt	g	ag	1140
OY	1141	caacat	gga	ca	gccc	ag	ta	aa	atg	ccc	cg	aa	1200
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OY	1201	gcca	aggt	ctc	gt	tacc	ccg	gg	ag	gc	ctt	g	1260
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QY 1888 gggggcggggagagagcgt 1947
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QY	1948	cagacgtagaataaagtcagcagccggaagcagtggttaagccggaagcgcggaagaa	2007
Db	144756	CAGACGTAGAATAAAGTCACACACGGAAGCAGTGGTTAAGCCGGAGGCGTCGGAAGAACG	144815
QY	2008	gcacgtttctcttcgcgaagaattatataggggctgaatgaagcttcggaagcctgtt	2067
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QY	2068	accgtttctatctgcacacagaagaagaacgcgtctgtctccctccggaattctct	2127
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QY	2128	ctttaagacgtgaatgcgcgtgcgtgcgtgagttcatttctgttttcttccctct	2187
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QY	2248	ctggaggttggtgtaactcgttccacacagaaacccgagccctattcttgccaagaa	2307
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QY	2368	tcaagaagagctg 2380	
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DEFINITION	Sequence 1 from Patent DE19847779.	DNA	linear
ACCESSION	AX026089		
VERSION	AX026089.1		
KEYWORDS	GI:10187520		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Mueller-Schilling, M., Kramer, P. and Oren, M.		
JOURNAL	Novel Receptor dna useful for identifying apoptosis-modulating		
FEATURES	substances potentially useful for cancer chemotherapy		
DEUTSCHES	KREBSFORSCH (DE)		
LOCATION/Qualifiers	1..3212		
BASE COUNT	778 a 784 c 809 g 841 t		
ORIGIN	778 a 784 c 809 g 841 t		
Query Match	79.8%; Score 1899.6; DB 6; Length 3212;		
Best Local Similarity	84.9%; Pred. No. 0;		
Matches 2348; Conservative	0; Mismatches 24; Indels 394; Gaps 4;		
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QY	61	ggctataaagataagtaagtaaggaagatcacatctgtaagctgctgcttaaat	120
Db	508	GGCTTAATAGATTAAGTAAGTAAGGAAGATCACATATGAGTGTGCTGGTTATAT	567
QY	121	tcaacctaagaagataagcttgcaatctgcttccctctctctctctcct	180
Db	568	TCACACTCAAGATATGATTTGTCAATGTCTTCCCTTTTCTCTCTCTCTCT	627
QY	181	cttccattctctctctcccttaacctctctctctctctccctcacaccccttctct	240
Db	628	CTTCCATCT	687
QY	241	cttcttaccatttttatttaataagaaacttctctcttctggaatagtttaagattca	300
Db	688	CTTTTACATTTTATTTAATGAAGACTTTCATTTTGAATAGTTTGAATTTCAAA	747
QY	301	aaatttcagagataaataagagaatgccaatataccatccctcttaccatctct	360
Db	748	AAATTTCAAGATTAATACAGAGATGCCATATACATCTCTCTCTCTCTCTCT	807
QY	361	tgtctctattagatgctcagaagtgctgcaagagcgtcggagccgaagctctctcat	420
Db	808	TGTGTATATAGATGCTCAGAGTGTGTGCACAGAGCTGGGACGCCAGGCTTCTCT	867
QY	421	ggcactaagctctactgaagtggaagagagacacacacacacacacacacacac	480
Db	868	GGCCTTACAGTCTACTGAAAGGTGGAACAGACAGACAGCTATACACACTTACAG	927
QY	481	gtgtaagtgagtgacagatgcaaaacacaggtgagtaagagccctcagaaggtaac	540
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QY	541	ctaacctagatttgagggcccaacagcctccagaagaagaatgtaactgagagagac	600
Db	988	CTAAGCTGATTTGAGGGGCC-ACAGGCTCCAGAAAGAAATGTCACTGAGAGAAC	1046
QY	601	tgaagatgaaacagtgaggctgaagcaaggttattatggtttattaaagggtgaact	660
Db	1047	TGAAGATGAAACAGTGGCTTAAGCAAGAGCTTATTAATGTGTATTAATGAGTGA	1106
QY	661	aattgggaaggaagaggttgcaagtgagtgagagcttggtgagagcttggaagag	720
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QY	781	atgcatatccaaatacctctctgttaaaatcaatcaatcaatcaatcaatcaatca	840
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Db	1467	TTGAGAAATTAATAAGGGGCTCTCTTTTCAAGAGCTTATGCGCAACATCTGTAC	1526
QY	1081	tttttctatggttaactgtcattccaggaagctgtgtgaagctctcatggtgagcca	1140
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QY	1141	caacatggaagccagctcaaatgcccgaagctctctctctgagtgactcagaacatta	1200
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QY 1621 gtgacttggttgagctgagcctgagggcgagcctgacacgagacacccctgagcgagcc 1680
DB 1622 GTGACTTGGCTGGAGCCTCAGGGCGGCGGACCTGCAGACACCCCTGAGCCGACGCC 1681
QY 1681 tggctgcccagagcgagcgtcctctctcccgag 1715
DB 1682 TGGCTGCCCCAGCGGAGCTGCTCTCTCTCCCGG 1716

RESULT 7
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LOCUS HSAPT1
DEFINITION H.sapiens APT gene, exon 1.
ACCESSION X81335
VERSION X81335.1 GI:537410
KEYWORDS APO-1 gene; apt gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1877)
AUTHORS Behnman, I., Walczak, H. and Kramer, P. H.
JOURNAL Eur. J. Immunol. 24 (12), 3057-3062 (1994)
MEDLINE 95104292
REFERENCE 2 (bases 1 to 1877)
AUTHORS Kramer, P. H.
JOURNAL Submitted (03-SEP-1994) P. H. Kramer, German Cancer Research
Center, Tumor Immunology Program, Im Neuenheimer Feld 280, 69120
Heidelberg, FRG

FEATURES
Source Location/Qualifiers
1. 1877
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QY 61 ggcataatgataagtaagtaagaagatcacacatgtaagtgctgctataat 120
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QY 121 tcaacacaaagatactgatttgcataatgcttccctccctcagaccccttccctc 180
DB 122 TCACACTCAAGATATGATGATTTGTCATTTGCTTCCCTTTTCTCTCTCCCT 181
QY 181 ccttcatcctcttccctcctacccctccttccctcctcctcagaccccttccctc 240
DB 182 CCTTCATTCCTCTTCCCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241
QY 241 cctttacatttttttttttttttttttttttttttttttttttttttttttt 300
DB 242 CTTTTCATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 301
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Db 302 AANPTGACAGATATATACAGAGATGCCATATACCATCCCTCCCTTCCACTTCTTT 361
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 Oy 421 ggccttaacagctcactggaaggtggaacagagaagcctatacaacactacaagctg 480
 Db 422 GGCCTTACAGTCTACTGGAAGGTGGAACAGAGACCAAGCCTATCACCTAC-AGACTG 480
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 Db 601 TGAAGGATGAACAGTGGGCTAAAGCAAGGCTTATATATGTTATTAATGGGTTGAATCT 660
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RESULT 8
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 LOCUS H.sapiens Fas, Apo-1 gene (promoter and exon 1).
 DEFINITION X82279.
 ACCESSION X82279.
 VERSION X82279.1 GI:673405
 KEYWORDS APO-1 gene; Fas gene.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS Cheng, J., Liu, C., Koopman, W.J. and Mountz, J.D.
 TITLE Characterization of human Fas gene. Exon/Intron organization and promoter region
 JOURNAL J. Immunol. 154 (3), 1239-1245 (1995)
 MEDLINE 95123075
 REFERENCE 2 (bases 1 to 1608)
 AUTHORS Cheng, J.
 TITLE Direct Submission
 JOURNAL Submitted (20-OCT-1994) J. Cheng, Univ. of Alabama at Birmingham, Birmingham, AL 35294-0007, USA
 COMMENT
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 location/Qualifiers
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 BASE COUNT 398 a 421 c 423 g 366 t
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 Best local Similarity 99.4%; Pred No. 0;
 Matches 1388; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Oy 320 agagaaatgcccataatcactccttccatccactcttctgtgtctatgagatgca 379
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 Oy 380 gagtgtgtgcaagaagcttgcaagccagaggtcttctcaatgcaactaagactactga 439
 Db 67 GAGTGTGTGCAACAGGCTGACAGCCCAAGGCTCTCTCTCATGACACTAAGTCTACTGA 126

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QY 440 aagtgagacagagacagacccatcacacaccctacagactggtgtaagtgcagtgacag 439
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Db 187 ATGCAAAACAGAGGTGATGGAAGCCCTCAGAGAGGTAACTTAACCTAAGATTGAGGGC 246
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Db 487 CTTTCTGTAATAATCTCTGCTTAACCTTAAGAGCTATCTACCGTTCCAAAGCAATAGTG 546
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Db 1206 CTGACACACCGGGGCTTTTCGTGAGCTGCTCTCTATCTCCGGCAAGAGTGCACACAGT 1265
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RESULT 9
AX347321/c 1608 bp DNA linear PAT 01-FEB-2002
LOCUS AX347321/c
DEFINITION Sequence 2392 from Patent WO0200928.
ACCESSION AX347321
VERSION AX347321.1 GI:18495209
KEYWORDS
SOURCE
ORGANISM synthetic construct.
artificial construct.
REFERENCE
1 (sites)
AUTHORS Olek A., Piepenbrock, C. and Berlin K.
TITLE Diagnosis of diseases associated with the immune system
JOURNAL Patent: WO 0200928-A 2392 03-JAN-2002;
Epigenomics AG (DE)
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source Location/Qualifiers
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/note="chemically treated genomic DNA (Homo sapiens)"
BASE COUNT 366 a 51 c 421 g 770 t
ORIGIN

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Best Local Similarity 77.1%; Pred. No. 1,1e-216;
Matches 1083; Conservative 0; Mismatches 321; Indels 1; Gaps 1;
QY 320 agagaatgcccataaccatccctccctatccactcttctgctatagatgctca 379
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QY 560 ccaaacagagctccagaagaanaatgtcaactgagaagagcctgaagagatggaacagtgagc 619
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RESULT 11	AX026090	720 bp	DNA	linear	PAT 16-SEP-2000			
	AX026090	Sequence 2 from Patent DE1984779.						
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	AX026090.1	GI:10187521						
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		Homo sapiens						
		Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
		1 (bases 1 to 720)						
		Mueller-Schilling,M., Krammer,P. and Oren,M.						
		Novel receptor dna useful for identifying apoptotic-modulating						
		substances potentially useful for cancer chemotherapy						
		PATENT: DE 1984779-C 2 03-FEB-2000;						
		DEUTSCHES KREBSFORSCH (DE)						
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142 a 181 c 216 g 181 t
ORIGIN
BASE COUNT
Query Match 25.7% Score 611.8 DB 6 Length 720

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QY	1826	gacctcaagaagccaagccaaggtccgctccggcgcggtgagtgaatgcgcgcgcc	1885	
Db	166	GGCCTACAAAGCCAAAGCCAAAGGTCGCTCGGGCGGGTGGGAGAGTGGCGCGGCC	225	
QY	1886	gcgggggcggggagagagagcctgcagccttcagaacagatattgtcaattcttcggagtt	1945	
Db	225	GGGGGGGCGCGGAGAGAGCCTTACAGCCTTCAGAACATATGTCTCATTTTCTTGCGATT	285	
QY	1946	ctcagaacgtaggaataaataatcagcaccggaagcagtggttaagccggaaggctcggaa	2005	
Db	286	CTCAGACGTAGGAATAATTAATGACACCGAAGCAGTGGTTAAGCCGGAGGCGCTCGAAGAA	345	
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Db	406	TTAOCGTTTTTATTTGTCACACAGAAAAGAAATGCCCTTGCTCCCTTCGGGAATTC	465	
QY	2126	ctctttaaagactgtaagtcgctgcctgcagtgagtttcaattcttctgtcttcctgcctt	2185	
Db	466	CTCTTTAAGACTGTAAAGTCGCTGCCTGAGTGGTTTCATTGTTTGTGTTTCTTGCCCTT	525	
QY	2186	ctcttctctctcttgcccttctctactgaacttgtaactccaatggtgatctctgtgtctcc	2245	
Db	526	CTCTTTCTCTTTTGCCCTTCTTACGCTTCACTCCACTCCATGGGATTCGTGCTGGCTCC	585	
QY	2246	tgctggaggttggtgtgtaactcgttccacgcgacagaaacccggcgactaatctggcgaag	2305	
Db	586	TGCTGGGGTGGTGGTACTCGTTCCACCGCACAGAAACCGGCGCCTTATTTATGGCCAA	645	
QY	2306	aaacttgaagacgcgtcttgaagaatccctcgtctcgaagaatgcagcttgcagatgct	2365	
Db	646	AAACTTGAGACGCCTGTTTGAAGAAGTCCCTCGCTCAGAAATGGCAGCTTCACATGGCT	705	
QY	2366	aatcaagaagagctg 2380		
Db	706	AATCAAGAAGACGTG 720		

RESULT	12
LOCUS	G27038
DEFINITION	G27038 SHC-20908 Human Homo sapiens STS genomic, linear STS 30-MAR-2000
ACCESSION	G27038
VERSION	G27038.1
KEYWORDS	STS, sequence tagged site.
SOURCE	GI:1375288
ORGANISM	human.
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	1 (bases 1 to 398); Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Olivier, M. and Cox, D.R.
TITLE	Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL	Unpublished
COMMENT	

Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave., 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: oliviereshgc.stanford.edu
Primer A: GTCTCCCTCCGGCAATTC
Primer B: AACCCACGACAGAACCCCA


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Db      181  CTGGCAGGAGACACACCTGAGCCGCTGGCTGCCAGCGAGCTGCTCTTCTCC 240
QY      1711  cgcgg 1715
Db      241  CGCGG 245

RESULT 14
LOCUS   HSA279011
DEFINITION Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas), exon 1
ACCESSION AJ279011 GI:13539238
VERSION   Apo-1 Fas; CD95 antigen; CD95 gene.
KEYWORDS  human.
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 702)
AUTHORS   Muschen,M., Re,D., Jungnickel,B., Diehl,V., Rajewsky,K. and
          Kuppers,R.
TITLE     Somatic mutations of the CD95 gene in human B cells as a
          side-effect of the germinal center reaction
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 702)
AUTHORS   Muschen,M., Re,D., Brauningner,A., Wolf,J., Hansmann,M.L., Diehl,V.,
          Kuppers,R. and Rajewsky,K.
TITLE     Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
          cells
JOURNAL   Unpublished
REFERENCE 3 (bases 1 to 702)
AUTHORS   Muschen,M.
TITLE     Direct Submission
JOURNAL   Submitted (19-SEP-2000) Muschen M., Department of Immunology,
          Institute for Genetics, LFI E4 R705, Joseph-Steitzmann-Str. 9, 50931
          Koeln, GERMANY
COMMENT   Related sequences: D31968 X89101 AJ279012 AJ279013.
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                    /protein_id="CAC35539.1"
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BASE COUNT 107 a 198 c 264 g 133 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7e-45;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      1500  gagctctctccatcctctgaccacggggtcttcgtgagctcgtctgattcgc 1559
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Db      1560  cgcgaagtgacacacaggtgttcaaaagccttccttgaggatgaggagcggttacg 1619
QY      61  CGCAAGAGTGACACACAGGTTCTCAAGAGCGCTTCGGGAGTGAGGAAACGGGTTACG 120
Db      1620  agtgaacttgctgagagcctcgaaggcggcgaactgtgacgaacacaccctgagcgacc 1679
QY      121  AGTGACTTGCTGGAGACCTTCAGAGCGGGGACATGGACGGAACACACCTTGAGGCCAGCC 180
Db      1680  ctgagctgccagcgagagctctctctcccgagg 1715
QY      181  CTGGCTGCCAGGCGGAGCTGCTTTCGCCGG 216

RESULT 15
LOCUS   HSA279012
DEFINITION Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas), exon 1, polymorphic allele (+275).
ACCESSION AJ279012 GI:13539240
VERSION   Apo-1 Fas; CD95 antigen; CD95 gene.
KEYWORDS  human.
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 702)
AUTHORS   Muschen,M., Re,D., Jungnickel,B., Diehl,V., Rajewsky,K. and
          Kuppers,R.
TITLE     Somatic mutations of the CD95 gene in human B cells as a
          side-effect of the germinal center reaction
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 702)
AUTHORS   Muschen,M., Re,D., Brauningner,A., Wolf,J., Hansmann,M.L., Diehl,V.,
          Kuppers,R. and Rajewsky,K.
TITLE     Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
          cells
JOURNAL   Unpublished
REFERENCE 3 (bases 1 to 702)
AUTHORS   Muschen,M.
TITLE     Direct Submission
JOURNAL   Submitted (19-SEP-2000) Muschen M., Department of Immunology,
          Institute for Genetics, LFI E4 R705, Joseph-Steitzmann-Str. 9, 50931
          Koeln, GERMANY
COMMENT   Related sequences: D31968 X89101 AJ279011 AJ279013.
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                    /number=1
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                    /translation="MGIWTLPLV"
                    314..>702

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/number=1
BASE COUNT 107 a 197 c 264 g 134 t
ORIGIN

Query Match 9.1%; Score 216; DB 9; Length 702;
Best Local Similarity 100.0%; Pred. No. 7e-45; Indels 0; Gaps 0;
Matches 216; Conservative 0; Mismatches 0;

OY 1500 gaggtccttccatctctctgacacgaggttctgtagctcgtctctgacatcg 1559
|||
Db 1 GAGGCTTCCTCCATCTCTCTGACACCGGGGCTTTCGTGAGCTCTCTCTGATCTCG 60
|||
OY 1560 cgcagaagtgacacacaggtgttcaagaagctctctgaggaggaagcggttacg 1619
|||
Db 61 CGCAAGAGTGACACACAGGTGTTCAAAGACGCTCTGGGAGTGAGGAGGAGCGTTTACG 120
|||
OY 1620 agtgacttgctgaggtcagggcgagtgcaactgacgagacacacccctgagggcagcc 1679
|||
Db 121 AGTGACTTGGCTGGAGCTTCAGGGGGGCGGCACTGCGACGAGACACACCTGAGGCCAGCC 180
|||
OY 1680 ctggctgcccagcgagagctgctctctctcccgag 1715
|||
Db 181 CTGGCTGCCCAAGGCGAGCTGCTCTCTCCCGCG 216
|||

Search completed: September 7, 2002, 18:30:49
Job time: 29348 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:40:35; Search time 1139.19 Seconds
(without alignments)
3586.984 Million cell updates/sec

Title: US-09-834-291-3
Perfect score: 2380
Sequence: 1 agctatttggtacattt.....tggtacttaagaagagcgtg 2380

Scoring table: IDENTITY-NIC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N.GeneSeq_032802.*

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- 23: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1372.8	57.7	1608	17	Fas promoter regio
2	879.4	36.9	1608	24	Human immune syste
3	856.8	36.0	1608	24	Human immune syste
4	190.4	8.0	859	21	Human colon cancer
5	161	6.8	266	21	Human CD95 recepto
6	155	6.5	2551	21	DNA encoding a hum
7	129	5.4	2471	16	Fas-delta-TM cDNA
8	129	5.4	2471	20	Soluble Fas recept
9	129	5.4	2534	13	Human cell surface

10	129	5.4	2534	16	AAQ95297	Plasmid pF58 contg
11	129	5.4	2534	17	AA16303	hFas coding sequen
12	129	5.4	2534	19	AAV32933	Fas cDNA. Mammali
13	127.4	5.4	2534	18	AAV07002	Human Fas antigen
14	63.6	2.7	19307	17	AA175557	Shuttle vector pad
15	62.6	2.6	9972	17	AA175557	Shuttle vector pad
16	60	2.5	2435	19	AA168854	Human lung tumour
17	59.8	2.5	35100	22	AA168854	Human lung tumour
18	59.8	2.5	38258	24	AA168854	Human lung tumour
19	59.2	2.5	8888	20	AA168854	Human lung tumour
20	56.2	2.4	36901	20	AA168854	Human lung tumour
21	56.2	2.4	38886	20	AA168854	Human lung tumour
22	54.6	2.3	13545	22	AA168854	Human lung tumour
23	54.6	2.3	6172	24	AA168854	Human lung tumour
24	54.4	2.3	8342	24	AA168854	Human lung tumour
25	54.2	2.3	404	22	AA168854	Human lung tumour
26	54	2.3	10640	21	AA168854	Human lung tumour
27	53.4	2.2	4406	22	AA168854	Human lung tumour
28	53.2	2.2	2467	22	AA168854	Human lung tumour
29	53	2.2	5893	24	AA168854	Human lung tumour
30	52.8	2.2	162450	21	AA168854	Human lung tumour
31	52.6	2.2	15484	22	AA168854	Human lung tumour
32	52.4	2.2	8622	22	AA168854	Human lung tumour
33	52	2.2	11960	22	AA168854	Human lung tumour
34	51.8	2.2	399	22	AA168854	Human lung tumour
35	51.8	2.2	20813	22	AA168854	Human lung tumour
36	51.6	2.2	556	20	AA168854	Human lung tumour
37	51.6	2.2	12404	22	AA168854	Human lung tumour
38	51.6	2.2	24259	22	AA168854	Human lung tumour
39	51.6	2.2	39380	22	AA168854	Human lung tumour
40	51.4	2.2	1734	22	AA168854	Human lung tumour
41	51.2	2.2	6519	22	AA168854	Human lung tumour
42	51.2	2.2	12669	24	AA168854	Human lung tumour
43	51.2	2.2	16854	22	AA168854	Human lung tumour
44	51	2.1	562	22	AA168854	Human lung tumour
45	51	2.1	562	22	AA168854	Human lung tumour

ALIGNMENTS

RESULT 1	AA163162	standard; DNA; 1608 BP.
XX	AA163162:	
XX	22-OCT-1996	(first entry)
XX	Fas promoter region.	
XX	Fas gene promoter; apoptosis; ageing; autoimmune disease;	
XX	T-cell senescence; ss.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	Promoter	1..1074
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XX	protein_bind	/note= "Fas gene promoter region"
XX	protein_bind	147..151
XX	protein_bind	/*tag= b
XX	protein_bind	/function= "GFI transcription factor binding site"
XX	protein_bind	168..174
XX	protein_bind	/*tag= c
XX	protein_bind	/function= "EBP20 transcription factor binding site"
XX	protein_bind	272..276
XX	protein_bind	/*tag= d
XX	protein_bind	/function= "Myb transcription factor binding site"
XX	protein_bind	/note= "G1ain 9"
XX	protein_bind	349..353
XX	protein_bind	/*tag= e

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 Qy 1520 ctgaccacgagcggtcttcgtgagctcgctctgctatctcgagagagatgacacaggt 1579
 Db 1206 ctgacacacgagcggtcttcgtgagctcgctctgctatctcgagagagatgacacaggt 1265
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RESULT 2
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 ID ABL34419 standard; DNA; 1608 BP.
 XX ABL34419;
 XX
 DT 26-MAR-2002 (first entry)
 DE Human immune system associated gene SEQ ID NO: 2392.
 XX Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antihaemic; cytosolic; neotropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antineoplastic; antiarthritic; antidiabetic; antipsoriatic;
 KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 KW gene; ds.
 XX Homo sapiens.
 OS
 PN NC0200200928-A2.
 XX
 PD 03-JAN-2002.
 PF 02-JUL-2001; 2001MO-EP07537.
 PR 30-JUN-2000; 2000DE-1032539.
 PR 01-SEP-2000; 2000DE-1043826.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 PL Olek A, Piepenbrock C, Berlin K;
 DR WPI: 2002-130909/17.
 XX
 PT Nucleic acid comprising fragment of chemically modified gene, useful
 PT for diagnosis and treatment of diseases associated with abnormal
 PT cytosine methylation -
 PS Claim 1; SEQ ID NO 2392; 32pp + Sequence Listing; German.
 XX
 CC The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention.
 CC
 XX Sequence 1608 BP; 366 A; 51 C; 421 G; 770 T; 0 other;

Query Match 36.9%; Score 879.4; DB 24; Length 1608;
 Best Local Similarity 77.1%; Pred. No. 2,7e-235;
 Matches 1083; Conservative 0; Mismatches 321; Indels 1; Gaps 1;

Qy 320 agagaatgcccatacatcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 379
 Db 1602 ACAAAATATACCTATATACCTATATACCTATATACCTATATACCTATATACCTAT 1543
 Qy 380 gagggtgagcagagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 439
 Db 1542 AAATATATATACCAATATATACCAATATATACCAATATATACCAATATATACCA 1483
 Qy 440 aagtgagcagagcagagcagagcagagcagagcagagcagagcagagcagagcagag 499
 Db 1482 AAAAT 1423
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 Db 1422 ATACAAAT 1363
 Qy 560 ccaaacagcctccag 619
 Db 1362 CCAAAAT 1303
 Qy 620 taagcag 679
 Db 1302 TAAAT 1243
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 Db 1182 TATCCTAT 1123
 Qy 800 cctctgtaaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 859
 Db 1122 CCTCTAT 1063
 Qy 860 acttgagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 919
 Db 1062 ACTTAAAT 1003
 Qy 920 ggcag 979
 Db 1002 AACCAAAAT 943
 Qy 980 ggcag 1039
 Db 942 AACCTAT 883
 Qy 1040 ggcag 1099
 Db 882 AAACCT 823
 Qy 1100 tccatccag 1159
 Db 822 TCCATCT 763
 Qy 1160 aatgcccag 1219
 Db 762 AAAT 703
 Qy 1220 ggcag 1279
 Db 702 AACCAAACT 643
 Qy 1280 gaactaag 1339
 Db 642 AAAT 583
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QY 1508	cttcaccatctctctgacacacgaggtcttcgtgagctcgtctgatatctcgcgcaag	1567	1567	1567	1567
DB 19	cgctccgccacgctcgcacgaggggtcttcgtgagctcgtctgatatctcgcgcaag	78	78	78	78
QY 1568	tgacaacacaggtgttcaaaagacgtctctgaggaggtgaggaacggtttacagagta	1627	1627	1627	1627
DB 79	tgacaacacaggtgttcaaaagacgtctctgaggaggtgaggaacggtttacagagta	138	138	138	138
QY 1628	ggctggagcctcaagggcgagcactggaacggaacacacccctgaagcgaacgctggtgc	1687	1687	1687	1687
DB 139	ggctggagcctcaagggcgagcactggaacggaacacacccctgaagcgaacgctggtgc	198	198	198	198
QY 1688	ccaggcgagctgcctcttctccgcgg	1715	1715	1715	1715
DB 199	ccaggcgagctgcctcttctccgcgg	226	226	226	226
RESULT 5					
AAZ88700	AAZ88700 standard; DNA; 266 BP.				
AC	AAZ88700;				
XX	11-MAY-2000 (first entry)				
DT					
XX					
DE	Human CD95 receptor intron 1 fragment.				
XX					
KW	p53; CD95 receptor; human; screening; apoptosis-modulation;				
XX	cancer chemotherapy; ss.				
OS	Homo sapiens.				
XX					
XX	Key	Location/Qualifiers			
FT	protein_bind	160..179			
FT		/tag=a			
FT		/bound_moiety=p53			
XX	DE1984779-C1.				
XX					
PN	03-FEB-2000.				
PD					
XX					
XX	16-OCT-1998;	98DE-1047779.			
PF					
XX	16-OCT-1998;	98DE-1047779.			
PR					

XX WPI: 1995-200120/26.
 DR P-PSDB; AAW76238.
 XX New nucleic acid encoding Fas protein without its trans-membrane region
 PT - and related vectors, transfected cells, transgenic animals, protein and
 PT antibodies, useful for control of Fas mediated apoptosis
 XX
 XX Claim 3; Fig.3-1 to 3-4; 38pp; English.
 PS
 CC mRNA was obtd. from human lymphocytes and PCR was used to make
 CC cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane
 CC region) mRNA. The PCR product was ligated into pBluescript and the
 CC recombinant plasmid was used to transfect E. coli DH5-alpha cells. The
 CC insert sequence of pBluescript-Fas-delta-TM is given in AAO93879.
 XX
 SQ Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;

Query Match 5.4%; Score 129; DB 16; Length 2471;
 Best Local Similarity 100.0%; Pred. No. 3.2e-25;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1587 gacgctctcggagagtgaggaagcgtttacagagtgacttgcttgagcctcagggcg 1646
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 gacgctctcggagagtgaggaagcgtttacagagtgacttgcttgagcctcagggcg 60

OY 1647 ggcactggcagcagacacacccctgagccagcctgtgctccagggagctgctctt 1706
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 DB 61 ggcactggcagcagacacacccctgagccagcctgtgctccagggagctgctctt 120

OY 1707 ctccgcgcg 1715
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 DB 121 ctccgcgcg 129

RESULT 8
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 ID AAX24878 standard; DNA: 2471 BP.

AC AAX24878;
 XX
 DT 21-JUN-1999 (first entry)

XX Soluble Fas receptor DNA.

DE Fas receptor; Fas ligand; FasL; proinflammatory; immunosuppressive;
 KW graft versus host disease; autoimmune disease; psoriasis;
 KW rheumatoid arthritis; systemic lupus erythematosus; gene therapy;
 SS.
 KW
 XX
 OS Mammalia.

XX Mammalia.

XX Key Location/Qualifiers

XX CDS 195..1139
 FT /*tag= a
 FT /transl_except= (pos:519..521, aa:Gly)

FT sig_peptide 195..242
 FT /*tag= b

FT mat_peptide 243..1136
 FT /*tag= C

FT polyA_signal 2349..2354
 FT /*tag= d

FT polyA_signal 2455..2460
 FT /*tag= e

XX W09903999-A1.

XX 28-JAN-1999.

XX 16-JUL-1998; 98WO-US14771.

XX 17-JUL-1997; 97US-0052829.

XX (UNMI) UNIV MICHIGAN.

XX Chen J, Nabel GJ;

XX WPI: 1999-132243/11.

XX P-PSDB; AAW98070.

PT Inhibition of proinflammatory responses - using an agent which
 PT modulates FasL stimulation, used for treating graft versus host
 PT disease or autoimmune disease

PS Disclosure: Fig 4B; 71pp; English.

XX This present sequence is a DNA clone encoding soluble Fas receptor
 CC (see AAW98070). The invention provides a method for inhibiting a
 CC proinflammatory response in a cell mixture by administering an
 CC immunosuppressive agent which inhibits the proinflammatory activity
 CC of Fas ligand (FasL). In some embodiments, FasL is coadministered
 CC with the immunosuppressive agent, and the cell mixture comprises
 CC neutrophil cells. The method can be practised in vitro, ex vivo or
 CC in vivo. Suitable immunosuppressive agents include antisense
 CC molecules that inhibit endogenous FasL expression, soluble Fas
 CC receptors, ribozymes that inhibit the endogenous expression of
 CC FasL, drugs that inhibit FasL signalling, agents that induce the
 CC endogenous expression of transforming growth factor (TGF)-beta,
 CC and polynucleotides coding for an immunosuppressive agent such as
 CC TGF-beta. The method can be used for treating diseases associated
 CC with an undesired FasL-mediated proinflammatory response, e.g.
 CC graft versus host disease, or an autoimmune disease such as
 CC systemic lupus erythematosus, rheumatoid arthritis and psoriasis.
 CC The invention also provides a method for identifying agents which
 CC modulate FasL stimulation of a proinflammatory response.

SQ Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;

Query Match 5.4%; Score 129; DB 20; Length 2471;
 Best Local Similarity 100.0%; Pred. No. 3.2e-25;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1587 gacgctctcggagagtgaggaagcgtttacagagtgacttgcttgagcctcagggcg 1646
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DB 1 gacgctctcggagagtgaggaagcgtttacagagtgacttgcttgagcctcagggcg 60

OY 1647 ggcactggcagcagacacacccctgagccagcctgtgctccagggagctgctctt 1706
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DB 61 ggcactggcagcagacacacccctgagccagcctgtgctccagggagctgctctt 120

OY 1707 ctccgcgcg 1715
 ||||||||

DB 121 ctccgcgcg 129

RESULT 9

AAQ29959
 ID AAQ29959 standard; cDNA to mRNA: 2534 BP.

XX AAQ29959;

XX 12-MAR-1993 (first entry)

XX Human cell surface antigen.

XX Fas antigen; apoptosis; pF58; NGFR/TNFR family; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX sig_peptide 195..242
 FT /*tag= a

FT mat_peptide 243..1139
 FT /*tag= b

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FT conflict /product= Fas_antigen
FT 1046 /tag= C
FT /note= "this residue is not present in pF3"
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FT polyA_signal /tag= d
FT polyA_signal 2352..2357
FT polyA_signal /tag= e
FT polyA_signal 2518..2523
FT /tag= f
FN EP510691-A.
XX 28-OCT-1992.
XX 24-APR-1992; 92EP-0107060.
XX 26-APR-1991; 91JP-0125234.
XX (OSAB-) OSAKA BIOSCIENCE INST.
XX PI Itoh N, Nagata S, Yonehara S;
XX WPI; 1992-356914/44.
XX P-PSDB; AAR28084.
XX DNA encoding human cell surface antigen - used to clarify
XX apoptosis mechanism of various types of cell, and to prepare
XX monoclonal antibodies that react with tumour cells expressing Fas
XX
XX Claim 3; Fig 1 and 2; 27pp; English.
XX
XX A cDNA library was prepared from polyA+ RNA from the human lymphoma
XX cell line KT-3. The cDNA was ligated to BstXI-cut vector pCEV4 via
XX BstXI linkers. The KT3 cDNA library was used to transfect monkey COS-
XX 7 cells which were then suspended in buffer containing murine anti-Fas
XX Ab. The cells were "panned" on plates pre-coated with goat anti-mouse
XX antibodies. The Fas-expressing cells adhered to the plates.
XX Extrachromosomal DNA was prepared from adhered cells and used to
XX transform E.coli VMI00 cells. A 520bp XhoI-BamHI fragment from a
XX positive clone (pF3) was used to screen the KT-3 cDNA library. The
XX longest cDNA clone was designated pF58 and contains an ORF corresp.
XX to a 335 amino acid pre-protein and a 319 amino acid mature protein
XX (i.e. human Fas antigen).
XX
XX Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
XX
XX Query Match 5.4%; Score 129; DB 13; Length 2534;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-25;
XX Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX QY 1647 ggcactgacgagcaacacaccttgagcgccactgctgctgccagggcgagctgctctt 1706
XX |||||||
XX Db 61 ggcactgacgagcaacacaccttgagcgccactgctgctgccagggcgagctgctctt 120
XX
XX QY 1707 ctcccgcg 1715
XX |||||||
XX Db 121 ctcccgcg 129
XX
XX RESULT 10
XX AAQ95297
XX ID AAQ95297 standard; cDNA; 2534 BP.
XX AC AAQ95297;
XX XX 19-FEB-1996 (first entry)
XX DT
XX XX

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DE Plasmid pF58 contg. human Fas cDNA.
XX
XX Plasmid pF58; human Fas cDNA; soluble membrane protein;
XX antibody production; diseases; treatment; prevention; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 195..1202
XX FT /tag= a
XX FT sig_peptide 195..242
XX FT /tag= b
XX FT mat_peptide 243..1199
XX FT /tag= c
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XX JP07115988-A.
XX
XX 09-MAY-1995.
XX
XX 26-OCT-1993; 93JP-0267644.
XX
XX 26-OCT-1993; 93JP-0267644.
XX
XX (NIBS) JAPAN TOBACCO INC.
XX
XX WPI; 1995-202847/27.
XX P-PSDB; AAR78606.
XX
XX Preparation of soluble membrane proteins - for their use in antibody
XX production for the treatment and prevention of related diseases
XX
XX Example 1; Pages 15-17; 51pp; Japanese.
XX
XX AAQ95297 is the plasmid pF58 which contains the human Fas cDNA. The
XX plasmid was used in the construction of an expression vector for
XX the prodn. of recombinant soluble membrane proteins. The proteins
XX can be used in antibody prodn. for the treatment and prevention of
XX related diseases.
XX
XX Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
XX
XX Query Match 5.4%; Score 129; DB 16; Length 2534;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-25;
XX Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX
XX QY 1647 ggcactgacgagcaacacaccttgagcgccactgctgctgccagggcgagctgctctt 1706
XX |||||||
XX Db 61 ggcactgacgagcaacacaccttgagcgccactgctgctgccagggcgagctgctctt 120
XX
XX QY 1707 ctcccgcg 1715
XX |||||||
XX Db 121 ctcccgcg 129
XX
XX RESULT 11
XX AAT16303
XX ID AAT16303 standard; cDNA; 2534 BP.
XX AC AAT16303;
XX XX 06-SEP-1996 (first entry)
XX DT
XX XX hFas coding sequence from plasmid pCEV4/hFas.
XX DE
XX XX Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
XX KW rheumatoid arthritis; serum; systemic lupus erythematosus; ss.
XX OS Synthetic.
XX

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:23:12 ; Search time 212.3 Seconds
(without alignments)
2753.687 Million cell updates/sec

Title: US-09-834-291-3
Perfect score: 2380
Sequence: 1 agcttttggctacattt.....tggctaataaagagagctg 2380

Scoring table:
IDENTITY-NUC
Gapop 10.0 , Gapect 1.0

Searched: 383533 seqs, 122816752 residues
Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA: *
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3: /cgn2_6/ptodata/2/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/Backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	155	6.5	2551	4	US-09-290-640-1
2	129	5.4	2471	1	US-08-444-231-18
3	129	5.4	2471	1	US-08-152-443A-18
4	129	5.4	2534	2	US-08-219-237B-1
5	129	5.4	2534	4	US-08-468-560C-1
6	129	5.4	2534	4	US-09-180-100-16
7	71.8	3.0	7218	1	US-08-232-463-14
8	67.4	2.8	7218	1	US-08-232-463-14
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13	62.6	2.6	4476	3	US-08-801-344-2
14	62.4	2.5	4476	4	US-09-488-599-2
15	59.8	2.5	35100	5	US-08-306-691B-19
16	59.8	2.5	35100	5	PCT-US93-06251-19
17	51.6	2.2	556	4	US-09-018-584A-25
18	50.8	2.1	370	2	US-08-332-766A-8
19	50	2.1	376	2	US-08-623-906A-18
20	49.8	2.1	5751	4	US-09-417-455-7
21	49.8	2.1	5751	4	US-09-348-942-7
22	49.2	2.1	361	4	US-09-018-584A-9
23	48.4	2.0	50	2	US-08-713-557B-35
24	48.4	2.0	15144	3	US-08-458-454A-6
25	48	2.0	421	1	US-08-480-784-24
26	48	2.0	421	1	US-08-483-553-24
27	48	2.0	421	1	US-08-487-002-24

28	48	2.0	421	1	US-08-483-554B-24	Sequence 24, Appl
29	48	2.0	421	1	US-08-488-011B-24	Sequence 24, Appl
30	48	2.0	421	1	US-08-850-727-24	Sequence 24, Appl
31	48	2.0	421	5	PCT-US95-10202-24	Sequence 24, Appl
32	48	2.0	421	5	PCT-US95-10203-24	Sequence 24, Appl
33	48	2.0	421	5	PCT-US95-10220-24	Sequence 24, Appl
34	47.6	2.0	421	5	US-08-332-766A-11	Sequence 11, Appl
35	47.4	2.0	1679	2	US-08-365-486A-11	Sequence 11, Appl
36	47.4	2.0	1679	4	US-08-880-342-11	Sequence 11, Appl
37	47.4	2.0	12141	4	US-09-488-671-10	Sequence 10, Appl
38	47.4	2.0	80246	4	US-09-078-294-3	Sequence 3, Appl1
39	47.4	2.0	80595	4	US-09-018-584A-8	Sequence 8, Appl1
40	47.2	2.0	235	2	US-08-332-766A-11	Sequence 11, Appl1
41	47.2	2.0	325	2	US-08-332-766A-26	Sequence 26, Appl1
42	47.2	2.0	446	2	US-08-332-766A-10	Sequence 10, Appl1
43	46.8	2.0	434	2	US-09-018-584A-19	Sequence 19, Appl1
44	46.6	2.0	444	4	US-08-623-906A-13	Sequence 13, Appl1
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ALIGNMENTS

RESULT 1
US-09-290-640-1
Sequence 1, Application US/09290640
Patent No. 6204055
GENERAL INFORMATION:
APPLICANT: Marcussen, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPP-0351
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2551
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (221)..(1228)
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 267
ISSUE: 15
PAGES: 10709-10715
DATE: 1992-05-25
DATABASE ACCESSION NUMBER: X63717/Genbank
DATABASE ENTRY DATE: 1996-07-19
US-09-290-640-1

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Best Local Similarity 100.0%: Pred. No. 1.5e-32:
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		US-08-444-231-18	

Sequence 18, Application US/08444231
Patent No. 5652210
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,231
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152,443
FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 195..1136
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243
US-08-444-231-18

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Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1707 ctcccgagg 1715
Db 121 CTCCTGGCGG 129

RESULT 3
US-08-152-443A-18
Sequence 18, Application US/08152443A
Patent No. 5663070
GENERAL INFORMATION:

APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,443A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 195..1136
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243
US-08-152-443A-18

Query Match 5.4%; Score 129; DB 1; Length 2471;
Best Local Similarity 100.0%; Pred. No. 1.9e-25;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1587 gacgcttcgagagtgagagagcggtttagagtgacttgctgagcctcagggcg 1646
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QY 1647 ggcactggcagcagacacacccctgagggccagcctgctgcccagggcagcctctt 1706
Db 61 GGCACTGGCAGCAGGAGACACCTTGAGGCCAGCCTGTGCTGCCAGGCGAGCTGCTCTT 120

QY 1707 ctcccgagg 1715
Db 121 CTCCTGGCGG 129

RESULT 4
US-08-219-237B-1
Sequence 1, Application US/08219237B
Patent No. 5874546
GENERAL INFORMATION:
APPLICANT: MAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 516762
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: pCEV4
CLONE: clone PF58
FEATURE:
NAME/KEY: CDS
LOCATION: 195..1202
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus

FEATURE:
NAME/KEY: sig_peptide
LOCATION: 195..242
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243..1199
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 1831..1836
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 2352..2357
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 2518..2523
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
US-08-219-237B-1

Query Match 5.4%; Score 129; DB 2; Length 2534;
Best Local Similarity 100.0%; Pred. No. 2e-25;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GACGCTTCGGGAGGTAGGGAACGGGTTTACAGTACTTGGCTGGAGCCTCAGGGGCG 60
QY 1647 gacactggcagcagacacacccctagcagccctgctgctgcccagggcgagctgctctt 1706
Db 61 GGACGTGGCAGCAACACACCCTTGAGCCAGCCCTGGCTGCCAGGGCAGACTGCTCTT 120
QY 1707 ctccgcgcg 1715
Db 121 CTCGCCGCG 129

RESULT 5
US-08-468-560C-1
Sequence 1, Application US/08468560C
Patent No. 6270998
GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,560C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20-4393P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 195..1202
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 195..242
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243..1199
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 1831..1836
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 2352..2357
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 2518..2532

RESULT 10
US-09-427-048A-10
; Sequence 10, Application US/09427048A
; Patent No. 6203975
GENERAL INFORMATION:
APPLICANT: Trustees of the University of Pennsylvania
Wilson, James M.
Fisher, Krishna J.
Chen, Shu-Jen
Weltzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
Methods of Use Thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/427,048A
FILING DATE: 21-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,022
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNPVN 008PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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Matches 93; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
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RESULT 11
US-08-836-022A-3/C
; Sequence 3, Application US/08836022A
; Patent No. 6001557
GENERAL INFORMATION:
APPLICANT: Trustees of the University of Pennsylvania
Wilson, James M.
Fisher, Krishna J.
Chen, Shu-Jen
Weltzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
Methods of Use Thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,022A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,381
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNPVN 008PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9972 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
US-08-836-022A-3
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Matches 92; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
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DB 2860 ttTACACGTCGTGACTGGGAA 2840

	NUMBER OF SEQUENCES:	10	
	CORRESPONDENCE ADDRESS:		
	ADDRESSEE: Howson and Howson		
	STREET: Spring House Corporate Cntr, P O Box 457		
	CITY: Spring House		
	STATE: Pennsylvania		
	COUNTRY: USA		
	ZIP: 19477		
	COMPUTER READABLE FORM:		
	MEDIUM TYPE: floppy disk		
	COMPUTER: IBM PC compatible		
	OPERATING SYSTEM: PC-DOS/MS-DOS		
	SOFTWARE: PatentIn Release #1.0, Version #1.30		
	CURRENT APPLICATION DATA:		
	APPLICATION NUMBER: US/09/427,048A		
	FILING DATE: 21-Oct-1999		
	CLASSIFICATION: <unknown>		
	PRIOR APPLICATION DATA:		
	APPLICATION NUMBER: 08/836,022		
	FILING DATE: <unknown>		
	ATTORNEY/AGENT INFORMATION:		
	NAME: Bak, Mary E.		
	REGISTRATION NUMBER: 31,215		
	REFERENCE/DOCKET NUMBER: GNVN.008PCT		
	TELECOMMUNICATION INFORMATION:		
	TELEPHONE: 215-540-9200		
	TELEFAX: 215-540-5818		
	INFORMATION FOR SEQ ID NO: 3:		
	SEQUENCE CHARACTERISTICS:		
	LENGTH: 9972 base pairs		
	TYPE: nucleic acid		
	STRANDEDNESS: double		
	TOPOLOGY: unknown		
	MOLECULE TYPE: CDNA		
	SEQUENCE DESCRIPTION: SEQ ID NO: 3:		
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	; Sequence 2, Application US/08801344		
	; Patent No. 6087140		
	GENERAL INFORMATION:		
	APPLICANT: Cameron, Douglas C.		
	APPLICANT: Shaw, Anita J.		
	APPLICANT: Altaras, Nedim E.		
	TITLE OF INVENTION: MICROBIAL PRODUCTION OF 1,2-PROPANEDIOL		
	TITLE OF INVENTION: FROM SUGAR		
	NUMBER OF SEQUENCES: 11		
	CORRESPONDENCE ADDRESS:		
	ADDRESSEE: Demilt Ross & Stevens S.C.		
	STREET: 8000 Excelsior Drive, Suite 401		
	CITY: Madison		
	STATE: WI		
	COUNTRY: U.S.A.		
	ZIP: 53717-1914		

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,344
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER: 09820.037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
TELEFAX: 608-831-2106
INFORMATION FOR SEQ. ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Vector pSE380
US-08-801-344-2

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Best Local Similarity 75.0%; Pred. No. 4,4e-07;
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DB        583 ctgcagaaagtactagtgcacgctggggccgatgcaccttaagctt 626

RESULT 14
US-09-498-599-2
; Sequence 2, Application US/09498599
; Patent No. 6303352
; GENERAL INFORMATION:
; APPLICANT: Cameron, Douglas C.
; APPLICANT: Shaw, Anita J.
; APPLICANT: Altaras, Nedim E.
; TITLE OF INVENTION: MICROBIAL PRODUCTION OF
; TITLE OF INVENTION: 1,2-PROPANEDIOL FROM SUGAR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Demilt Ross & Stevens S.C.,
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patenlin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498.599
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara Charles S.
; REFERENCE/DOCKET NUMBER: 09820.037
; TELECOMMUNICATION INFORMATION:

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[illegible]

sequence 19, Application US/08306691B
Patent No. 5734039

GENERAL INFORMATION:

APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz

TITLE OF INVENTION: ANTISENSE

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' TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES
' NUMBER OF SEQUENCES: 55

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CORRESPONDENCE ADDRESS:
ADDRESSEE: 3043-1

STREET: Two Penn Center, Suite 1800
ADDRESS: Seidel, Gonda, Lavorigna & Monaco, P.C.

CITY: Philadelphia
STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19102
COMPUTER READABLE FORM

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2
OPERATING SYSTEM:

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: FIS/08/2306 6011

FILING DATE: September 15, 1994

CLASSIFICATION: 514
PRIOR APPLICATION DATA

APPLICATION NUMBER:
FBI TWO 0188

FILED DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.
REGISTRATION NUMBER:

REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8

TELECOMMUNICATION INFORMATION
TELEPHONE 401 733 3333

TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549

TELEX: NO. 5734039e
INFORMATION FOR CTO TO

SEQUENCE CHARACTERISTICS: 19;

LENGTH: 35100 base pairs
TYPE: nucleotide

STATE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
S-08-306-691B-19

CT 0700

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[illegible]

Search completed: September 7, 2002, 18:26:08
Job time: 29062 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:32:06 ; Search time 13836.9 Seconds
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3721.275 Million cell updates/sec

Title: US-09-834-291-3
Perfect score: 2380
Sequence: 1 agccttttgctacattt.....tgctaatcaagagacgtg 2380

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues 143959072

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Pending_Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2380	100.0	2827	US-09-834-291-10	Sequence 10, Appl
3	1923.4	80.8	45121	US-09-834-291-1	Sequence 1, Appl
4	1899.6	79.8	3212	US-09-665-615B-94	Sequence 94, Appl
5	1713.4	72.0	2165	US-09-802-669-94	Sequence 1, Appl
6	1713.4	72.0	2165	US-08-377-522-1	Sequence 1, Appl
7	1372.8	57.7	1608	US-08-377-522-1	Sequence 1, Appl
8	1372.8	57.7	1608	US-08-377-522-1	Sequence 1, Appl
9	1372.8	57.7	1608	US-08-377-522-1	Sequence 1, Appl
10	706	29.7	3814	US-60-324-185-29531	Sequence 29531, A
11	611.8	25.7	720	US-09-834-291-2	Sequence 2, Appl
12	424.2	17.8	449	US-09-404-284-674	Sequence 674, Appl
13	424.2	17.8	449	US-09-524-038-674	Sequence 674, Appl
14	319.6	13.4	458	US-09-306-3508-14682	Sequence 14682, A
15	319.6	13.4	458	US-09-909-629-3705	Sequence 3705, Ap
16	296.8	12.3	254	US-09-652-816-3367	Sequence 3367, Ap
17	244	10.3	254	US-09-652-816-3367	Sequence 3367, Ap
18	239.2	10.1	2871	US-09-652-124-8816	Sequence 8816, Ap
19	239.2	10.1	2871	US-09-717-350-4919	Sequence 4919, Ap
20	239.2	10.1	2871	US-09-726-172-2083	Sequence 2083, Ap
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26	234.4	9.8	2641	US-60-172-373-15844	Sequence 15844, A
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29	190.4	8.0	859	PCT-US00-05883-187	Sequence 187, App
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RESULT      3
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; Sequence 10, Application US/09997722
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 45121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-997-722-10

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Query Match	80.8%	Score 1923.4	DB 36	Length 45121
Best Local Similarity	85.1%	Pred. No. 0		
Matches 2359	Conservative	0	Mismatches 21	Indels 393
				Gaps
QY 1	agcttttttggcacaatttttlaattgttaagaagcgaagttaataacacacactacg	60		
Db 8441	agccttttggctcacattttttattgttaagaagtttaataacacacacacacg	8500		
QY 61	ggcctataatgataagatgaatgaagaagaatccacataatgtagtgcgtgcttaaat	120		
Db 8501	ggcctataatgataagccttaagaagaagatccacataatgtagtgcgtgcttaaat	8560		
QY 121	tcacactcaagaagatactgattttgtgcaatgctctccctttttctctccct	180		
Db 8561	tcacactcaagaagatactgattttgtgcaatgctctccctttttctctccct	8620		
QY 181	ccttccactcctctctcccttaactctcctttccttccctcaaacccctttctcctt	240		

QY 2008 gcacattctctccgaaagatataatggtggtcgtgaatgagctctggaggtctgtt 2067
Db 10841 gacattctctctccgaaagatataatggtggtcgtgaatgagctctggaggtctgtt 10900
QY 2068 accgtttttatgttcaacagaaagaaactgctgtctccctccggaaattctt 2127
Db 10901 accgtttttatgttcaacagaaagaaactgctgtctccctccggaaattctt 10960
QY 2128 cttaagactgaatgctgctgagtggtttcaattgtttgtttcttccctct 2187
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QY 2308 acttgagcagctgttttgaagagtcctcgcagaaatgagcagcttgagatgctaa 2367
Db 11141 acttgagcagctgttttgaagagtcctcgcagaaatgagcagcttgagatgctaa 11200
QY 2368 tcaagagacgtg 2380
Db 11201 tcaagagacgtg 11213

RESULT 4
US-09-834-291-1
Sequence 1, Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: P53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 3212
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-834-291-1

Query Match 79.8%; Score 1899.6; DB 32; Length 3212;
Best Local Similarity 84.9%; Pred. No. 0;
Matches 2348; Conservative 0; Mismatches 24; Indels 394; Gaps 4;

QY 1 agctttttgctaatattttttatgtgaagtaagtttaataacatcatcgtactg 60
Db 448 agctttttgctaatattttttatgtgaagtaagtttaataacatcatcgtactg 507
QY 61 ggcataataatgaatgaatgaagaaagatccacataatgtaattgtgtgctataat 120
Db 508 ggcataataatgaatgaatgaagaaagatccacataatgtaattgtgtgctataat 567
QY 121 tcaacacccaagagatactgattgttcaatgtcttccctctttttttcttccct 180
Db 568 tcaacacccaagagatactgattgttcaatgtcttccctctttttttcttccct 627
QY 181 ccttcaatctcttccctcttctctctctctctctctctccctcaacaccccttctctct 240
Db 628 ccttcaatctcttccctcttctctctctctctctctctccctcaacaccccttctctct 687

QY 241 cttttacatttttttatttaaatgaacttttcaatttggaaatgttttagatttcaaa 300
Db 688 cttttacatttttttatttaaatgaacttttcaatttggaaatgttttagatttcaaa 747
QY 301 aaattggcagaagataaacaagagaaatgcccataatccctcttccattctt 360
Db 748 aaattggcagaagataaacaagagaaatgcccataatccctcttccattctt 807
QY 361 tgtgtctatagaatgctcaagagtggtgcaagagcgtggaagcccgaggtctccat 420
Db 808 tgtgtctatagaatgctcaagagtggtgcaagagcgtggaagcccgaggtctccat 867
QY 421 ggcactaaagcttactgtaagagtggaacagagacacccataacacactacaagatg 480
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QY 541 ctactagatttggaggtcccaacagagctccagagaaatgtcaactgagagagacc 600
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QY 601 tgaagatgaacagtggtgtaagcaagaggttattatgttattatgttgaatct 660
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Db 1167 aacttgaaacctttagtggtccagctgtaagctgtaacccaattcaagttcagtaatg 1226
QY 781 atgtcatctcccaacatacctctgttaaaattcatgtaacccaattcaagttcagtaatg 1286
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QY 1201 gccaaggtccttaccacagcgagcctctgagctgagctcatctctcccaagac 1260
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Db 302 aaattgcaagagataataacagagaatgccaataacatccctcttaaccactcttt 361
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RESULT 6
US-09-802-669-94
? Sequence 94, Application US/09802669
? GENERAL INFORMATION:
? APPLICANT: Dean, Nicholas M.
? APPLICANT: Marcusson, Eric G.
? APPLICANT: Wyatt, Jacqueline
? APPLICANT: Zhang, Hong
? TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
? FILE REFERENCE: ISPH-545
? CURRENT APPLICATION NUMBER: US/09/802,669
? PRIOR APPLICATION NUMBER: US 2001-03-09
? PRIOR FILING DATE: 2000-09-18
? PRIOR APPLICATION NUMBER: US 09/665,615
? PRIOR FILING DATE: 1999-04-12
? NUMBER OF SEQ ID NOS: 180
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 94
? LENGTH: 2165
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1782)...(1813)
us-09-802-669-94

Query Match 72.0%; Score 1713.4; DB 31; Length 2165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1714; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agcttttggctacaatttttatttgtaaagtaagtttaataatcaatcactcaactg 60
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Db 62 ggtcataatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 121
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Db 1022 tttgagaaataataaactaaag 1081
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QY 1141 caacatgag 1200
Db 1142 caacatgag 1201
QY 1201 gcaag 1260
Db 1202 gcaag 1261
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QY 1321 ctccgaagtgctctacatgaagtgagcatgccaagcactgcaagaaagagagagagagagag 1380
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QY 1381 tggccattgtgcaagaaacccctgactctctctcaactgacttctccctctctctctctct 1440
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QY 1681 tggctgccaagcag 1715
Db 1682 tggctgccaagcag 1716

RESULT 7
US-08-377-522-1
Sequence 1, Application US/08377522
GENERAL INFORMATION:
APPLICANT: Mountz, John D.
APPLICANT: Liu, Changdan
APPLICANT: Cheng, Jianhua
APPLICANT: Koopman, William J.
APPLICANT: Zhou, Tong
TITLE OF INVENTION: Human Fas Gene Promoter Region
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,522
FILING DATE: 20-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Serlich, Gary J.
REGISTRATION NUMBER: 34,430
REFERENCE/DOCKET NUMBER: USOB:034/SBR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

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; NAME/KEY: CDS
; LOCATION: 1467..1496
US-08-377-522-1

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Query Match	57.7%;	Score 1372.8;	DB 7;	Length 1608;
Best Local Similarity	99.4%;	Pred. No. 2.1e-285;		
Matches 1388;	Conservative	0;	Mismatches 7;	Indels 1.

12

QY	320	agagaatgcccataacacatcctcttatcccacttcctttgtgtcattatagatgctca	37
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QY	380	gagtgctgacaaagctctgcacgcccagggctctcccaatggaaactaaagcttactga	43
Db	67	GAGGTGTGCACAAGGCTGGCAGCCCAAGGGTCTTCTCATAGCACTAACGTCTACTGA	120
QY	440	aagttggaacgaaacaaagctatacaacactacaagaactggttgtaagtgcagtgacg	49
Db	127	AAGGTGAACAGAAACAAGCTTATCAACACCTTACAAACATGCTGTGAATGACATGACAG	186
QY	500	atgcacaacacagggtgatgtgaagccctcaaggagggttaacctaacttaatttgagggc	558
Db	187	ATGCAAAACACAGGCTGATGGAAAGCCCTCAGAGGGTTAACTTAATTTGAGGGC	246
QY	560	ccaaacggctcccaagaagaataatgtaactgagaggaaagcctgaagatgaacagtgagc	619
Db	247	CCAAACAGGCTCCAGAAAGAAATGTCAACTGAAAGGAAGCCTGAAGATGAACAGTGGC	306
QY	620	taagcaaaaggttatctaattgtctataatggttgtaacttaattggnaaggaagag	679
Db	307	TAAAGCAAGGGTATTAAATGTATTAAATGTTAAATCTTAATTTGGAAAGGAGAGAG	366
QY	680	ttgcagaatggaagtgacagagcttggtgcagatgcccagaagaatactgaacacttagtg	739
Db	367	TTGCAGATGAGGATGCGAGGCTTGGTGAGCGATGCCAAAGGAATACTGAAACCTTTAGTG	426
QY	740	tgctcaagcttggaactgcataccaattcaaggttcaagtgtaatgtaatgcatatccaaacata	799
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QY	860	acttgaacagtggtcacacagagccgaagaagaatatacaagtttcttttaagaagaact	919
Db	547	ACTTTGAACAGAGTGTCCACAGAGCAGAAAGATTAACAGATTTTTTTTAAAGAAATTT	606
QY	920	ggccaggaataatgaatgaagaagaaggaagaatctgtgaatgttaataatagctg	979
Db	607	GGCCAGGAATATATGATGATGAAAGAGCAAGGAAGTAATTTGGAATGTTTAATATAGCTGG	666
QY	980	ggctatgagatcttggtcttaagtgttgtaagcttggttccctcttgagaataaataaaga	1039
Db	667	GGCTATGCGATTTGGCTTAATGTTGTTAGCTTTGTTTTCCTTTGAGAAATTAACAACCTAAG	726
QY	1040	ggagccccccttttccaagccctatggcgcaacatctgtactttcataatggttaactg	1099
Db	727	GGGCCCCCTTTTCAAGGCCCTATGTGGCGAACAATCTGTACTTTTCAATATGTTACTG	786
QY	1100	tcaattccaggaacgtctgtgaagcctctcaatgttgcaagcacacaacatggacagcccaatc	1159
Db	787	TCCATTCCAGAAAGCTGTGAGAGCTCTCATGTTGGCAAGCAAGATGGACAGGCCCACTG	846
QY	1160	aaatgcccgcgaagcttctctcgtatgactccagaatataagcaagctcctctgatacca	1219
Db	847	AAATGCCCCCAAGGCTTTCTTGAGATGACTCCAGCAATTAAGCCAAGGCTCTGTACCCA	906
QY	1220	ggcaggaaactctgagctctgagctccatctccttcaagaaccccccaacttcccaggt	1279
Db	907	GGCAGACACTTCTGCTGTAGCTCATTTCTCCTTAAACACCTCCCAACTTCCAGGTT	966

QY	1280	gaactaagcagaagcgttttagaaaggcagagagccgcctctcgaagcttcactga	1339
Db	967	GAAGCTACAGCAGAAAGCCTTTATGAAGAGGACAGAGCGCGCTCTGAGAGTCTCACTGAA	1026
QY	1340	gttagcaltgcagccacttgtcagaagacgcccgcggagacgaatggccatttgtgaacgaa	1399
Db	1027	GTGAG-ATGCGACAGCACTGCAGGAAGCCCGGACACAGATGCCATTGTGTGAACGAA	1085
QY	1400	cccttgactccttctcaaccttgacttcctccctccctacccgcgcgaagccaagttgc	1459
Db	1086	CCCTGACTCTTCTCAACCTGTACTTCTCCCTCCTTACCCTACCCGGCGCAGAGCCAAAGTTGC	1145
QY	1460	tgaatcaalbgagccctccccaacccggcggttccccagagagcttccctccactcc	1519
Db	1116	TGAATCAATGAGACCCCTCCCAACCCGGGGGCTTCCCAAGGAAGCTTCTTCCATCTTC	1205
QY	1520	ctgaccaccggggcttcttcgtgagctcgtctctgatactcgcgcgaagatgacacagat	1579
Db	1206	CTGACCAACCGGGGCTTTTGATGAGCTGCACTTGATCTGGCCAAAGTGAACACAGGT	1265
QY	1580	gttcaaaagcagcttcctggggagtgaaagaaagggttlaagatgacttgcttggagccctc	1639
Db	1266	GTTCAAAAGACGTTTCTGGGGAGTGAAGGAGGGTTTACGAGTGAATTTGGCTGAGACCTTC	1325
QY	1640	agggcgaggcacttgcacggaacacacccctgagccagcccttgctgcgcagcgagagt	1699
Db	1326	AGGGCGGGGCACTGGCAGGAGAACACACCTGAGGGCAGCCTGCGTCCGCCAAGCGAGCTT	1385
QY	1700	gcctcttctccggag 1715	
Db	1386	GCTCTTCTCCCGGG 1401	

RESULT 8
US-08-377-522C-1

GENERAL INFORMATION:

TITLE OF INVENTION:	Human Fas Gene Promoter Region
NUMBER OF SEQUENCES:	1

CORRESPONDENCE ADDRESS:

CITY: Houston

ZIP: 77073

MEDIUM TYPE: 3.5 inch floppy

OPERATING SYSTEM: Macintosh

```

; CURRENT APPLICATION DATA:
APPLICATION NUMBER      DATE

```

FILING DATE: January 20, 1995
CLASSIFICATION: 425

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION.

REGISTRATION NUMBER: 35.423

TELECOMMUNICATION INFORMATION:

TELEFAX: (713) 777-6908

SEQUENCE CHARACTERISTICS:
LENGTH: 1600 bp

TYPE: nucleic acid

MOLECULE TYPE: linear

DESCRIPTION:	genomic DNA
--------------	-------------

HYPOTHEICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placental
IMMEDIATE SOURCE:
LIBRARY: (FIXIT: EMBL-SP6/T7
CLONE: FIX1, FIX2, FIX3; EMBL1, EMBL2, EMBL3
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
US-08-377-522C-1

Query Match 57.7%; Score 1372.8; DB 7; Length 1608;
Best Local Similarity 99.4%; Pred. No. 2.1e-285;
Matches 1388; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

320 agagaatgccatataccatccctccctacccactctcttctgtctatagatgctca 379
7 ACAGAGATGCCCTTATACCATCTCTTATCCACTCTTTTGTCTATTAGATGCTCA 66
380 gaatgtgtgcaagagctgtgagacgccaaggtcttccatgagcaatacagctactga 439
67 GAGGTGTGCAAGAGGCTGGCAGCCCGAGGCTTCTTCATGCGCATACAGTCTACTGA 126
440 aaggtgagacagacaaagcctatcaacactcaagaagctgtgtgtaagtgcagtgaag 499
127 AAGGTGAGACAGAGACAGCCTATCAACACTGATCAAGAGCTGTGTAGTGCAGTACAG 186
500 atgcaaaacacagagtgatgaaagccctccaggaaggtgaacactaagattgagagc 559
187 ATGCAAAACACAGGCTGTATGAAACCCCTCAGAGAGGTAACTTACCTGATTTGAGGCG 246
560 ccaaacagctccagagaagaaatgtcaactgagaggaagcctgaagatgaacagtggcg 619
247 CCAAAACAGCTCCAGAGAAATGTCAACTGAGAGAGCCTGAAGAGATGAACAGTGGCG 306
620 taagcaaaaggtatataatgtcttataatggtgttgatctaatgtggaagagagag 679
307 TAAGCAAAAGGTTATTAATGTATTAATGAGTTAACTTAATTTGGAGAGGAGAGAGG 366
680 ttgcagagtgaggtgagagagctgtgtgagcagatgcacaaaggaatctgaacctta 739
367 TTGCGAGAGTGTGAGAGCTGTGTGTGAGAGATGCCAAAGGAATACCAAACTTATG 426
740 tgcagctgtgagactgcatccaattcaggttcagtaagtgaatgtaattatccaata 799
427 TGTCCAGTCTGGAATGCAATCCAAATTCAGGTTCAGTAATGATGTCAATTAACAA 486
800 cctctgttaaatctcgtctaaactcctaaagagctactacagcttccaagcaatag 859
487 CCCTTGTGTAATAATTCAGTAACTTAACTTAAAGCTATCTACCCGTCCAAAGCAAT 546
860 acttgacagctgtcacccagagcagcaagaaattacaagaattcttttaagaagaat 919
547 ACTTTGAACAGTGTTCACAGAGACGAGCAAGAAATTAAGATTTTAAAGAAATTT 606
920 ggcaggaagaatagtaagtaagagcaggaagtaattgtgaatgtttaataagctg 979
607 GGCAGGAAGAAATAGTAAGTAAGAGACAGGAATTAATGTGAATGTTTATATAGCTG 666
980 ggcagcagatgttgcttaagtgtgagcttcttctcctcttgagaataaaaaaag 1039
667 GGTATGCGATTTGGCTTAATGTGTAGCTTGTTCCTCTTGAGAAATTAAGAACTAAG 726
1040 ggcgcctcccttccagagccctatgagcgaacatctgactcttctatagtgtaag 1099
727 GGGCCCTCCCTTTCAGAGCCCTATGAGGCAACATCTGTACTTTTCATATGTATAG 786
1100 tccatctcaggaagctgtgtagcctctcatgtgcaagccacaacatgacagccactc 1159

787 TCCATTCAGAGAGCTGTGTGAGCCCTCTCATGTTGAGCCACAGATGACAGCCAGTC 846
1160 aaatgcccagcaagctcttctcagtgactccagcaattagcaaggtctcgttaccga 1219
847 AAATGCCCGCAAGTCTTCTGTGAGTACTCCAGCAATTAAGCAAGGCTCCTGTACCCA 906
1220 ggcagacctctgagctgtgagctcaatctccttcaagagctccccaacttccaggt 1279
907 GGAAGACCTCTGGGCTGTGAGCTCCATTCCTTCAAGACCTCCCAACTTCCAGGTT 966
1280 gaactaagcaagaagcctttagaagaagcaggaagccggtctcaggtctcactga 1339
967 GAATTCAGAGAGAGGCTTTTGAAGAGGAGAGAGGCGGCTCTGAGGCTCTCACTGAA 1026
1340 gtgagatgccaagcactgcaagaagcccggaagcaagaatgccatgttgcaagaa 1399
1027 GTGAG-ATGCCAGCAGCTGAGAGAAAGCCCGGAGACAGAAATGCCATTTGTGACGAA 1085
1400 cctgactccttctcagcctgactctccctccctccctaccagcgagcagcaagctgc 1459
1086 CCGTACCTCTTCTCAGCCCTGACTTCTCCCTCTCTTACCCGCGGAGGCAAGTTGC 1145
1460 tgaatcaatgagccctcccaacccagcgcttcccaagagcttccctccactctc 1519
1146 TGAATCAATGAGCCCTCCCAACCCGCGGCTTCCAGAGGCTTCTTCCATCTCTC 1205
1520 ctgacacccagggcttctcgtgagctgtctctgtatctcgtgcaagatgacacaggt 1579
1206 CTGACACACGGGGCTTTCGTGAGCTGTCTGTGATCTGCGCAAGAGTGAACACAGGT 1265
1580 gtcaaaagcgtctctgagagtgaggaagcgtttacagatgactgtgctgagctc 1639
1266 GTTCAAGAGCGCTTCTGGGAGTGAAGAGGAGGTTTACAGATGACTGTGAGACCTTC 1325
1640 aggggagcagctgagcaggaacacacccctgagggcagccctggtcccaagcagagct 1699
1326 AGGGGCGGACAGTGCAGCAACACACCTGAGGCGACGCTGCTGCGCAGGAGGAGCT 1385
1700 gctctctcccgcg 1715
1386 GCCTCTTCTCCGCG 1401

RESULT 9
US-08-377-522D-1
Sequence 1. Application US/08377522D
GENERAL INFORMATION:
APPLICANT: Mounitz et al.
TITLE OF INVENTION: Human Fas Gene Promoter Region
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
STREET: 8011 Candle Lane
CITY: Houston
STATE: TX
ZIP: 77071
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,522D
FILING DATE: January 20, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5919


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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 415714.1
US-60-324-185-29531

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Query Match	29.7%;	Score 706;	DB 71;	Length 3814;
Best Local Similarity	99.9%;	Pred. No. 2e-141;		
Matches 717; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1

Y	999	agttgttagctgttcttctctctctgtgaaataaaactaaggagccctcccttttcag	1058
Db	1	agtgttttagctgttcttctctctctgtgaaataaaactaaggagccctcccttttcag	60
Y	1059	cccatgtgcgcaaacatcgttacttttccataatggttttactgtccatctccaggaagctctg	1118
Db	61	cccatgtgcgcaaacatcgttacttttccataatggttttactgtccatctccaggaagctctg	120
Y	1119	tgaagccttcaatgttgcagccacaacatgtgacgcccagttcaaatgtcccccgaagtctt	1178
Db	121	tgaagccttcaatgttgcagccacaacatgtgacgcccagttcaaatgtcccccgaagtctt	180
Y	1179	ctctgagagatccagcaatattagacaaggtccctgttaaccggagagagactctgcgtct	1238
Db	181	ctctgagagatccagcaatattagacaaggtccctgttaaccggagagagactctgcgtct	240
Y	1239	gagctccattctctctccaaagacccctcccaattcccaaggttgagattaaagagaagccct	1298
Db	241	gagctccattctctctccaaagacccctcccaattcccaaggttgagattaaagagaagccct	300
Y	1299	tggaaagggcagagagccgggctctctgagatccctccactggaaagtgaagcatgcccagactg	1358
Db	301	tggaaagggcagagagccgggctctctgagatccctccactggaaagtgaagcatgcccagactg	360
Y	1359	caggaacgcgccgggagacaggaatgccatttgtgaaacgaacccgtgactccttccatcc	1418
Db	361	caggaacgcgccgggagacaggaatgccatttgtgaaacgaacccgtgactccttccatcc	420
Y	1419	ctggaactctcccccctccctccacccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	1478
Db	421	ctggaactctcccccctccctccacccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	480
Y	1479	ccaaaccggcggtctcccccagcgaagctctctccctccactctctctgacccacggggtcttc	1538
Db	481	ccaaaccggcggtctctcccccagcgaagctctctccctccactctctctgacccacggggtcttc	540
Y	1539	gttgaagctgctctgtactctgc	1598
Db	541	gttgaagctgctctgtactctgc	600
Y	1599	gaatgagggagagcggtttacgaagtgaactgtgagcctcagggcgggcgaattggcac-	1658
Db	601	gaatgagggagagcggtttacgaagtgaactgtgagcctcagggcgggcgaattgggacac	660
Y	1658	ggaaacaaaccttgaagccagacccctgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	1718
Db	661	ggaaacaaaccttgaagccagacccctgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	718

RESULT 11
US-09-834-291-2
Sequence 2, Application US/09834291
GENERAL INFORMATION:
APPLICANT: Kraemer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834, 291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1

```

; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-03-834-291-2

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Query Match	25.7%	Score 611.8:	DB 32:	Length 720:
Best Local Similarity	99.7%	Pred. No. 2.4e-121:		
Matches 613; Conservative	0:	Mismatches 2:	Indels 0:	Gaps 0:

[illegible]

```

RESULT 12
US-09-404-284-674/c
: Sequence 674, Application US/09404284
:
: GENERAL INFORMATION:
:
: APPLICANT: Hyseq, Inc.
:
: TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
:
: TITLE OF INVENTION: From Various Libraries
:
: FILE REFERENCE: 20411-780
:
: CURRENT APPLICATION NUMBER: US/09/404,284
:
: CURRENT FILING DATE: 1999-09-21
:
: NUMBER OF SEQ. ID NOS: 4670
:
: SOFTWARE: Hy-patent.pl Version 3.1
:
: SEQ. ID NO 674
:
: LENGTH: 449

```


Search completed: September 7, 2002, 22:33:42
Job time: 43916 sec

OY 754 ctgcacccaatcaggttcaatgatgtcattatccaaacattactctctgaaatt 813
|||||
DB 221 ctgcattccaaattcaggttcaatgatgtcattatccaaacattactctgaaatt 163
OY 814 catgctaaactaactaagactaactcctacccgttccaaagcaatagtgacttgaacagt 873
|||||
DB 162 catgctaaactaactaagactaactcctacccgttccaaagcaatagtgacttgaacagt 104
OY 874 tcaccagagacgaagaattacagaattttttttaagaanaatt 919
|||||
DB 103 tcaccagagacgaagaattacagaattttttttctgcgcgatt 58

RESULT 15
US-09-909-629-14682/c
Sequence 14682, Application US/0909629
GENERAL INFORMATION:
APPLICANT: Dickson, Mark C.
APPLICANT: Dimanac, Radoje T.
APPLICANT: Jones, Lee W.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various CDNA Libraries
FILE REFERENCE: 20411-776
CURRENT APPLICATION NUMBER: US/09/909, 629
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/306,350
PRIOR FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 41304
SOFTWARE: pt_ct_1 Version 1.1
SEQ ID NO 14682
LENGTH: 458
TYPE: DNA
ORGANISM: Homo sapiens
US-09-909-629-14682

Query Match 13.4%; Score 319.6; DB 34; Length 458;
Best Local Similarity 96.3%; Pred. No. 2.3e-58;
Matches 391; Conservative 0; Mismatches 9; Indels 6; Gaps 6;
OY 514 gtgatggaaagccctcagagaggttaacctagatttgaggcccaacagctcca 573
|||||
DB 457 gtgatggaaagccctcagagaggttaacctagatttgaggcccaacagctcca 399
OY 574 gaagaaatgtcaactgagaggaagccctgaaggaatgaacagtggcttaagcaaggtta 633
|||||
DB 398 gaagaaatgtcaactgagaggaagccctgaaggaatgaacagtggcttaagcaaggtta 340
OY 634 ttaattgttatttaattgaggttgaatttaattggaaggaaggttgagagtgagt 693
|||||
DB 339 ttatattgtatttaattgaggttgaatttaattggaaggaaggttgagagtgagt 281
OY 694 gcagagcttggtgagagatgcacaaggaatgaactgaacactttagtggctcagcttgaa 753
|||||
DB 280 gcagagcttggtgagagatgcacaaggaatgaactgaacactttagtggctcagcttgaa 222
OY 754 ctgcattccaaattcaggttcaatgatgtcattatccaaacattactctgaaatt 813
|||||
DB 221 ctgcattccaaattcaggttcaatgatgtcattatccaaacattactctgaaatt 163
OY 814 catgctaaactaactaagactaactcctacccgttccaaagcaatagtgacttgaacagt 873
|||||
DB 162 catgctaaactaactaagactaactcctacccgttccaaagcaatagtgacttgaacagt 104
OY 874 tcaccagagacgaagaattacagaattttttttaagaanaatt 919
|||||
DB 103 tcaccagagacgaagaattacagaattttttttctgcgcgatt 58

Accession	Sequence	Position
OY	2128 ccttaagactgaagcgcgtgcagatggtttattttgtttgtttcttcgccttt	2187
OY	2128 ccttaagactgaagcgcgtgcagatggtttattttgtttgtttcttcgccttt	11020
Db	10961 ccttaagactgaagcgcgtgcagatggtttattttgtttgtttcttcgccttt	2247
OY	2188 ccttcctctcttgcctttccttaagctgaactccacatggtatcttcgctgtcttcg	11080
OY	11021 ccttcctctcttgcctttccttaagctgaactccacatggtatcttcgctgtcttcg	2307
OY	2248 ctggaggtctggatggaactcgtccacacgcacagaaaccggtgccttaatttggccaagaa	11140
Db	11081 ctggaggtctggatggaactcgtccacacgcacagaaaccggtgccttaatttggccaagaa	2367
OY	2308 accttgagcagcctgtttctgaaatgcctcgtctcagaatagcagcttgacatggtctaa	11200
Db	11141 accttgagcagcctgtttctgaaatgcctcgtctcagaatagcagcttgacatggtctaa	
OY	2368 tcaagagacgtg	
Db	11201 tcaagagacgtg	11213

US-10-011-154-674/c Application US/10011154

? SEQUENCE INFORMATION:
 ? APPLICANT: Drmanac, Radoje T.
 ? APPLICANT: Labat, Ivan
 ? APPLICANT: Stache-Cran, Birgit
 ? APPLICANT: Dickson, Mark C.
 ? APPLICANT: Jones, Lee W.
 ? TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
 ? FROM VARIOUS LIBRARIES
 ? FILE REFERENCE: 780CIP
 ? CURRENT FILING DATE: 2001-12-06
 ? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/524,038
 ? PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-13
 ? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/404,284
 ? PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-21
 ? NUMBER OF SEQ ID NOS: 4670
 ? SOFTWARE: Hy-patent.pl Version 3.1
 ? SEQ ID NO 674
 ? LENGTH: 449
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 ? US-10-011-154-674

Query Match	17.8%	Score 424.2	DB 7	Length 449
Best Local Similarity	99.3%	Pred. No. 7,2e-81		
Matches 426	Conservative	0	Mismatches 3	Indels 0
				Gaps 0
QY 1233	cgcctctagcttcattctctctcttccttcgaagacttccccaactccagttccacaggttgtaactacagaga	1292		
Db 449	CGTTCATAGCTCCATTTCTCCTTCAACACCTCCCCCAACTTCCGAGGTGTAACTACAGCAGA	390		
QY 1293	agcctcttagaaagcgacggagccggctctcgaggtctctacacttaagatgagcatgcccag	1352		
Db 389	AGCCTTTAGAAAGGACAGAGAGCGCGGTCTCGAGGTCTCACTGAAGTACACATGCGCAG	330		
QY 1353	cgccctacagaagacgcccgcggagcagcgagatgcacattgtgtgcaagaaacctgaactctcttc	1412		
Db 329	CCACTGCAGAGACGCCCGCGGACAGAGAAATGCCAATTTGTGCACAGAAACCTGTACTCTTTC	270		
QY 1413	ctcaacctgaattctccctctcctcactccgcgcgacgcccgaagtcgaagtcgtgatcaatgag	1472		
Db 269	CTCACCTGTGACTTCTCCCTCCCTCCCTCCCTCCGCGGACAGGCGCAAGTTGGTGATTCATGAG	210		
QY 1473	ccctccccaacccggcgctgtccccaagagaggtctctctcactctctctctgaacccgggg	1532		
Db 209	CCCTCCCAACCCGGGGGTTTCCCAAGGAGGCTTCCCTTCCATTCCTCCTGACACACCGGGG	150		

Db 29 GGCACGGG -

US-10-211-364-477 Application US/10211364

```

Sequence 4
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P1216C1N
CURRENT APPLICATION NUMBER: US/10/211,364
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: 09/760,486
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 1778
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 477
LENGTH: 772
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (392)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (594)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (704)
OTHER INFORMATION: n equals a,t,g, or c
US-10-211-364-477

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Query Match	DB 6	Score 237.4	Length 172	Gaps 0
Best Local Similarity	99.6%	Pred. No. 6,2e-41	Indels 1	
Matches 238	Conservative	Mismatches 1		
QY 1477	ccccaaaccggcggttccccagcagagcttccctccatctctctgacacacgggcttt	1536		
DB 9	cgcacacccggcggttccccagcagagcttccctccatctctctgacacacgggcttt	68		
QY 1537	tcgtagctcgtctctgatatctcgcgaaagatgacacacagtttcaaaagcgtctcg	1596		

6.5%;	Score 155;	DB 7;	Length 2551
100.0%;	Pred. No. 3.2e-23;		

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RESULT 10
US-10-035-832-1259
: Sequence 1259, Application US/10035832
: GENERAL INFORMATION:
: APPLICANT: Engelhard, David
: TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
: FILE REFERENCE: A-71249/RMS/DCF
: CURRENT APPLICATION NUMBER: US/10/035, 832
: CURRENT FILING DATE: 2002-07-22
: PRIOR APPLICATION NUMBER: US 09/747,377
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: US 09/758,586
: PRIOR FILING DATE: 2001-03-02
: NUMBER OF SEQ ID NOS: 1613
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1259
: LENGTH: 55996
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: misc.feature

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RESULT 13
US-10-113-872-1669/c
Sequence 1669, Application US/1011387Z
GENERAL INFORMATION:
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Sleath, Paul R.

Search completed: September 8, 2002, 01:12:00
Job time: 37198 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 14:51:36 ; Search time 8462.63 Seconds
(without alignments)
3795.836 Million cells updates/sec

Title: US-09-834-291-3
Perfect score: 2380
Sequence: 1 agcttttgcctacattt.....tgcttaacaaagagacgtg 2380

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_lin:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	465.4	19.6	467	9	AA704610	AA704610 zj19h02.s
2	438.4	18.4	793	10	B1763679	B1763679 603049567
3	298.4	12.5	603	9	AA058563	AA058563 z155b04.s
4	294.4	12.4	577	9	AA056275	AA056275 z155g03.s
5	286.4	12.0	442	9	AA011028	AA011028 z634d02.s
6	285.4	12.0	547	9	AA047220	AA047220 z149e11.s
7	285.4	12.0	447	9	AA057418	AA057418 z159h03.s
8	276.4	11.6	467	9	AA020992	AA020992 z65f07.s
9	270	11.3	368	10	H84298	H84298 y95e09.s1
10	259	10.9	297	9	AA018441	AA018441 z650e08.s1
11	254.4	10.7	381	10	H86544	H86544 y104f01.s1
12	253.6	10.7	381	10	H86544	H86544 y104f01.s1
13	197	8.3	419	10	R85827	AV715411 AV715411
14	185.2	7.8	696	9	AV715411	B1838027 603083875
15	181.8	7.6	828	9	B1838027	AW239285 x838402.Y
16	161	6.8	429	9	AW239285	BG288747 60238556
17	145.6	6.1	1339	10	BG288747	

18	124.2	5.2	300	9	AU100132	AU100132 AU100132
19	117	4.9	932	9	AL542093	AL542093 AL542093
20	105.4	4.4	1052	10	BM455788	BM455788 AGENCOURT
21	96	4.0	285	10	BM090262	BM090262 505440 MA
22	85	3.6	899	9	AL540709	AL540709 AL540709
23	72	3.0	506	10	BG659530	BG659530 TGESTZY22
24	70.6	3.0	1101	12	CNS00396	AL063921 Drosophila
25	65	2.7	286	10	B1029879	B1029879 T10-MT035
26	64.6	2.7	343	10	B1045052	B1045052 MR4-OT010
27	64.6	2.7	343	10	B1045052	B1045052 MR4-OT010
28	64	2.7	169	10	BG998195	BG998195 MR4-HT126
29	64	2.7	205	10	BG998195	BG998195 MR4-HT126
30	64	2.7	267	10	BG998195	BG998195 MR4-CT053
31	63.8	2.7	1027	12	CNS01637	AL106813 Drosophila
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33	63.6	2.7	316	10	B1004597	B1004597 MR4-HN005
34	63.6	2.7	549	9	AA521324	AA521324 aa86e09.s
35	63.6	2.7	583	9	AA521324	AA521324 aa86e09.s
36	63.4	2.7	280	10	BG998167	BG998167 MR4-HT126
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38	63	2.6	276	10	BG015436	BG015436 RC2-GN035
39	63	2.6	279	10	BG978282	BG978282 RC4-C1019
40	63	2.6	287	10	BF759346	BF759346 RC2-CT064
41	63	2.6	319	10	B1028532	B1028532 MR4-MT033
42	62.8	2.6	987	10	CNS016F1	AL106663 Drosophila
43	62.8	2.6	1101	12	CNS017XW	AL106638 Drosophila
44	62.6	2.6	613	12	AZ363784	AZ363784 IM0109020
45	62.4	2.6	185	10	B1009341	B1009341 MR4-RT004

ALIGNMENTS

RESULT 1
AA704610 467 bp mRNA linear EST 24-DEC-1997
LOCUS zj19h02.s1 Scores: fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA
DEFINITION clone IMAGE:450771 3', mRNA sequence.

AA704610
AA704610.1 GI:2714528

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

human.
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 467)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marita, M., Martin,
'J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisling, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project
Unpublished (1997)

TITLE JOURNAL
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
This clone is available royalty-free through INL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Seg primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 459.

FEATURES
source location/Qualifiers
1..467

/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:450771"

/clone_lib="Soares-fetal_liver_spleen_INFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)

Oy	2351	agcttcgagatgcatacaagaacacgtc	2380
Db	241	AGCTTCGAGATGGCTAATCAAGACACGTc	270
RESULT	10		
H86126			
LOCUS		398 bp	Linear EST 21-NOV-1995
DEFINITION	H86126	ys94g08.s1 Soares retina N2B5HR Homo sapiens	CDNA clone
ACCESSION	H86126	IMAGE:222494 3', mRNA sequence.	
VERSION	H86126.1	GI:1067705	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 398)		
JOURNAL	Hillier,L., Clark,N., Dubouque,T., Elliston,K., Hawkins,M., Holman,		
COMMENT	R., Williamson,A., Wohlschlag,P. and Wilson,R. The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu High quality sequence stops: 378 Source: IMAGE Consortium, LNLN. This clone is available royalty-free through LNLN; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 925 Std Error: 0.00 Seq primer: Promega -2im13 High quality sequence stop: 378. Location/Qualifiers 1..398 /organism="Homo sapiens" /db_xref="GDB:3851255" /db_xref="taxon:9606" /clone="IMAGE:222494" /clone_lib="Soares retina N2B5HR" /sex="male" /tissue_type="retina" /dev_stage="55 year old" /lab_host="DH10B (ampicillin resistant)" /note="Organ: eye; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - Oligo(dt) primer [5' TGTTACCATCTGCAGTCGAGCGGCCGCGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Faelima Bonaldo."		
BASE COUNT	74 a	93 c	105 g
ORIGIN		125 t	1 others
Query Match	10.98%	Score 259;	DB 10;
Best Local Similarity	99.68%;	Pred. No. 2.4e-36;	length 398;
Matches 270;	Conservative	0;	Mismatches 0;
			Indels 1;
			Gaps 1;
OY	2106	gtttcccttcgggaattcctcttaagaactgaagtgcgtgcttgagtggttcat	2165
Db	1	GTCTCCCTTCGGGAATTCTCTTTAAAGACTGTAAAGTCGCTGAGTGATTCATT	60

Oy	2166	tgttttgcttcttcgcacctcctcttcttcttcccttcttagtggacatg	2225
Db	61	TGTTTGTATTTCTCCCTTCCTTCTCTTGGCCCTTTAGCTTCACATGCCATG	120
Oy	2226	gtgatcttcgtcttgtcttcgtctgagtggttggtgactcgctccaccgcacagaacc	2285
Db	121	GGAATTTCGCTTGCGCTCCTGCTGGGCTTGGTGACTGCTTCCCAACCGACAAGAACC	180
Oy	2286	gagcgcatattatggccaagaaccttgacagcctgltttgaagaatgccctgcataaa	2345
Db	181	GCGCGCTATATTGGCCCAAGAACTGAGCAGCGCTGTTTGAAAAGTCCCGCTCAGAA	240
Oy	2346	atgccagcttgc-a-gatgctaatacaag	2375
Db	241	ATGCCAGCTTGACAGATGGCTAATCAAAGAG	271
RESULT 11			
AA018441		297 bp mRNA linear EST 05-AUG-1996	
LOCUS		ze50a08.s1 Soares retina NZB4RI Homo sapiens CDNA clone	
DEFINITION		IMAGE:362390 3', mRNA sequence.	
ACCESSION	AA018441		
VERSION	AA018441.1	GI:1481696	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
	1 (bases 1 to 297)		
	Hillier,L., Clark,N., Dubouque,T., Elliston,K., Hawkins,M., Holman		
	,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,		
	Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston		
	,R., Williamson,A., Wohldmann,P. and Wilson,R.		
JOURNAL	The WashU-Merck EST Project		
COMMENT	Unpublished (1995)		
	Contact: Wilison RK		
	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: est@watson.wustl.edu		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	Seq primer: -40M13 fwd. from Amersham		
	High quality sequence stop: 244.		
FEATURES	Location/Qualifiers		
SOURCE	1..297		
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	/db_xref="GBD:1279093"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:362390"		
	/clone_lib="Soares retina NZB4RI"		
	/sex="male"		
	/tissue_type="retina"		
	/dev_stage="55 year old"		
	/lab_host="DH10B (ampicillin resistant)"		
	/note="Organ: eye; Vector: pRT3D (Pharmacia) with a		
	modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st		
	strand cDNA was primed with a Not I - oligo(dT) primer [5'		
	TGTTACCATCTGAAAGTGGGAGACGGCCGCTTTTTTTTTTTTTTTT 3'] ,		
	double-stranded cDNA was size selected, ligated to Eco RI		
	adapters (Pharmacia), digested with Not I and cloned into		
	the Not I and Eco RI sites of a modified pRT3 vector		
	(Pharmacia). The retinas were obtained from a 55 year old		
	Caucasian and total cellular poly(A)+ RNA was extracted 6		
	hrs after their removal. The retina RNA was kindly		
	provided by Roderick R. McInnes M.D. Ph.D. from the		
	University of Toronto. Library constructed by Bento		
	Soares and M.Fatiema Bonaldo."		
BASE COUNT	59 a	78 c	62 g
ORIGIN			98 t

Query Match 10.7%; Score 254.4; DB 9; Length 297;
 Best Local Similarity 99.6%; Pred. No. 1.6e-35;
 Matches 255; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2083 caacagaaagaaagaaatgccttctcctccctccggaatctctcttaagaactga 2142
 Db 1 CACACAGAAAAAGAAAGCGCTGCTCCCTCCGGAATCTCTTAAGACTGTAG 60
 QY 2143 tgcctccagtagtggtttggtttgtttttcttgcctctctctcttgc 2202
 Db 61 TCGCTCCCTAGAGGCTTCTTTTGTGTTTGTGCTCCCTCTCTTTCTTTGCC 120
 QY 2203 cttcttaagcttgacacccatggtatcttctgcttgctcctccgaggttggtga 2262
 Db 121 CTTTCTTACCTTGACCTCCATGCTGATTTCTGCTGCTCCCTGCTGCTGCTGCTA 180
 QY 2263 ctcgttccacgcacagaaacccgagcctattattggcaagaactgaagcctgt 2322
 Db 181 CTCGTTCCACCGCACAGAAACCGCGCCCTATATGCGCAAGAACTGAGCAGCTGT 240
 QY 2323 ttgaaagtcctctg 2338
 Db 241 TTTGAAAGTCCCTCG 256

RESULT 12
 LOCUS H86544 381 bp mRNA linear EST 21-NOV-1995
 DEFINITION y104f01.s1 Soares retina N2b5HR Homo sapiens cDNA clone
 ACCESSION H86544
 VERSION H86544.1 GI:1068123
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 381)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
 Riklin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston
 R., Williamson, A., Wohlmann, P. and Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

High quality sequence stops: 361
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 882 Std Error: 0.00
 Seq primer: Promega -21ml3
 High quality sequence stop: 361.

FEATURES

1..381
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 /clone.lib="Soares retina N2b5HR"
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 /dev_stage="55 year old"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: eye; Vector: pUT73D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'

TCGTACCAATCTGAAGTGGAGCGCGGCTTTTCTTTTCTTTTCTTTT 3'),
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pUT73 vector
 (Pharmacia). The retinas were obtained from a 55 year old
 Caucasian and total cellular poly(A)+ RNA was extracted 6
 hrs after their removal. The retina RNA was kindly
 provided by Roderick R. McInnes M.D. Ph.D. from the
 University of Toronto. Library constructed by Bento
 Soares and M. Fatima Bonaldo.

Query Match 10.7%; Score 253.6; DB 10; Length 381;
 Best Local Similarity 96.6%; Pred. No. 2.2e-35;
 Matches 259; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2111 ccttcggaatctctcttgaagctgaagtcgctgcctgaagttcatttggtt 2170
 Db 1 CTTCCGGGAATTCCTCTTAAGACTGTAAGTCGCTGAGTGCTTCAATTTGTTT 60
 QY 2171 tgtttctgcctctctctctcttcttcttgccttcttaagcttaccctcgtgtat 2230
 Db 61 TGTCTTTCGCCCTCTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 120
 QY 2231 ttctgcttgctcctgctggttggttggttggttggttggttggttggttggttggt 2290
 Db 121 TTTGCTTGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 QY 2291 ctattatggcgaagaacttgagagcctgttttgaagaagtcctcctgcctgaagatgc 2350
 Db 181 CTATTATGGCCAGAAACTTGAGCAGCTGTGTAAGAACCTCCCTGCTCAGAAATGCC 240
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 Db 241 AGCTTGCAAGATGGCTATCAAGAGAGC 268

RESULT 13
 LOCUS R85827 419 bp mRNA linear EST 22-JAN-1999
 DEFINITION y922g10.s1 Soares retina N2b4HR Homo sapiens cDNA clone
 ACCESSION R85827
 VERSION R85827.1 GI:944233
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 419)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
 Riklin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston
 R., Williamson, A., Wohlmann, P. and Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

High quality sequence stops: 269
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 958 Std Error: 0.00
 Seq primer: Promega -21ml3
 High quality sequence stop: 269.

FEATURES

Location/Qualifiers

male. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT 253 a 181 c 194 g 200 t

ORIGIN

Query Match

Best Local Similarity 7.6%; Score 181.8; DB 10; Length 828;
Matches 198; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1959 aataagtcagcaaccgaagcagtggttaagcggagggctcgaagaagacgaccttctc 2018
DB 1 AATTAAGTCAGCACCGAAGCAGTGTAAAGCCGAGGCTCGAAGACGGCACCTTTTC 60
QY 2019 ttctcgaaaaagtataatggggctgaatgaagctctcgaagccttgtaacglttcta 2078
DB 61 TTCTCGAAAAAAGTTATATGGGGGCTGAATGAGCTTCTCGAGGCTGTATTACCGTTT 120
QY 2079 ttgtcaacacagaagaagaactgccttgctccttcgcgggaattctctcttaagactg 2138
DB 121 TTGTCACACAGAAAAAGAACTGCTGTGCTCCCTTCGCGAATTCTCTTTAAGACTG 180
QY 2139 taagtcgctgcctgagtggttcaatttgcttcttcgccc 2183
DB 181 TTCTTACGCTGTGCTAGATTATGTCCAAAAGTGAATGCCCC 225

Search completed: September 7, 2002, 14:51:47
Job time: 16206 sec

[illegible]

RESULT	9
HSZA279012	
LOCUS	
DEFINITION	702 bp DNA
ACCESION	Homo sapiens partial CD95 gene for
VERSION	1 polymorphic allele (+275). linear
KEYWORDS	A1279012.1 GI:13539240
SOURCE	Apo-1 Fas; CD95 antigen; CD95 gene.
ORGANISM	human.
PROJECT	PRI 02-APR-2001

REFERENCE AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 702)
TITLE	Kuppers, R., Re,D., Jungnickel, B., Diehl, V., Rajewsky, K. and Somatic mutations of the CD95 gene in human B cells as a side-effect of the germinal center reaction
JOURNAL REFERENCE AUTHORS	2 (bases 1 to 702) Kuppers, M., Re,D., Brauning, A., Wolf, J., Hansmann, M.L., Diehl, V., Kuppers, R. and Rajewsky, K. Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg cells
TITLE	Unpublished 3 (bases 1 to 702) Muschen, M. Direct Submission
JOURNAL REFERENCE AUTHORS	Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931 Köln, GERMANY
COMMENT FEATURES	Related sequences: D31968 X89101 AJ279011 AJ279013. 1. 702 Location/Qualifiers
SOURCE	

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db_xref="taxon:9606"
cell_type="Reed-Sternberg cells"
note="Hodgkin's disease tissue-polymorphic allele (+275)"
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<1..313
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/number=1
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/product="CD95 antigen"
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BASE COUNT	107 a	197 c	264 g	134 t
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Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 148; Conservative 0.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
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RESULT 10	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE
HSAA279011	702 bp	Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas), exon 1.	U02790.1	GI:13539238	Apo-1 Fas; CD95 antigen; CD95 gene.	human.

REFERENCE	Eukaryotes
AUTHORS	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 1 (bases 1 to 702)
TITLE	Muschen,M., Re,D., Jungnickel,B., Diehl,V., Rajewsky,K. and Kuppers,R.
JOURNAL	Somatic mutations of the CD95 gene in human B cells as a side-effect of the germinal center reaction
REFERENCE	2 (bases 1 to 702)
AUTHORS	Muschen,M., Re,D., Brauningner,A., Wolf,J., Hansmann,M.L., Diehl,V., Kuppers,R. and Rajewsky,K.
TITLE	Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg cells
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 702)
AUTHORS	Muschen,M.
TITLE	Direct Submission
JOURNAL	Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931 Koeln, GERMANY
COMMENT	Related sequences: D31968 X88101
FEATURES	location/Qualifiers
SOURCE	1..702

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    /note="Hodgkin's disease tissue"
    1..702
    /gene="CD95"
    <1..313
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    /gene="CD95"
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5'UTR
CDS

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Matches 147	Conservative	0	Mismatches 1	
QY 1	galtccgcctggcagagcgcgagctccgcgcgcctcccgagagaccactgcgtccacgtt	60		
Db 555	GACCCCGCGGGCAGACGGGGCAGCTCCGGGCGTCCTCGAGACACTGCGCTCCACGTT	614		
QY 61	gaagtcgagcctgaggggagcgagcaagaattgaagcggaagcttggaagctttgggtcgc	120		
Db 615	GAGGTGGCGCTGGCGGCGCGACGAGAAATTGAAGCGGAAAGCTGGGAACTTTAGGTCGC	674		
QY 121	tggaggggagaccgcggttgagagagaga	148		
Db 675	TGGAGGGGAGACCCGGGTTGGAGAGAGCA	702		
RESULT 11				
LOCUS HSA279013	HSA279013	702 bp	DNA	linear PRI 02-APR-2001
DEFINITION Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas), exon				
ACCESSION AJ279013.1	GI:13539242			
VERSION Apo-1 Fas; CD95 antigen; CD95 gene.				
KEYWORDS human.				
SOURCE Homo sapiens				
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE 1 (bases 1 to 702)				
AUTHORS Muschen.M., Re.D., Jungnickel.B., Diehl.V., Rajewsky.K. and				
Kuppers.R.				
TITLE Somatic mutations of the CD95 gene in human B cells as a				
JOURNAL Unpublished				
REFERENCE 2 (bases 1 to 702)				
AUTHORS Muschen.M., Re.D., Brauninger.A., Wolf.J., Hansmann.M.L., Diehl.V.,				
Kuppers.R. and Ralewsky.K.				
TITLE Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg				
JOURNAL Unpublished				
REFERENCE 3 (bases 1 to 702)				
AUTHORS Muschen.M.				
TITLE Direct Submission				
JOURNAL Submitted (19-SEP-2000) Muschen M., Department of Immunology,				
Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931				
Koeln, GERMANY				
COMMENT Related sequences: D31968 X89101 AJ279011 AJ279012.				
FEATURES				
source	Location/Qualifiers			
gene	1..702			
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	/cell_type="Reed-Sternberg cells"			
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Best Local Similarity	98.6%	Pred. No. 1,2e-23;	Indels 0;	Gaps 0;
Matches 146;	Conservative	0;	Mismatches 2;	
QY 1 gatccgcgtgacgagcgggagcagctccggcgctcctctggagaccactgcgtccacgtt 60	11			
Db 555 GACCCCGCTGGGCGAGCGGGGCGAGCTCCGGCGCTCTCTGGAGACACTGGCGCTCCAGGTT 614				
QY 61 gaaggctggcgtggggggcgagacgaatgaagcggaaagctctgggaagctttaagttcgc 120	11			
Db 615 GAGGTGGGCGATGGGGGGCGGACAGGAATTGAAGCGGAAAGTCGGGAACCTTTAGGGTCGC 674				
QY 121 tggagggggaccccggtctggagaagaga 148	11			
Db 675 TCGAGGGGGGACCCCGGTGGAGAGAGGA 702				

RESULT 12	HUMFAS	2165 bp	DNA	linear	PRI 14-APR-2000
LOCUS	HUMFAS	Human DNA for Fas antigen, promoter region.			
DEFINITION	D31968				
ACCESSION	D31968.1	GI:961455			
VERSION					
KEYWORDS	Fas antigen.				
SOURCE	Homo sapiens blood DNA, clone pF7.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 2165) Wade, N., Matsumura, M., Ohba, Y., Kobayashi, N., Takizawa, T. and Nakanishi, Y.				
TITLE	Transcription stimulation of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection				
JOURNAL	J. Biol. Chem. 270 (30), 18007-18012 (1995)				
MEDLINE	95355401				
REFERENCE	2 (bases 1 to 2165)				
AUTHORS	Nakanishi, Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Ishikawa 920-0934, Japan (E-mail: nakanaka@pbs.p.kanazawa-u.ac.jp, Tel: 076-234-4424, Fax: 076-234-4480)				
FEATURES	location/Qualifiers				
source	1. .2165 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="pF7" /tissue_type="blood" 79. .87 /bound_moiety="NF-IL6" 276. .284 /bound_moiety="NF-IL6" 481. .489 /bound_moiety="NF-IL6" 772. .780 protein_bind				

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/ complement(<36507. .36887)
/ gene="JPH3"
/ note="JP3"
/ complement(<36507. .36887)
/ gene="JPH3"
/ note="component of the junctional complex between plasma
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/ product="junctionophilin 3"
/ protein_id="AAL40941.1"
/ db_xref="GI:17646245"
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BASE COUNT 29056 a 32731 c 30696 g 28283 t 4254 others
ORIGIN

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Best Local Similarity 12.4%; Pred. No. 0.0032;
Matches      80; Conservative 293; Mismatches 269;

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	QY	19	gagcagctcgcgcgcctccgcgagaccctcgcgcacccgttgagtgagcgtggagc	78	
Db	50777	SBSTBMGCTMCCKBSAASVDYRYKBTMYRVRVCSMYVYKBSMSYARSKSGKR	50836		
QY	79	gagcaggaattgaagcggaaatctctggaagatcttaagctctcggagggagaccgcagt	138		
Db	50837	VRSSMKCSRRKAKMSTVSMMRSMKDRKCSCHSHYKSKSMKWTSDYDRCVAAA	50896		

[illegible][illegible]

Accession	Sequence	Position
Db	51317 YKRMGKCTCTMMNSMRKRCMGMSAGGSMNGAKYSIMWSTSKYGRWTCMRSCMYMCTSC	613
Qy	614 GGCACAGAACCCGGGCGCCATTATGCGCAAGAAACTGAGCAGCCT	51376
Db	51377 MTRSCCMGMCCTCTCTSMKRGYTSRRCYCAIYMSKCSYSYCMRCGM	51423
RESULT	14	
LOCUS	166494	
DDPBYSEQUENCE	7218 bp	22

KEYWORDS	VERSION
166494.1 GI:2724471	
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 7218)
AUTHORS	Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
TITLE	Recombinant fowlpox virus
JOURNAL	Patent: US 5670367-A 14 23-SEP-1997;
FEATURES	Location/Qualifiers 1..7218
BASE COUNT	/organism="unknown" 1944 a 1491 c 1486 g 1929 t 368 others
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Query Match	7.5%; Score 54; DB 6; Length 7218; Best Local Similarity 8.2%; Pred. No. 0.02; Matches 24; Conservative 159; Mismatches 109; Indels 0; Gaps 0;
OY	401 ctgtgtaacgcttttattatgtcacacagagaagaaagcgccttcctcccgga 460
Db	1194 yyy 1253
OY	461 attctctctaagactgaagtgcgtcgtcgtggtttcatlgtttttctg 520
Db	1254 yyy 1313
OY	521 ccctctctctctctcttcttgccctctcttgatgtcacaccatgtgatctctg 580
Db	1314 yyy 1373
OY	581 tctctcgtgggttgtgtgacctgtcccacagacagaccgcgcctatatgtg 640
Db	1374 yyy 1433
OY	641 ccagaagaactgagcagcctgtttgaaaagtcctcgtcctagaatgccag 692
Db	1434 ygtaccaaatctttctamctcttttAACACTTGCAATGATAATTACAG 1485
RESULT 15	
LOCUS	AP004479 41820 bp DNA linear PLN 14-DEC-2001
DEFINITION	Lotus japonicus genomic DNA, chromosome 1, clone:LjT03H13, TM0012b,
ACCESSION	complete sequence.
VERSION	AP004479
KEYWORDS	AP004479.1 GI:17736846
SOURCE	HTG.
ORGANISM	Lotus japonicus DNA, clone_LjT library clone:LjT03H13. Lotus japonicus Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus. 1 (sites) Sato, S., Kaneko, T., Nakamura, Y., Asamizu, E., Kato, T. and Tabata, S. Structural Analysis of a Lotus japonicus genome. 1. Sequence Features and Mapping of Fifty-six YAC clones which cover the 5.4 Mb Regions of the Genome Unpublished 2 (bases 1 to 41820) Nakamura, Y. Direct Submision Submitted (13-DEC-2001) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research, 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:yinakamukazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:81-458-52-3935, Fax:81-458-52-3934) location/Qualifiers 1..41820 Location/Qualifiers 1..41820

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Best Local Similarity	58.6%;	Pred. NO. 0.56;		
Matches 102; Conservative	0;	Mismatches 69;	Indels 3;	Gaps 1

[illegible]

Search completed: September 7, 2002, 18:26:31
Job time: 29090 sec

[illegible]

	RESULT 15				
AP004479/c	AP004479	41820 bp	DNA	linear	PLN 14-DEC-2001
LOCUS	Lotus japonicus genomic DNA, chromosome 1,				clone: jT03H13, TM0012b
DEFINITION	complete sequence.				
ACCESSION	AP004479				
VERSION	AP004479.1	GI:17736846			
KEYWORDS	HTG.				
SOURCE	Lotus japonicus DNA, clone: jT03H13.				
ORGANISM	Lotus japonicus				

REFERENCE	1 (sites)	
AUTHORS	Sato, S., Kaneke, T., Nakamura, Y., Asamizu, E., Kato, T. and Tabata, S.	
TITLE	Structural Analysis of a Lotus japonicus Genome. I. Sequence Features and Mapping of Fifty-six TAC clones which cover the 5.4 Mb regions of the genome	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 41820)	
AUTHORS	Nakamura, Y.	
TITLE	Submitted	
JOURNAL	Submitted (13-DEC-2001) Yasukazu Nakamura, Kazuo DNA Research Department of Plant Gene Research: 1532-3, Yana,	

FEATURES	location/Qualifiers
source	1. .41820
	/organism="Lotus japonicus"
	/db_xref="taxon:343305"

[illegible]

PA (HYSE-) HYSEQ INC.
Tang YT. I-III C. Remanec pm.

XX	(HYSE-) HYSEQ INC.
PA	Tang YT, Liu C, Drmanac RT;
PI	WPI, 2001-514838/56.
XX	P-PSDB; AAO02346.
DR	Isolated nucleic acids and polypeptides, useful for preventing
XX	diagnosing and treating e.g. leukaemia, inflammation and immune
PT	disorders -
PT	
XX	Claim 1; SEQ ID NO 2337; 1399pp + Sequence Listing; English.
XS	The invention relates to human polynucleotides (AAI79941-AAI93841) and
PS	the encoded proteins (AAO00010-AAO1910) that exhibit activity elating to
CC	cytokine, cell proliferation or cell differentiation or which may induce
CC	production of other cytokines in other cell populations. The
CC	polynucleotides and polypeptides have various cytokine-like activities,
CC	e.g. stem cell growth factor activity, haematopoiesis regulating
CC	activity, tissue growth factor activity, immunomodulatory activity and/or
CC	activin/inhibin activity and may be useful in the diagnosis and/or
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC	inflammation.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_ptc_sequences.
XX	
SQ	Sequence 386 BP; 213 A; 30 C; 52 G; 72 T; 19 other:
	Query Match 6.3%; Score 45.6; DB 22; Length 386;
	Best Local Similarity 52.8%; Pred No. 0.0037;
	Matches 93; Conservative 0; Mismatches 83; Indels 0; Gaps 0
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OY	472 aagactgtaagtgcgtcgctgaagtggttcatattgttttgttttctgcctctctt 531
Db	173 TTTTTTYTAATCCCCCCCCCCCNNNTTTTTTTTTTTTTTTTTTTTTTTTTTTT 114
OY	532 ctctcttgcctctcttagcttgaacctccatggtgatcttcgttggtcctg 587
Db	113 TTNG 58
RESULT	5
AAI82334/c	
ID	AAI82334 standard; cDNA: 423 BP.
AC	AAI82334;
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XX	06-NOV-2001 (first entry)
DT	
XX	
XX	Human polynucleotide SEQ ID NO 2394.
DE	
XX	Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW	vaccine; peptide therapy; stem cell growth factor; haematopolesis;
KM	tissue growth factor; immunomodulatory; cancer; leukaemia;
KW	nervous system disorders; arthritis; inflammation; ss.
OS	Homo sapiens.
PN	WO200164835-A2.
PD	07-SEP-2001.
PF	26-FEB-2001; 2001WO-US04927.
PR	28-FEB-2000; 2000US-0515126.

18-MAY-2000; 2000US-0577409.
 (HYSE-) HYSEQ INC.
 Tang YT, Liu C, Drmanac RT;
 WPI: 2001-514838/56.
 P-PSDB: AA002403.

Isolated nucleic acids and polypeptides, useful for preventing
 disorders -
 diagnosing and treating e.g. leukaemia, inflammation and immune

Claim 1: SEQ ID NO 2394; 1399pp + Sequence Listing; English.

The invention relates to human polynucleotides (AA179941-AA193841) and
 the encoded proteins (AA000010-AA013910) that exhibit activity relating to
 cytokine, cell proliferation or cell differentiation or which may induce
 production of other cytokines in other cell populations. The
 polynucleotides and polypeptides are useful in gene therapy, vaccines or
 peptide therapy. The polypeptides have various cytokine-like activities,
 e.g. stem cell growth factor activity, haematopoietic regulating
 activity, tissue growth factor activity, immunomodulatory activity and
 treatment of cancer, leukaemia, nervous system disorders, arthritis and
 inflammation.
 Note: The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/published_pcl_sequences.

Sequence 423 BP; 205 A; 43 C; 87 G; 88 T; 0 other;

Query Match
 Best Local Similarity 6.3%; Score 45.4; DB 22; Length 423;
 Matches 97; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
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 Db 253 ttttttttAAAGGCCCCCCCCCTTTTTCCTCCCGCGGGGAAATAATTTT 194
 QY 532 ctctcttgccttcttgcctgacatggtatctgctgctgctcctctt 194
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 QY 592 ggt 594
 Db 133 GTT 131

RESULT 6
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 ID AA192484 standard; cDNA; 442 BP.

AA192484;

06-NOV-2001 (first entry)

Human polynucleotide SEQ ID NO 12544.

Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation; ss.
 OS Homo sapiens.
 XX
 XX
 PN MO200164835-A2.

07-SEP-2001.
 26-FEB-2001; 2001WO-US04927.
 28-FEB-2000; 2000US-0515126.
 18-MAY-2000; 2000US-0577409.
 (HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;
 WPI: 2001-514838/56.
 P-PSDB: AA012553.

Isolated nucleic acids and polypeptides, useful for preventing
 disorders -
 diagnosing and treating e.g. leukaemia, inflammation and immune

Claim 1: SEQ ID NO 12544; 1399pp + Sequence Listing; English.

The invention relates to human polynucleotides (AA179941-AA193841) and
 the encoded proteins (AA000010-AA013910) that exhibit activity relating to
 cytokine, cell proliferation or cell differentiation or which may induce
 production of other cytokines in other cell populations. The
 polynucleotides and polypeptides are useful in gene therapy, vaccines or
 peptide therapy. The polypeptides have various cytokine-like activities,
 e.g. stem cell growth factor activity, haematopoietic regulating
 activity, tissue growth factor activity, immunomodulatory activity and
 treatment of cancer, leukaemia, nervous system disorders, arthritis and
 inflammation.
 Note: The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/published_pcl_sequences.

Sequence 442 BP; 175 A; 73 C; 104 G; 83 T; 7 other;

Query Match
 Best Local Similarity 6.3%; Score 45.4; DB 22; Length 442;
 Matches 82; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
 QY 412 ttttattgacacagaagaagaactgctgtccctcgcgggaattctctt 471
 Db 319 ttttttttTGCCCCCAAAATAATTTTCCTCCCGCGGGTtttttttttt 260
 QY 472 aagaactgaagtcgctgctgagtggttcaattgtttgttttcttctctt 531
 Db 259 ttttttttAAAGGCCCCCCCCCTTTTTCCTCCCGCGGGTtttttttttt 200
 QY 532 ctctcttgccttcttgcctgacatggtatctgctgctgctcctctt 554
 Db 199 ttttttttTTTtt 177

RESULT 7
 AA185304/C
 ID AA185304 standard; cDNA; 404 BP.

AA185304;

06-NOV-2001 (first entry)

Human polynucleotide SEQ ID NO 5364.

Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation; ss.
 OS Homo sapiens.
 XX
 XX
 PN MO200164835-A2.

XX 07-SEP-2001.
 PD 26-FEB-2001; 2001WO-US04927.
 PF 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI: 2001-514838/56.
 DR P-PSDB; AAO05373.
 XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX Claim 1; SEQ ID NO 5364; 1399pp + Sequence Listing; English.
 PS The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 SQ Sequence 404 BP; 205 A; 47 C; 82 G; 62 T; 8 other;

Query Match 5.9%; Score 42.4; DB 22; Length 404;
 Best Local Similarity 51.6%; Pred. No. 0.031; 91; Indels 0; Gaps 0;
 Matches 97; Conservative 0; Mismatches 91;

QY 412 tttttatgtcacagaaagaagaactgccttccttcggaattctctctt 471
 DB 250 ttttttttttcccccaaaaaaaatatttttcccccggggaataattttt 191
 QY 472 aagactgtaagtcgctgagctgattcatttctgttttcttcgacctctt 531
 DB 190 ttttttttccccccccccccctttttttttttttttttttttttttttt 131
 QY 532 ctcttttgccttctttagctgacctccatgtagttctgttctgtctcgtcg 591
 DB 130 tt 71
 QY 592 ggttcgtg 599
 DB 70 AGATCGAG 63

RESULT 8
 AA183979/c
 ID AA183979 standard; cDNA: 416 BP.
 XX
 AC AA183979;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 4039.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorders; arthritis; inflammation; ss.
 XX Homo sapiens.
 OS
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PR 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI: 2001-514838/56.
 DR P-PSDB; AAO04048.
 XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX Claim 1; SEQ ID NO 4039; 1399pp + Sequence Listing; English.
 PS The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 SQ Sequence 416 BP; 210 A; 44 C; 91 G; 66 T; 5 other;

Query Match 5.8%; Score 41.6; DB 22; Length 416;
 Best Local Similarity 51.7%; Pred. No. 0.054;
 Matches 89; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 412 tttttatgtcacagaaagaagaactgccttccttcggaattctctctt 471
 DB 292 ttttttttcccccccccaaaaaaaatatttttcccccggggaataattttt 233
 QY 472 aagactgtaagtcgctgagctgattcatttctgttttcttcgacctctt 531
 DB 232 ttttttttccccccccccccnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 173
 QY 532 ctctttgaccttctttagctgacctccatgtagttctgttctgtctcgtcg 583
 DB 172 tt 121

RESULT 9
 AA189184/c
 ID AA189184 standard; cDNA: 420 BP.
 XX
 AC AA189184;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 9244.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 XX nervous system disorders; arthritis; inflammation; ss.
 OS Homo sapiens.
 XX WO200164835-A2.
 PN 07-SEP-2001.
 PD 26-FEB-2001; 2001WO-US04927.
 XX 28-FEB-2000; 2000US-0515126.
 XX 18-MAY-2000; 2000US-0577409.
 PR (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-514838/56.
 DR P-PSDB; AA009253.
 XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX Claim 1; SEQ ID NO 9244; 1399pp + Sequence Listing; English.
 PS The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA00010-AA013910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polypeptides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX Sequence 420 BP; 204 A; 73 C; 65 G; 75 T; 3 other;
 SQ

Query Match
 Best Local Similarity 5.7%; Score 41.2; DB 22; Length 420;
 Matches 97; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

412 ttttttttgcacagaaagaactgctgtctccctccgggaattctctt 471
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 403 TTTTGTGGGGGCCCAAAAATTTTCCCGCCCGCGCGGATTAATTTT 344
 472 aagactgaagtcgctgcgcgagtggttcaattgttttttccctctt 531
 343 TTTTATATGGGGCCCGCCCGCCCGCCCGCGCGGATTAATTTT 284
 532 cttctttcccttcttctgactgacccatgltgattctgctcgcgcg 591
 283 TTTTATATGGGGCCCGCCCGCCCGCCCGCGCGGATTAATTTT 224
 592 ggttggtgact 604
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 223 TTTTATATGGGGCCCGCCCGCCCGCCCGCGGATTAATTTT 211

DB 592 ggttggtgact 604
 OY 223 TTTTATATGGGGCCCGCCCGCCCGCCCGCGGATTAATTTT 211
 DB 223 TTTTATATGGGGCCCGCCCGCCCGCCCGCGGATTAATTTT 211

RESULT 10
 AAS44777/c
 ID AAS44777 standard; DNA; 424 BP.
 XX AAS44777;
 AC AAS44777;
 XX 18-DEC-2001 (first entry)

XX Human contig polynucleotide sequence #30.
 DE
 XX
 KW Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
 KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
 KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
 KW nervous system disorder; inflammatory disorder; cell differentiation; ds;
 KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
 KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
 KW cytostatic; antineoplastic; antiarthritic; vulnery; antiinflammation;
 KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
 KW neuroprotective; osteopathic; antidiabetic; antisthmatic; antiallergic;
 KW immunostimulant; analgesic; gene therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200164834-A2.
 PN 07-SEP-2001.
 PD 26-FEB-2001; 2001WO-US04926.
 XX 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 PR 17-JUN-2000; 2000US-0597707.
 PR 14-JUL-2000; 2000US-0616807.
 PR 19-SEP-2000; 2000US-0664641.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
 PI Drmanac R;
 DR WPI; 2001-589862/66.
 DR P-PSDB; AAU21877.
 XX Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis, treatment of
 PT cancer, neurological, inflammatory disorders and for use in arrays for
 PT detection -
 XX Claim 1; SEQ ID NO 374; 153pp; English.
 PS Sequences AAS4576-AAS44919 represent full-length polynucleotides and
 XX contig polynucleotides encoding polypeptides of the invention. The DNA
 CC and protein sequences are useful for the treatment, diagnosis and
 CC prevention of various types of disorder in a mammalian subject such as a
 CC human, dog, monkey, mouse, hamster or rat. The disorders include cancers
 CC such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
 CC as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
 CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
 CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
 CC chorea, anyotropic lateral sclerosis, spinal muscular atrophy and
 CC Menckie disease, inflammatory disorders such as nephritis, Crohn's
 CC disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
 CC bowel disease. The sequences exhibit activity relating to angiogenesis,
 CC cell proliferation, cell differentiation, stem cell growth factor,
 CC activin or inhibin, therefore, they can be used to manipulate stem cells
 CC in culture or to give rise to neuroepithelial cells that can be used to
 CC disorders. The sequences may also be used for regeneration of bone,
 CC cartilage, tendons and ligaments and in tissue repair and burn healing.
 CC Note: Some sequences for this patent did not form part of the printed
 CC specification, but were obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX Sequence 424 BP; 138 A; 60 C; 110 G; 110 T; 6 other;
 SQ

Query Match
 Best Local Similarity 5.7%; Score 40.8; DB 22; Length 424;
 Matches 97; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

Best Local Similarity 52.7%; Pred.No. 0.1;
Matches 88; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

DQ 412 ttttattgttcacagaaagaagaacctgccttgctcccttcgggaatctcctctt 477
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Db 396 tttttttttgaggcccccaaaaaaaaaaacctttcccctcccccccgaaaaaaaatttt 53

Dy 472 aaagactgtaagtcgcgtccctgaagtgttcatctgtttcgtllrlrccgcacccccccc
| | | | | | | | | | | | | | | | | | | |
Db 336 ttttttttttAAAGGGCCCCCCCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTT 27

[illegible]

RESULT	12
AAI89131/c	
AAI89131	standard; cDNA; 410 BP
ID	

XX	AA189131;
AC	
XX	
DT	06-NOV-2001 (first entry)

XX	Human polynucleotide SEQ ID NO 9191.
XX	Human: cytokine; cell proliferation; cell differentiation; gene therapy.
XX	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KM	tissue growth factor; immunomodulatory; cancer; leukaemia;
KM	nervous system disorders; arthritis; inflammation; ss.

XX Homo sapiens.
OS
XX
PN W0200164835-A2.
XY

AA	07-SEP-2001.
PD	
XX	
PF	26-FEB-2001; 2001WO-US04927
XX	

PR 28-FEB-2000; 2000US-0515128
PR 18-MAY-2000; 2000US-0577409
XX
PA (HYSE-) HYSEQ INC.
XX

aa Tang YT, Liu C, Drmanac RT
PI
XX
DR WPI; 2001-514838/56.
DR P-PSDB; AAO09200.

XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 1; SEQ ID NO 9191; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA1759941-AA193441) and
CC the encoded proteins (AA000010-AA013510) that exhibit activity eliciting
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

XX
SQ Sequence 410 BP; 197 A; 36 C; 119 G; 50 T; 8 other


```

XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA00010-AA01910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/Published_pct_sequences.
XX
SQ Sequence 398 BP; 162 A; 72 C; 71 G; 81 T; 12 other:

Query Match          5.6%; Score 40.4; DB 22; Length 398;
Best Local Similarity 46.5%; Pred. No. 0.12;
Matches 107; Conservative 0; Mismatches 123; Indels 0; Gaps 0

QY 407 tacggttttatgtgcacacagaaagaactgcctgtcccttcgggaattctc 466
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DB 387 TCCGATTTTTTGGGCCCCCAAAAAAATTTTTTCCCCCGGGGTTTAT 328
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QY 467 tccttaagactgtaagtcgctgagtggttcattgtttgttttcgccttc 526
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 327 TTTTTTTTTTTTAAAGGGCCCCCCCCNNNNNNNNNNATATTTTTTTTTTT 268
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QY 527 tcttctctttgcaccttcttagcttgcactcccatggtgatttctgctgtcct 586
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DB 267 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATATAGTCACTCCAGGTTTATG 208
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QY 587 gctggggtgtgtgtaactcgtccacacgcacagaaccggcgccattta 636
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DB 207 GAGGGTTCTTACTATTAAGGACTTTGCGCTGGAAGGAGGCTTCACA 158
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Job time: 29927 sec

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Job time: 29927 sec

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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:21:19 ; Search time 212.3 Seconds
(without alignments)
833.048 Million cell updates/sec

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Perfect score: 720
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues
Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_NA:*

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- 2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/prodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/PCRTUS_COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	54	7.5	7218	1	US-08-232-463-14
2	44	6.1	7218	1	US-08-232-463-14
3	38.4	5.3	3133	1	US-08-162-809-1
4	37.8	5.2	257	2	US-08-520-678A-24
5	37.8	5.2	257	4	US-08-897-126-24
6	37.4	5.2	72604	4	US-09-268-992-7
7	37.2	5.2	123	4	US-09-007-005-1
8	36.6	5.1	123	4	US-09-244-796-1
9	36.6	5.0	152331	3	US-09-339-964-1
10	35.4	4.9	372	4	US-09-128-135-16
11	35.2	4.9	3168	2	US-09-018-584A-13
12	35.2	4.9	3168	2	US-08-659-251-14
13	35.2	4.9	3168	5	US-09-256-490-14
14	35.2	4.9	10163	2	US-09-256-490-14
15	35.2	4.9	10163	2	US-09-256-490-14
16	35.2	4.9	10163	2	US-09-256-490-14
17	35.2	4.9	10163	2	US-09-256-490-14
18	34.6	4.8	289	4	US-09-007-005-17
19	34.6	4.8	289	4	US-09-244-796-17
20	34.6	4.8	291	1	US-07-922-723A-7
21	34.6	4.8	291	1	US-07-922-723A-7
22	34.6	4.8	291	1	US-08-074-275-7
23	34.6	4.8	291	1	US-08-480-366-7
24	34.6	4.8	291	2	US-07-952-277A-7
25	34.6	4.8	361	4	US-09-018-584A-9
26	34.2	4.8	289	4	US-09-007-005-17
27	34.2	4.8	289	4	US-09-244-796-17

28	34.2	4.8	1635	3	US-09-234-332-4	Sequence 4, Appl
29	34.2	4.8	5433	3	US-08-929-329-1	Sequence 1, Appl
30	34.2	4.8	20303	1	US-08-370-975B-6	Sequence 6, Appl
31	34.2	4.8	26764	1	US-08-370-975B-1	Sequence 1, Appl
32	34	4.7	1431	4	US-09-054-782-1	Sequence 1, Appl
33	34	4.7	1431	6	5465783-1	Patent No. 546783
34	33.8	4.7	295	4	US-09-018-594A-8	Sequence 8, Appl
35	33.8	4.7	1209	4	US-09-105-537-21	Sequence 12, Appl
36	33.8	4.7	1798	2	US-08-557-128-12	Sequence 3, Appl
37	33.8	4.7	13613	3	US-09-105-537-3	Sequence 19, Appl
38	33.8	4.7	38506	3	US-09-320-878-19	Sequence 11, Appl
39	33.6	4.7	1065	1	US-08-145-006C-11	Sequence 107, App
40	33.4	4.6	291	4	US-09-329-796-1	Sequence 107, App
41	33.4	4.6	7208	3	US-09-166-186-107	Sequence 1, Appl
42	33.4	4.6	7208	4	US-09-313-932-107	Sequence 1, Appl
43	33.2	4.6	1065	5	US-08-854-764-1	Sequence 1, Appl
44	33.2	4.6	1065	5	PCRT-US95-09377-1	Sequence 10, Appl
45	33.2	4.6	1600	4	US-09-434-288-10	

ALIGNMENTS

RESULT 1
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ9pt-fls
; US-08-232-463-14

Query Match	6.1%;	Score 44;	DB 1;	Length 7218;
Best Local	Similarity	2.68;	Pred. No. 0.0055;	
Matches	8;	Conservative	180;	Mismatches 120;
				Indels 0;

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101 ctgggaagctttaggtcgtcgtgaggggaccccggttgagagaggaagcgcgaactccta 160
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1149 RRRRRRR 1142

06-102-809-1
Sequence 1, Application US/08162809

APPLICANT: Sajjadi, Fereydoon G.
TITLE OF INVENTION: NOVEL AND

ADDRESSEE: CAMPBELL AND FLORES

COUNTRY: United States of America
ZTP: 93132

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

FILED DATE: 03/06/102,809
CLASSIFICATION: 514

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-I-T 9503

----- (013/ 000 0543
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS

STRANDEDNESS: both
TOPOLOGY: linear

LOCATION: join(3..419, 421..2858)


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; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE OF INVENTION: AND TREATING CHROMOSOME-10p RELATED DISORDERS
; FILE REFERENCE: 7653-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; CURRENT FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: 09/236,134
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 72604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: all n positions
; OTHER INFORMATION: n-a, c, g, or t
US-09-268-992-7

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Query Match          5.2%; Score 37.4; DB 4; Length 72604;
Best Local Similarity 58.6%; Pred. No. 1.1;
Matches 65; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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RESULT 7
US-09-007-005-1/c
; Sequence 1, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/35003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 123
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-007-005-1

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Query Match          5.2%; Score 37.2; DB 4; Length 123;
Best Local Similarity 39.1%; Pred. No. 0.091;
Matches 36; Conservative 29; Mismatches 27; Indels 0; Gaps 0;

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DB 115 TTTTCTTTTCTTTTCTTTGTYTCYAGGYTCYTCYTCYTCYTCYTCYTCYTCY 56
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QY 558 ctcccatgtagtattcgtctgctcgtcgtcgtcgtcgtcgtcgtcgtcgt 589
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DB 55 YTYCYAGGYTCYTCYTCYTCYTCYTCYTCYTCYTCYTCYTCYTCYTCYTCY 24
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RESULT 8
US-09-244-796-1/c
; Sequence 1, Application US/09244796
; Patent No. 6283444
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/35007
; CURRENT APPLICATION NUMBER: US/09/244,796
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 123
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-244-796-1

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Query Match          5.2%; Score 37.2; DB 4; Length 123;
Best Local Similarity 39.1%; Pred. No. 0.091;
Matches 36; Conservative 29; Mismatches 27; Indels 0; Gaps 0;

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QY 558 ctcccatgtagtattcgtctgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 589
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RESULT 9
US-09-339-964-1
; Sequence 1, Application US/09339964
; Patent No. 6025198
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-2 EXPRESSION
; FILE REFERENCE: RTS-0065
; CURRENT APPLICATION NUMBER: US/09/339,964
; CURRENT FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 4743
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(3988)
US-09-339-964-1

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,251
FILING DATE: No. 5883081 yet assigned
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,441
FILING DATE: 26-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 02307E-056410US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3168
OTHER INFORMATION: /label=pol
OTHER INFORMATION: /note="HIV-2KR subsequence encoding
US-08-659-251-14

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Best Local Similarity 49.5%; Pred. No. 1.3;
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
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DB 308 GCAAAATCCTCTGCGCCCTCTTTGTGTGCTCTCTCTCTGTCAGGTGAGTAAGTCC 249
QY 495 tggttcatttggtttcttctcgcctctctctctctctctctctctctctct 554
DB 248 CTGTACACCTCTGTATGTCATTTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 189
QY 555 gcaaccacatgttatttctgtctgtctcctcgtcgtgggttggtgtaactcgtccacc 614
DB 188 ACTTCTTAAGCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129
QY 615 gcac 618
DB 128 GGAC 125

RESULT 13

US-09-256-490-14/c
Sequence 14, Application US/09256490
Patent No. 6235881
GENERAL INFORMATION:
APPLICANT: Kraus, Guenter
APPLICANT: Wong-Straal, Florsie
APPLICANT: Talbot, Randy
APPLICANT: Poeschia, Eric
TITLE OF INVENTION: Isolation of No. 6235881el HIV-2 Proviruses
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/256,490
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/659,251
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 02307E-056410US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3168
OTHER INFORMATION: /label=pol
OTHER INFORMATION: /note="HIV-2KR subsequence encoding
US-09-256-490-14

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Best Local Similarity 49.5%; Pred. No. 1.3;
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
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QY 495 tggttcatttggtttcttctcgcctctctctctctctctctctctctctct 554
DB 248 CTGTACACCTCTGTATGTCATTTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 189
QY 555 gcaaccacatgttatttctgtctgtctcctcgtcgtgggttggtgtaactcgtccacc 614
DB 188 ACTTCTTAAGCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129
QY 615 gcac 618
DB 128 GGAC 125

RESULT 14

PCT-US96-11445-14/c
Sequence 14, Application PC/TUS9611445
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Isolation of Novel HIV-2 Proviruses
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

GenCore version 4.5
Copyright (c) 1993 - 2000 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:31:48 ; Search time 13836.9 Seconds
(without alignments)
1125.764 Million cell updates/sec

Title: US-09-834-291-2

Perfect score: 1 gatccgcctgagcagcg95.....tgctaatcaagagacgtg 720

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	720	100.0	720	32	US-09-834-291-2	Sequence 2, Appl1
2	716.8	99.6	45121	36	US-09-997-722-10	Sequence 10, Appl1
3	713	99.0	3212	32	US-09-834-291-1	Sequence 1, Appl1
4	611.8	85.0	2380	32	US-09-834-291-3	Sequence 3, Appl1
5	611.8	85.0	287	32	US-09-834-291-4	Sequence 4, Appl1
6	296.8	41.2	467	56	US-09-834-291-32	Sequence 32, Appl1
7	262.8	36.5	266	32	US-09-834-291-32	Sequence 32, Appl1
8	203.4	28.2	419	18	US-09-489-036-818	Sequence 818, Appl1
9	203.4	28.2	419	18	US-09-489-036-818	Sequence 818, Appl1
10	203.4	28.2	419	18	US-09-489-036-818	Sequence 818, Appl1
11	190.2	26.4	466	17	US-09-817-500-2214	Sequence 2214, Appl1
12	190.2	26.4	466	17	US-09-817-500-2214	Sequence 2214, Appl1
13	188.4	26.2	532	29	US-09-726-788-5938	Sequence 5938, Appl1
14	186.4	25.9	362	19	US-09-522-303-847	Sequence 847, Appl1
15	186.4	25.9	362	19	US-09-522-303-847	Sequence 847, Appl1
16	182.6	25.4	473	16	US-09-234-611-3879	Sequence 3879, Appl1
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18	182.6	25.4	473	16	US-09-234-611-3879	Sequence 3879, Appl1
19	182.6	25.4	473	16	US-09-234-611-3879	Sequence 3879, Appl1
20	182.6	25.4	473	16	US-09-234-611-3879	Sequence 3879, Appl1
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22	179.6	24.9	443	19	US-09-524-843-23549	Sequence 23549, Appl1
23	178.8	24.8	462	28	US-09-716-475-3862	Sequence 3862, Appl1
24	178.8	24.8	462	28	US-09-716-475-3862	Sequence 3862, Appl1
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26	173.8	24.1	2760	25	US-09-652-127-7930	Sequence 7930, Appl1
27	173.8	24.1	2760	25	US-09-652-127-7930	Sequence 7930, Appl1
28	173.8	24.1	2760	25	US-09-652-127-7930	Sequence 7930, Appl1
29	173.8	24.1	2760	25	US-09-652-127-7930	Sequence 7930, Appl1
30	166.4	23.1	263	12	US-08-869-540-581	Sequence 581, Appl1
31	166.4	23.1	263	12	US-08-869-540-581	Sequence 581, Appl1

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c 34 166 23.1 404 17 US-09-904-013-3927 Sequence 3927, Ap
c 35 165.4 23.0 1655 56 US-60-173-373-10224 Sequence 10224, A
c 36 163 22.6 495 25 US-09-653-911-4924 Sequence 4924, A
c 37 159 22.1 318 25 US-09-652-127-2780 Sequence 2780, Ap
c 38 158.4 22.0 1732 25 US-09-644-867-7725 Sequence 7725, Ap
c 39 158.4 22.0 1732 25 US-09-652-911-10283 Sequence 10283, A
c 40 146 20.3 324 17 US-09-396-087-4122 Sequence 4122, Ap
c 41 109.4 15.2 2165 26 US-09-665-615B-94 Sequence 94, Appl
c 42 109.4 15.2 2165 31 US-09-802-669-94 Sequence 94, Appl
c 43 85 11.8 355 18 US-09-431-517-12091 Sequence 12091, A
c 44 85 11.8 355 18 US-09-431-517-12154 Sequence 12154, A
c 45 85 11.8 371 18 US-09-489-036-24990 Sequence 24990, A

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ALIGNMENTS

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RESULT 1
US-09-834-291-2
; Sequence 2, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Kramer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: P53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834, 291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-2

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Query Match          100.0%; Score 720; DB 32; Length 720;
Best Local Similarity 100.0%; Pred. No. 2, 4e-152;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 tggaggggagcccggtcttgagagagagagcagcactcctggaacaagccctgaagccaa 180
    |||||||
Db 121 tggaggggagcccggtcttgagagagagagcagcactcctggaacaagccctgaagccaa 180
    |||||||
QY 161 gccaaagctccgcctccgcgcggtgtgagtgcgcgccgcgcgcggcggggagagaga 240
    |||||||
Db 161 gccaaagctccgcctccgcgcggtgtgagtgcgcgccgcgcgcggcggggagagaga 240
    |||||||
QY 241 gagctacagccttcagaaacacatatgtctcttcttgcaattctcagaagtaagaaa 300
    |||||||
Db 241 gagctacagccttcagaaacacatatgtctcttcttgcaattctcagaagtaagaaa 300
    |||||||
QY 301 taagtcagacacagcagcttgtaagccgagaggtcgcgaagaacggaacggaacgtttctt 360
    |||||||
Db 301 taagtcagacacagcagcttgtaagccgagaggtcgcgaagaacggaacggaacgtttctt 360
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QY 361 ctccgaaaagctatatttggtgggtctgaatgagctcttggaaggtctgtttacgtttttatt 420
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Db 361 ctccgaaaagctatatttggtgggtctgaatgagctcttggaaggtctgtttacgtttttatt 420
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Db 421 gtccacagaaaaggaacactgcctgtctccctccgcgaattctctcttaagactgta 480
    |||||||
QY 481 agtcgctgcgcctgagtggtttcaatttctgttttcttgcctctctcttcttctt 540
    |||||||
Db 481 agtcgctgcgcctgagtggtttcaatttctgttttcttgcctctctcttcttctt 540
    |||||||
QY 541 cccttcttaagctgaactccatctgattcttctgtctgtctgtctgtctgtgtgtgtgt 600
    |||||||
Db 541 cccttcttaagctgaactccatctgattcttctgtctgtctgtctgtctgtgtgtgtgt 600
    |||||||
QY 601 tactgttccacccagcagacagaccgcgcctattatttgccaaagaactgacagcct 660
    |||||||
Db 601 tactgttccacccagcagacagaccgcgcctattatttgccaaagaactgacagcct 660
    |||||||
QY 661 gttttgaaaagctccctgcctcagaaatgacagcttgacagatgcttaacaaagacgtg 720
    |||||||
Db 661 gttttgaaaagctccctgcctcagaaatgacagcttgacagatgcttaacaaagacgtg 720
    |||||||

```

```

RESULT 2
US-09-997-722-10
; Sequence 10, Application US/09997722
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997, 722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747, 377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798, 586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 45121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-997-722-10

```

```

Query Match          99.6%; Score 716.8; DB 36; Length 45121;
Best Local Similarity 99.7%; Pred. No. 3, 2e-151;
Matches 718; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 gatccgcctgggagcagcgagcagctccgcgctcctcgagaccactgcctccagctt 60
    |||||||
Db 10494 gatccgcctgggagcagcgagcagctccgcgctcctcgagaccactgcctccagctt 10553
    |||||||
QY 61 gaggtggcgctgggggagcgagcaggaattgaagcgggaagcttggaagcttcgc 120
    |||||||
Db 10554 gaggtggcgctgggggagcgagcaggaattgaagcgggaagcttggaagcttcgc 10613
    |||||||
QY 121 tggaggggagcccggtcttgagagagagagcagcactcctggaacaagccctgaagccaa 180
    |||||||
Db 10614 tggaggggagcccggtcttgagagagagagcagcactcctggaacaagccctgaagccaa 10673
    |||||||
QY 181 gccaaagctccgcctccgcgcggtgtgagtgcgcgccgcgcgcggcggggagagaga 240
    |||||||
Db 10674 gccaaagctccgcctccgcgcggtgtgagtgcgcgccgcgcgcggcggggagagaga 10733
    |||||||
QY 241 gagctacagccttcagaaacacatatgtctcttcttgcaattctcagaagtaagaaa 300
    |||||||
Db 10734 gagctacagccttcagaaacacatatgtctcttcttgcaattctcagaagtaagaaa 10793
    |||||||
QY 301 taagtcagacacagcagcttgtaagccgagaggtcgcgaagaacggaacggaacgtttctt 360
    |||||||
Db 10794 taagtcagacacagcagcttgtaagccgagaggtcgcgaagaacggaacggaacgtttctt 10853
    |||||||

```


QY 346 cggacacatttcttctcgaagaaatataatgagggcgaatgagcttctgagagctgt 405
|||||
Db 2006 cggacacatttcttctcgaagaaatataatgagggcgaatgagcttctgagagctgt 2065
QY 406 ttacgctttttatttctcagacagaaagaaagaaactgtctctcctccggagattct 465
|||||
Db 2066 ttacgctttttatttctcagacagaaagaaagaaactgtctctcctccggagattct 2125
QY 466 ctcttaagacgttaagtcgctgctgagtggttcatctttgtttttctccctt 525
|||||
Db 2126 ctcttaagacgttaagtcgctgctgagtggttcatctttgtttttctccctt 2185
QY 526 ctcttctcttcttctgac 585
|||||
Db 2186 ctcttctcttcttctgac 2245
QY 586 tgcctgggt 645
|||||
Db 2246 tgcctgggt 2305
QY 646 aaacttgagcagcctgttttgaagaaagtcctcgcgtcagaaatgcagcttcagatgt 705
|||||
Db 2306 aaacttgagcagcctgttttgaagaaagtcctcgcgtcagaaatgcagcttcagatgt 2365
QY 706 aatcaagaagacgtg 720
|||||
Db 2366 aatcaagaagacgtg 2380

RESULT 5

US-09-834-291-4
; Sequence 4, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2827
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-4

Query Match 85.0%; Score 611.8; DB 32; Length 2827;
Best Local Similarity 99.7%; Pred. No. 9.2e-128;
Matches 613; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 106 aagcttagagctgctgagagggagagagagagagagagagagagagagagagagagagag 165
|||||
Db 2213 aagcttagagctgctgagagggagagagagagagagagagagagagagagagagagagag 2272
QY 166 ggcctgcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 225
|||||
Db 2273 ggcctgcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2332
QY 226 ggcggggcggggag 285
|||||
Db 2333 ggcggggcggggag 2392
QY 286 ctgagagctagagaaatagtagacacagagagagagagagagagagagagagagagagagag 345
|||||
Db 2393 ctgagagctagagaaatagtagacacagagagagagagagagagagagagagagagagagag 2452

QY 346 cggacacatttcttctcgaagaaatataatgagggcgaatgagcttctgagagctgt 405
|||||
Db 2453 cggacacatttcttctcgaagaaatataatgagggcgaatgagcttctgagagctgt 2512
QY 406 ttacgctttttatttctcagacagaaagaaagaaactgtctctcctccggagattct 465
|||||
Db 2513 ttacgctttttatttctcagacagaaagaaagaaactgtctctcctccggagattct 2572
QY 466 ctcttaagacgttaagtcgctgctgagtggttcatctttgtttttctccctt 525
|||||
Db 2573 ctcttaagacgttaagtcgctgctgagtggttcatctttgtttttctccctt 2632
QY 526 ctcttctcttcttctgac 585
|||||
Db 2633 ctcttctcttcttctgac 2692
QY 586 tgcctgggt 645
|||||
Db 2693 tgcctgggt 2752
QY 646 aaacttgagcagcctgttttgaagaaagtcctcgcgtcagaaatgcagcttcagatgt 705
|||||
Db 2753 aaacttgagcagcctgttttgaagaaagtcctcgcgtcagaaatgcagcttcagatgt 2812
QY 706 aatcaagaagacgtg 720
|||||
Db 2813 aatcaagaagacgtg 2827

RESULT 6

US-60-172-360-3705/c
; Sequence 3705, Application US/60172360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE REFERENCE: GX-0007 P
; CURRENT APPLICATION NUMBER: US/60/172,360
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 29838
; SOFTWARE: PERL Program
; SEQ ID NO 3705
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO: 038693.2C
US-60-172-360-3705

Query Match 41.2%; Score 296.8; DB 56; Length 467;
Best Local Similarity 99.3%; Pred. No. 9.1e-57;
Matches 298; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 421 gtacacagaaagaaagaaactgtctgtctcctcccggaattctctttaaagctgta 480
|||||
Db 467 gtacacagaaagaaagaaactgtctgtctcctcccggaattctctttaaagctgta 408
QY 481 agtcgctgctgagtggttcatctttgtttttcttctgacacacacacacacacacacac 540
|||||
Db 407 agtcgctgctgagtggttcatctttgtttttcttctgacacacacacacacacacacac 348
QY 541 ccttctcttagcttgac 600
|||||
Db 347 ccttctcttagcttgac 288
QY 601 tactgttccacacagacagaaac 660
|||||
Db 287 tactgttccacacagacagaaac 228


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; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: US 09/235,076
; EARLIER FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: US 09/234,611
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: US 09/240,371
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: US 09/277,227
; EARLIER FILING DATE: 1999-03-25
; EARLIER APPLICATION NUMBER: US 09/271,490
; EARLIER FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: US 09/293,972
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 09/274,861
; EARLIER FILING DATE: 1999-03-23
; EARLIER APPLICATION NUMBER: US 60/125,453
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: US 60/126,605
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: US 09/306,350
; EARLIER FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/399,720
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: US 09/404,284
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 10451
; SOFTWARE: PL_CT_genes Version 1.0
; SEQ ID NO 315
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (465)...(578)
; OTHER INFORMATION: similar to g1178067 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-471-275-3315

```

```

Query Match      28.2%; Score 203.4; DB 18; Length 575;
Best Local Similarity 99.5%; Pred. No. 1.2e-35;
Matches 204; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gatccgcgttgaggagcgggagcagctccgcgcctctcgagagaccactgcgtccacgtt 60
   |||
Db 313 GACCCCGCTGGGAGGAGCGGGGAGCTCCGGCGCTCTCGAGACCTGCGCTCCACGTT 254
   |||
QY 61 gaggttgagcgttgaggagcgggagcaggaattgaagcggaagctctggaagcttaaggtcgc 120
   |||
Db 253 GAGGTGGGCGGTGGGGGCGGACAGAAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTGC 194
   |||
QY 121 tggagggggagcccggttggagagagagcggagactcttgacaagccctacaaagccaa 180
   |||
Db 193 TCGAGGGGAGCCCGGCTGGAGAGAGAGCGGAAGCTCTTGAGCAAGCCCTGAGCAAGCCAA 134
   |||
QY 181 gccaaagtcgcgtccggggcgaggt 205
   |||
Db 133 GCCAAGGTCCGCTCCGGCGGGGT 109

```

```

RESULT 11
US-09-333-909-2214
; Sequence 2214, Application US/09333909
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: HUMAN OSTEOBLAST LIBRARY
; CURRENT APPLICATION NUMBER: US/09/333,909
; CURRENT FILING DATE: 1999-06-16

```

```

; EARLIER APPLICATION NUMBER: 60/089,519
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/135,628
; EARLIER FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 2409
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2214
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(466)
; OTHER INFORMATION: n = A,T,C or G
US-09-333-909-2214

```

```

Query Match      26.4%; Score 190.2; DB 17; Length 466;
Best Local Similarity 87.7%; Pred. No. 1.1e-32;
Matches 207; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 288 cagacgtaggaaataagtcacagcagcagcagtggttaagccggagggctcggaagacg 347
   |||
Db 15 cggacgtaggaaataagtcacagcagcagcagcagtggttaagccggagggctcggaagacg 74
   |||
QY 348 gcaacgtttcttctcgaaaaagtataatgagggtgaatagctcttgagagctgttt 407
   |||
Db 75 gcaacgtttcttctcgaaaaagtataatgagggtgaatagctcttgagagctgttt 134
   |||
QY 408 accgtttttatgtccacagaaagaaagacgtcctgtctccctccgggaatttctc 467
   |||
Db 135 accgtttttatgtccacagaaagaaagacgtcctgtctccctccgggaatttctc 194
   |||
QY 468 ctttaagactgttaagtcgctgctgagtggtttcaattttgtttttctgcc 523
   |||
Db 195 ctttaagactgttcaagctgtgtgtgtagattatcgtccaaagtgttaattgcc 250

```

```

RESULT 12
US-09-817-500-2214
; Sequence 2214, Application US/09817500
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: HUMAN OSTEOBLAST LIBRARY
; CURRENT APPLICATION NUMBER: US/09/817,500
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/089,519
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: US 60/135,628
; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: US 09/333,909
; NUMBER OF SEQ ID NOS: 2409
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2214
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(466)
; OTHER INFORMATION: n = A,T,C or G
US-09-817-500-2214

```

```

Query Match      26.4%; Score 190.2; DB 31; Length 466;
Best Local Similarity 87.7%; Pred. No. 1.1e-32;
Matches 207; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 288 cagacgtaggaaataagtcacagcagcagcagtggttaagccggagggctcggaagacg 347

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Mon Sep 9 09:30:27 2002

us-09-834-291-2.rmp

Page 8

Search completed: September 7, 2002, 22:32:03
Job time: 43817 sec

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Db 10794 taagcagacacgagcagtggttaagccgaggggctcggaaagagcccttctt 10853
Qy 361 ctgcaaaagtataatggtggtgagtgatgagctctgagagctgtttaccgtttat 420
Db 10854 ctgcaaaagtataatggtggtgagtgatgagctctgagagctgtttaccgtttat 10913
Qy 421 gtcacacagaaagaaagcagctctgctcctcccggaatctctcttgaactgta 480
Db 10914 gtcacacagaaagaaagcagctctgctcctcccggaatctctcttgaactgta 10973
Qy 481 agtcgctgagcagtggtttcaatttctgttttcttccctctctctcttctt 540
Db 10974 agtcgctgagcagtggtttcaatttctgttttcttccctctctctcttctt 11033
Qy 541 cccctcttaagctgacatccatgtagtttctgtctgtctgctgaggtgtgtg 600
Db 11034 cccctcttaagctgacatccatgtagtttctgtctgtctgctgaggtgtgtg 11093
Qy 601 tactgcttccacgcagacagaccgcgccttattatgccaagaacttgaagcagct 660
Db 11094 tactgcttccacgcagacagaccgcgccttattatgccaagaacttgaagcagct 11153
Qy 661 gtttgaagaagtcctctgctgtagaataatgccaagctgcaagatgtaacaaagagctg 720
Db 11154 gtttgaagaagtcctctgctgtagaataatgccaagctgcaagatgtaacaaagagctg 11213
```

RESULT 2

```
US-10-222-927-123/c
; Sequence 123, Application US/10222927
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM006CIN
; CURRENT APPLICATION NUMBER: US/10/222,927
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 09/758,465
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; NUMBER OF SEQ ID NOS: 1276
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 123
; LENGTH: 710
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-222-927-123
```

```
Query Match 5.7%; Score 40.8; DB 6; Length 710;
Best Local Similarity 59.5%; Pred. No. 2.9;
Matches 69; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
Qy 469 tttaagactgaatgcgcgcctgagtggttcaatttctgttttcttgcctctc 528
Db 706 ttctgagatcgcgagcgccgcttcttcttcttcttcttcttcttcttctt 647
Qy 529 ttcttcttgccttcttcttcttcttcttcttcttcttcttcttcttcttct 584
Db 646 ttttttttttcccaaaacttggcctgatatgcgaatggttttcaatttgaatc 591
```

RESULT 3

```
US-10-198-846-8585
; Sequence 8585, Application US/10198846
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
```

```
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 8585
; LENGTH: 931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21,
; LOCATION: 22, 24, 27, 28, 36, 66, 68, 78, 86, 87, 115, 117, 133, 142,
; LOCATION: 143, 157, 158, 162, 165, 173, 176, 177, 183, 184, 186, 188,
; LOCATION: 200, 201, 203, 206, 207, 213, 214, 215, 217, 221, 222
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 229, 231, 234, 256, 294, 295, 299, 309, 310, 317, 331, 334,
; LOCATION: 339, 344, 357, 360, 361, 363, 366, 369, 380, 387, 397, 407,
; LOCATION: 412, 418, 424, 426, 428, 432, 437, 441, 444, 456, 459, 460,
; LOCATION: 462, 463, 470, 471, 472, 478, 503, 506, 520, 528, 538
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 541, 542, 544, 550, 554, 555, 557, 561, 569, 580, 595, 597,
; LOCATION: 607, 629, 638, 658, 660, 663, 666, 675, 701, 703, 710, 712,
; LOCATION: 718, 724, 726, 728, 732, 735, 746, 749, 754, 759, 761, 764,
; LOCATION: 770, 773, 779, 780, 792, 800, 801, 822, 824, 825, 826
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 832, 833, 843, 845, 854, 858, 872, 874, 885, 892, 897, 900,
; LOCATION: 909, 929, 930
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-8585
```

```
Query Match 5.7%; Score 40.8; DB 6; Length 931;
Best Local Similarity 44.5%; Pred. No. 3.1;
Matches 81; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
```

```
Qy 58 gttaggttggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 117
Db 717 gnggggngngngngngngngngngngngngngngngngngngngngngngngng 776
Qy 118 cgttgaggggagaccgcggttggaagagagagcgaactcttgacaagccctgaacgc 177
Db 777 gnnnggggggagatgngagatgnnngggggcgagaaagagagannnaagannag 836
Qy 178 caagccaaaggtccgcctcgcgcgcgtggtggtggtggtggtggtggtggtggt 237
Db 837 gaggccngngagacaagngnggggaggggggngngngngngngngngngngngng 896
Qy 238 ag 239
Db 897 ng 898
```

RESULT 4

```
US-10-098-754-7588/c
; Sequence 7588, Application US/10098754
; GENERAL INFORMATION:
; APPLICANT: Harrington, John J.
; APPLICANT: Jackson, P. David
; APPLICANT: Sherf, Bruce A.
; APPLICANT: Cain, Scott
; APPLICANT: Rundlett, Stephen E.
```


PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 325093
LENGTH: 787
TYPE: DNA
ORGANISM: Human
US-10-027-632-325093

Query Match 5.6%; Score 40; DB 7; Length 787;
Best Local Similarity 55.6%; Pred. No. 4.7;
Matches 70; Conservative 3; Mismatches 53; Indels 0; Gaps 0;
QY 424 acacagaaaggaactgctgtccctccggaattctctcttaagaactgaagt 483
DB 556 AAAAAAAAAAACTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 497
QY 484 cgcctgcctgagtgcttcttcttcttcttcttcttcttcttcttcttcttcc 543
DB 496 TTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 437
QY 544 tttctt 549
DB 436 TTTCTT 431

RESULT 11
US-10-103-313-632
Sequence 632, Application US/10103313
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P20707C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 633
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 632
LENGTH: 6573
TYPE: DNA
ORGANISM: Homo sapiens
US-10-103-313-632

Query Match 5.6%; Score 40; DB 7; Length 6573;
Best Local Similarity 47.9%; Pred. No. 8;
Matches 115; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
QY 358 ttctcgaaaagtataatgggggctgaatgagctctcggagcttgtaaccgttttt 417
DB 3892 tctatcgagataatcatgtgttttctcattgtctcttaagtgaatgaacttt 3951
QY 418 attgcaacagaaagaaactgctgtctccttcggaattctctcttaagact 477
DB 3952 attgttgcataatgctcaaccgctgcattcccaaggagaaagcaactgacatg 4011
QY 478 gtaagtcgctcgtgagtgcttcttcttcttcttcttcttcttcttcttctt 537
DB 4012 gtttctgagtgcctgcgtgattcaattcccaagatttattgagatttgcacaa 4071

QY 538 ttgccttcttagctgacatcccatgtgattctctctctctctctctctgagtg 597
DB 4072 tgttcacagcatatgctcgaatttcaatttcttcttcttcttcttcttctt 4131
RESULT 12
US-10-125-540-561/c
Sequence 561, Application US/10125540
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P211401
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 561
LENGTH: 6573
TYPE: DNA
ORGANISM: Homo sapiens
US-10-125-540-561

Query Match 5.6%; Score 40; DB 7; Length 6573;
Best Local Similarity 47.9%; Pred. No. 8;
Matches 115; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
QY 358 ttctcgaaaagtataatgggggctgaatgagctctcggagcttgtaaccgttttt 417
DB 2682 tctatcgagataatcatgtgttttctcattgtctcttaagtgaatgaacttt 2623
QY 418 attgcaacagaaagaaactgctgtctccttcggaattctctcttaagact 477
DB 2622 ATTGATTGGATATGCTGAACCAAGCTTGATTCCTAGGAGTGAAGCACTGATCATG 2563
QY 478 gtaagtcgctcgtgagtgcttcttcttcttcttcttcttcttcttcttctt 537
DB 2562 gtttttcgagtgctcgtcgaatttccatgttcttcttcttcttcttcttctt 2503
QY 538 ttgccttcttagctgacatcccatgagcttctctctctctctctctcttctt 597
DB 2502 TGTTCATCAGGATATGCTGAACCAAGCTTGATTCCTAGGAGTGAAGCACTGATCATG 2443

RESULT 13
US-10-158-057-375
Sequence 375, Application US/10158057
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P20505C1
CURRENT APPLICATION NUMBER: US/10/158,057
CURRENT FILING DATE: 2002-06-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 375
LENGTH: 6573
TYPE: DNA
ORGANISM: Homo sapiens
US-10-158-057-375

Query Match 5.6%; Score 40; DB 7; Length 6573;
Best Local Similarity 47.9%; Pred. No. 8;
Matches 115; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
QY 358 ttctcgaaaagtataatgggggctgaatgagctctcggagcttgtaaccgttttt 417
DB 3892 tctatcgagataatcatgtgttttctcattgtctcttaagtgaatgaacttt 3951

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 14:51:28 ; Search time 8462.63 Seconds
(without alignments)
1148.320 Million cell updates/sec

Title: US-09-834-291-2
Perfect score: 720
Sequence: 1 gatccgcctggcagcagcggg.....tgctatcaagaagacgtg 720

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapect 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
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9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	294.4	40.9	577	9	AA058575
4	286.4	39.8	442	9	AA011028
5	286.4	39.6	547	9	AA047220
6	285.4	38.4	447	9	AA057418
7	276.4	38.4	467	9	AA020992
8	270	37.5	376	10	H84298
9	259	36.0	398	10	H86126
10	254.4	35.3	297	9	AA018441
11	253.6	35.2	381	10	H86544
12	197	27.4	419	10	R85827
13	190	26.4	899	9	AL540709
14	185.2	25.7	666	9	AV715411
15	181.8	25.2	828	10	BI838027
16	177	24.6	506	10	BG659530
17	148.4	20.6	599	10	BF569266

C 18	142.2	19.7	1140	10	BG121070
C 19	140	19.4	617	9	AV695647
C 20	124	17.2	359	9	AV692383
21	96	13.3	285	10	BM090262
22	63.4	8.8	800	10	BI463384
23	62.4	8.7	291	9	AA383161
C 24	52	7.2	1101	12	CNS00LJC
C 25	51	7.1	844	12	CNS0052P
C 26	49.6	6.9	912	12	CNS006N3
C 27	47.4	6.6	821	10	BI956860
C 28	47.4	6.6	925	12	CNS0091P
C 29	47	6.5	1101	12	CNS00BOM
C 30	46.8	6.5	931	12	CNS005QH
C 31	46.8	6.5	1035	9	AL578906
C 32	46.4	6.4	910	12	CNS006ON
C 33	46.2	6.4	854	10	BI950608
C 34	46	6.4	272	9	AW185154
C 35	45.8	6.4	696	10	BM558974
C 36	45.8	6.4	1326	9	AW731214
C 37	45.6	6.3	474	10	BG520290
C 38	45.6	6.3	985	12	CNS02R29
C 39	45.6	6.3	1101	12	CNS00GFB
C 40	45.2	6.3	802	12	CNS02R43
41	45.2	6.3	851	9	AL514003
42	44.8	6.2	631	9	AL566993
C 43	44.8	6.2	724	12	AG058793
C 44	44.8	6.2	1050	10	BF248086
45	44.6	6.2	1064	12	CNS016P9

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
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603049567F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189752 5',
mRNA sequence.
BI763679.1 GI:15755257
ACCESSION
BI763679
VERSION
KEYWORDS
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 793)
NIH-MGC http://mgs.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LLM11474 row: e column: 17
High quality sequence stop: 786.
Location/Qualifiers
1..793
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5189752"
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/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is

FEATURES

source

[illegible][illegible]

QY 540 gcccttcttaacttgcaatcccatggtgtaattctgcttgcttcctgctcggtgtgtg 539
Db 121 gccctttcttaacttgcaatcccatggtgtaattctgcttgcttcctgctcggtgtgtg 180
QY 600 gtaccggttcaccgcgcagacagagaccggcgccattattgtggccaagaaccttgaagcc 659
Db 181 gtactcggtttccaccgcgcagacagagaccggcgccattattgtggccaagaaccttgaagcc 240
QY 660 tgttttgaagaagtcctctgctcagaatltgcagctltgcagatlgctaatcacaagaagagt 719
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Db 301 g 301

RESULT	5	547 bp	mrna	linear	EST
AA047220					02-FEB-1997
LOCUS					
DEFINITION					
ACCESSION	AA047220	z49gell.1	Soares retina	Nb4hr	Homo sapiens cDNA clone
VERSION	AA047220	IMAGE:380300	3'		mrna sequence.
KEYWORDS	AA047220.1	GI:1525120			
SOURCE	EST.				
ORGANISM	human.				
	Homo sapiens				

REFERENCE

HILLIER, L., Lennon, G., Becker, M., Bonaldó, M.F., Chiappelli, R.
1 (bases 1 to 547)

TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
COMMENT Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through IMML: contact the
IMMGE Consortium (info@imge.jini.gov) for further information.
Insert Length: 893 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 471.

FEATURES
SOURCE

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`/db_xref="GDB:1288557"`
`/db_xref="taxon:9606"`
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`/clone_lib="Soares retina N2b4HR"`
`/sex="male"`
`/tissue_type="retina"`
`/dev_stage="55 year old"`
`/lab_host="PH10B (ampicillin resistant)"`
`/note="Organ: eye; Vector: pRTT3D (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' GTTGACATCTCGAATGGAGGCGGCCCTTTTTTTTTTTTTT 3'] , double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRTT3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento`

BASE COUNT	131 a	128 c	125 g	158 t	5 others
ORIGIN					

Query Match	39.8%	Score 286.4;	DB 9;	Length 547;
Best Local Similarity	99.3%;	Pred. No. 3.4e-43;		
Matches 298; Conservative	0;	Mismatches 1;	Indels 1;	Gaps 1

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Db 1 gtcacacagaaaggaaactgcctgtccctccgcgggaattctctctttaagaactgta 60

481 agtcgcctgcctgagtgtgttcaatttggtttctgtccctctctctctt 540

[illegible]

Db 121 CCCTTCTAGCTGCACCTCCCATGCTGATTCTGCTGGTCTCTGCTGGGTTGGTGG 180

601 tactcgttccaccacgcgacagaaccgcgcctatttggccagaacttgacagcct 660

D5	TACTCGTTCACCCGACAGAACCCGGCCCTATTATTTGGCCCAAGAACTTGAGCAGCCT	240
OY	gttttgaataatcccttcctcagaaaattgggacacttgc	

241 GTTGTAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCTAACTAAGAGAGAGCT 300

RESULT 6

LOCUS	AA057418	447 bp	mRNA	linear	EST 18-SEP
DEFINITION	z559h03.s1 Soares retina N2b4d home				

[illegible]

KEYWORDS	EST.
SOURCE	human.

ORGANISM: Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homininae: Homo

REFERENCE AUTHORS	1 (bases 1 to 447) Hillier, L., Clark, N., Dubugue, T., Elliston, K., Hawkins, M., M. Hultman, M. Roberts, P. Schmitt, J. Smith, S. Staden, R. Young, Holm
----------------------	---

R. Williams, A. Wohlmann, P. and Wilson, R.
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E.,
Waterson, J., Williams, M., Woodard, T., Le, M., Lennon, G., Marra, M.,
Parsons

Project
the wasnu-Merck ESF
Unpublished (1995)
Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Tel.: 1 202 1000
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham

High quality sequence stop: 339.	FEATURES
Location/Qualifiers	source
1 447	

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        /db_xref="GDB:1289526"

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/ad_xref="taxon:9606"
/clone="IMAGE:381269"
/clone_lib="Soares retina N2hp4r"

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/sex="male"
/tissue_type="retina"
/day_start="55 Nov 2014"

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/vec_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pRTT3D (Pharmacia) with a

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modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer

QY 294 tagaataatcagccagcaagctgtttaagcccgagagctctcgaaagcaagcaccct 353
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Db 61 TTTTCGAAAAAGTTATATGGGGCTTGATGACCTTCTGAGGCTGTGTTACCGTTTTTTA 12

OY 419 ttgtcaacacagaaagaaactgctgtctcccttccgggaattctctcttaagactg 478
 |||||
 Db 121 TTGTACACACAAAGAAAGAACTGCTGTCTCCCTTCGGGAATTCTCTTAAGACTG 180
 OY 479 taagtcgctgacctgagtggttcaatttggtttcttgccc 523
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 Db 181 TTCTTACGCTGTGTGCTAGATTATCGTCCAAAGTGTTAATGCC 225

Search completed: September 7, 2002, 14:51:33
 Job time: 16192 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 14:51:16 ; Search time 8462.63 Seconds
(without alignments)
31.898 Million cell updates/sec

Title: US-09-834-291-1_COPY_44_63
Perfect score: 20
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_iny:*
15: em_gss_pln:*
16: em_gss_vtc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	17.4	87.0	282	9	BB573416
2	17.4	87.0	475	10	BM420516
3	17.4	87.0	677	10	BC410123
4	17.4	87.0	735	9	BB630820
5	17.4	87.0	796	12	BB393256
6	17.4	85.0	627	9	AL575246
7	17.4	85.0	948	9	AL551725
8	16.8	84.0	200	12	AZ766513
9	16.8	84.0	291	9	AA400303
10	16.8	84.0	302	10	BF835617
11	16.8	84.0	314	10	BF994308
12	16.8	84.0	322	12	AZ718811
13	16.8	84.0	326	9	BB508020
14	16.8	84.0	365	10	D60325
15	16.8	84.0	377	9	AM879474
16	16.8	84.0	385	10	BF994425
17	16.8	84.0	394	12	AZ231468

18	16.8	84.0	411	12	A0173492
19	16.8	84.0	498	10	BG726816
20	16.8	84.0	532	10	BM054898
21	16.8	84.0	535	9	AM704890
22	16.8	84.0	546	12	A0992080
23	16.8	84.0	563	10	BF191086
24	16.8	84.0	578	12	AZ909829
25	16.8	84.0	667	12	AG037563
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27	16.8	84.0	783	12	AG094259
28	16.8	84.0	809	12	A0860057
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32	16.4	82.0	270	9	BB195068
33	16.4	82.0	339	9	BB224461
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35	16.4	82.0	443	9	A0023648
36	16.4	82.0	468	12	A0887814
37	16.4	82.0	469	9	A1682696
38	16.4	82.0	480	9	AM643847
39	16.4	82.0	481	12	AZ583912
40	16.4	82.0	496	12	AQ05214
41	16.4	82.0	525	12	AZ120201
42	16.4	82.0	548	10	BE750959
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44	16.4	82.0	644	12	AZ336189
45	16.4	82.0	649	9	BB645432

ALIGNMENTS

RESULT 1
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LOCUS BB573416/c
DEFINITION RIKEN full-length enriched, adult male testis (DH10B) Mus musculus
ACCESSION BB573416
VERSION BB573416.1
KEYWORDS GI:11469960
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 282)
Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arahawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hirooka, T., Hirozane, T., Hodozane, Y., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shiga, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Watanabe, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A., Muramatsu, M., and Hayashizaki, Y.
RIKEN Mouse ESTs (Aizawa, K. et al. 2000)

TITLE JOURNAL
COMMENT Unpublished (2000)
Contact: Yoshinori Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitama-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Thermolabile and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Katsunari, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki

Db 46 GAGATGCCCAACTGTTT 28

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RESULT 4 735 bp mRNA linear EST 26-OCT-2001
LOCUS BB630820
DEFINITION BB630820 RIKEN full-length enriched, 16 days neonate thymus Mus
musculus cDNA clone A130029622 5', mRNA sequence.

ACCESSION BB630820
VERSION BB630820.1 GI:16467689

KEYWORDS EST.
SOURCE house musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 735)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Sasaki,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M., and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.go.jp/
URL: http://genome-resgsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,
M., Kono,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matshiki,M., Yoneda,Y., Ishikawa,T., Oawa,K., Tanaka,T., Matsura,
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,
Y., and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanka,I., Aizawa,
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.resgsc.riken.go.jp) for
further details.
e mouse tissues.

FEATURES

source

Location/Qualifiers
1. 735
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A130029622"
/clone_1lb="RIKEN full-length enriched, 16 days neonate
thymus"
/tissue_type="thymus"
/dev_stage="16 days neonate"
/lab_host="DH10B"
/note="Site_1: Sali; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken

BASE COUNT 175 a 171 c 195 g 193 t 1 others
ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 735;
Best Local Similarity 94.7%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agagatgcccaactgttt 19
|||||
Db 316 AGAGCTGCCCAACTGTT 298

RESULT 5

BB393256 796 bp DNA GSS 11-DEC-2001
LOCUS AG-ND-165J5.TF ND-TAM Anopheles gambiae genomic clone AG-ND-165J5,
DEFINITION DNA sequence.

ACCESSION BB393256
VERSION BB393256.1 GI:17339397
KEYWORDS GSS.
SOURCE African malaria mosquito.

ORGANISM

Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae

REFERENCE 1 (bases 1 to 796)
AUTHORS Sheaty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL Unpublished (2001)
COMMENT Other GSSs: AG-ND-165J5.TF
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjoftus@igf.org

This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 For
Class: BAC ends.
Location/Qualifiers
1. 796
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-165J5"
/clone_1lb="ND-TAM"
/note="Vector: pECBAC1, Site_1: HindIII"

FEATURES

source

BASE COUNT 227 a 164 c 178 g 227 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 12; Length 796;
 Best Local Similarity 94.7%; Pred. No. 2.5e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agagatgcccaactgttt 19
 |||||
 Db 762 AGAGATGCCCAACTGT 780

RESULT 6
 AL575246 627 bp mRNA linear EST 16-FEB-2001
 LOCUS AL575246 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1062YB12 5
 DEFINITION prime, mRNA sequence.
 ACCESSION AL575246
 VERSION AL575246.1 GI:12936226
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 627)
 AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
 Source
 Location/Qualifiers
 1..627
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0D1062YB12"
 /clone_lib="LTI_NFL006_PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : filang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 146 a 175 c 130 g 158 t 18 others
 ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 627;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gatgcccaactgttt 20
 |||||
 Db 59 GATGCCCAACTGT 75

RESULT 7
 AL551725 948 bp mRNA linear EST 16-FEB-2001
 LOCUS AL551725 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1062YB12 3
 DEFINITION prime, mRNA sequence.
 ACCESSION AL551725
 VERSION AL551725.1 GI:12889952
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 948)
 AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
 Source
 Location/Qualifiers
 1..948
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0D1062YB12"
 /clone_lib="LTI_NFL006_PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : filang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 236 a 261 c 212 g 235 t 4 others
 ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 948;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gatgcccaactgttt 20
 |||||
 Db 618 GATGCCCAACTGT 634

RESULT 8
 A2766513 200 bp DNA linear GSS 16-FEB-2001
 LOCUS A2766513
 DEFINITION IM0564H07F Mouse 10kb Plasmid UGCM1 library Mus musculus genomic
 clone UGCM10564H07 F. DNA sequence.
 ACCESSION A2766513
 VERSION A2766513.1 GI:12883665
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 200)
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
 and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel.: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0564 row: H column: 07
 Seq primer: CGTGTAAACGACGCCACAGT
 Class: Plasmid ends
 High quality sequence stop: 200.
 Location/Qualifiers
 1..200

FEATURES
 Source

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0564H07"
/clone_lib="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (91473211419b|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 63 a 32 c 35 g 70 t

ORIGIN

Query Match 84.0%; Score 16.8; DB 12; Length 200;
Best Local Similarity 90.0%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agagatgcccaactgttt 20
|||||
Db 137 AGAATGCCCAACTGATT 118

RESULT 9 291 bp mRNA linear EST 16-MAY-1997
AA400303
LOCUS AA400303
DEFINITION 5', mRNA sequence.
ACCESSION AA400303.1 GI:2054192
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 291)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R., and Wilson, R.
Washu-Merck EST Project 1997
Unpublished (1997)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 205.

FEATURES
source
1..291
/organism="Homo sapiens"
/db_xref="GDB:5929684"
/db_xref="taxon:9606"

/clone="IMAGE:742732"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAGAGGAGCGCGCCCAATTTTCTTTT 3']
Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3D vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 80 a 62 c 46 g 103 t

ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 291;
Best Local Similarity 90.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agagatgcccaactgttt 20
|||||
Db 25 AGAGTCCCAACTGCTT 6

RESULT 10 302 bp mRNA linear EST 13-JAN-2001
BP835617
LOCUS BP835617
DEFINITION RC4-HT0890-151100-017-ell HT0890 Homo sapiens cDNA, mRNA sequence.
ACCESSION BP835617
VERSION BP835617.1 GI:12186834
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 302)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=RC4&t2=RC4-HT0890-151100-017-ell&t3=2000-11-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 302.

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0890"
/dev_stage="Adult"
/note="Organ: head, neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTRS PCR (U.S. Letters Patent application

BASE COUNT	REFERENCE	ORGANISM	FEATURES
92 a	BB508020 BB508020.1	GI:9516983	EST. house mouse. Mus musculus
53 c	1 (bases 1 to 326)		Ekukayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
68 g	Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Arkawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hoti, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadoya, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugihara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomihaga, N., Toya, T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamana, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.		RIKEN Mouse ESTs (Kono, H., et al.)
113 t	Unpublished (2000)		Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsr.riken.go.jp, URL: http://genome-gsc.riken.go.jp/ Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S., Sasaki, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Thermotabilization and thermocatalysis of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2): 520-524 (1998) Itoh, M., Kishimoto, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5): 463-470 (1999) Carninci, P. and Hayashizaki, Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome-rtc.riken.go.jp) for further details.
			Location/Qualifiers
			1..326
			/organism="Mus musculus"
			/db_xref="taxon:10090"
			/clone="D730015M05"
			/clone_1lb="RIKEN full-length enriched, 10 days lactation, adult female mammary gland"
			/sex="female"
			/tissue_type="mammary gland"
			/dev_stage="10 days lactation, adult"
			/lab_host="DH10b"
			/note="Site_1: SalI. Site_2: BamHI. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'] GAGAGAGAGCGCGCCCACTCGAGTTTCTTTTCTTTTATN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'] GAGAGAGAGATTCGAGTTCAATTAATTAATTCACCCCGCCCGCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

Query Match	84.0%;	Score 16.8;	DB 9;	Length 326;
Best Local Similarity	90.0%;	Pred. No. 4e+02;		
Matches 18; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	agagatgcccaactgtttt 20		
		11		
Db	72	AGAGATTCGCAACTGTATT 53		
RESULT 14				
D60325/c		365 bp	mRNA	linear
LOCUS				EST 28-AUG-1995
DEFINITION				
ACCESION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
COMMENT				
FEATURES				
source				
BASE COUNT				
ORIGIN				
Query Match	84.0%;	Score 16.8;	DB 10;	Length 365;
Best Local Similarity	90.0%;	Pred. No. 4.2e+02;		
Matches 18; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	agagatgcccaactgtttt 20		
		11		
Db	221	AGAGATGCCCTAAATCTTTT 202		
RESULT 15				
AM879474/c		377 bp	mRNA	linear
LOCUS				EST 23-MAY-2000
DEFINITION				
ACCESION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				

TITLE 'M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 JOURNAL Shotgun sequencing of the human transcriptome with ORF expressed
 MEDLINE sequence tags
 COMMENT Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202863
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=8t2=PM0-OT0019-180>)
 400-003-f04kt3-2000-04-18&tl=1)
 Seq primer: puc 18 forward
 High quality sequence start: 27
 High quality sequence stop: 377.
 Location/Qualifiers

FEATURES

source
 1..377
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="OT0019"
 /dev_stage="Adult"
 /note="Organ: ovary; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 94 a 91 c 82 g 110 t
 ORIGIN

Query Match

Best Local Similarity 84.0%; Score 16.8; DB 9; Length 377;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 agagatgcccaactgttt 20
 ||||| ||||| ||||| |||||
 Db 341 ACAGAGCGCCCAACTGTTT 322

Search completed: September 7, 2002, 14:51:20
 Job time: 16179 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 8, 2002, 01:09:16 ; Search time 1826.34 Seconds
(without alignments)
33.350 Million cell updates/sec

Title: US-09-834-291-1_COPY_44_63
Perfect score: 20
Sequence: 1 agagatgcccaactgtttt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2036664 seqs, 1522705736 residues

Total number of hits satisfying chosen parameters: 4073328

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_MA_New:*
1: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US12_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US13_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	45121	6 US-10-035-832-1262	Sequence 1262, Ap
2	17	85.0	34547	7 US-10-105-299-7482	Sequence 7482, Ap
3	16.8	84.0	251	5 US-09-975-254-17065	Sequence 17065, A
4	16.8	84.0	253	5 US-09-975-254-2234	Sequence 2234, Ap
5	16.8	84.0	680	7 US-10-027-632-205156	Sequence 205156, A
6	15.8	79.0	289	5 US-09-540-2108-20774	Sequence 20774, A
7	15.8	79.0	364	5 US-09-785-276A-2716	Sequence 2716, Ap
8	15.8	79.0	416	5 US-09-785-276A-11885	Sequence 11885, A
9	15.8	79.0	440	5 US-09-785-276A-21743	Sequence 21743, A
10	15.8	79.0	440	5 US-09-785-276A-22947	Sequence 22947, A
11	15.8	79.0	440	5 US-09-785-276A-27588	Sequence 27588, A
12	15.8	79.0	440	5 US-09-785-276A-28808	Sequence 28808, A
13	15.8	79.0	451	5 US-09-785-276A-33057	Sequence 33057, A
14	15.8	79.0	451	5 US-09-785-276A-41983	Sequence 41983, A
15	15.8	79.0	451	5 US-09-785-276A-43780	Sequence 43780, A
16	15.8	79.0	454	5 US-09-785-276A-13790	Sequence 13790, A
17	15.8	79.0	458	5 US-09-785-276A-4621	Sequence 4621, Ap
18	15.8	79.0	472	5 US-09-918-995-1867	Sequence 1867, Ap
19	15.8	79.0	482	5 US-09-785-276A-34930	Sequence 34930, A
20	15.8	79.0	516	5 US-09-539-331D-35569	Sequence 35569, A
21	15.8	79.0	534	5 US-09-918-002-6997	Sequence 6997, A
22	15.8	79.0	864	6 US-10-098-754-20906	Sequence 20906, A
23	15.8	79.0	893	7 US-10-027-632-254882	Sequence 254882, A
24	15.8	79.0	909	5 US-09-886-492-18251	Sequence 18251, A
25	15.8	79.0	1157	1 PCT-US02-09188-136	Sequence 136, App

C 26	15.8	79.0	1157	1 PCT-US02-09257-91	Sequence 91, Appl
C 27	15.8	79.0	1157	1 PCT-US02-09370-140	Sequence 140, App
C 28	15.8	79.0	1157	1 PCT-US02-09922-85	Sequence 85, Appl
C 29	15.8	79.0	1157	7 US-10-105-299-180	Sequence 180, App
C 30	15.8	79.0	1179	5 US-09-919-002-1295	Sequence 1295, Ap
C 31	15.8	79.0	1195	1 PCT-US02-23913-396	Sequence 396, App
C 32	15.8	79.0	1195	6 US-10-205-823-396	Sequence 878, App
C 33	15.8	79.0	1195	6 US-10-144-678A-878	Sequence 1, Appl
C 34	15.8	79.0	1195	7 US-10-011-095-1	Sequence 1, Appl
C 35	15.8	79.0	1195	7 US-10-010-667A-1	Sequence 3023, Ap
C 36	15.8	79.0	1212	7 US-10-179-131-3023	Sequence 112, App
C 37	15.8	79.0	1294	5 US-09-620-325-172	Sequence 45839, A
C 38	15.8	79.0	2037	8 US-60-360-039-45839	Sequence 6, Appl
C 39	15.8	79.0	2037	7 US-10-011-095-6	Sequence 1214, Ap
C 40	15.8	79.0	3627	7 US-10-010-667A-6	Sequence 2023, App
C 41	15.8	79.0	3627	7 US-10-035-832-1214	Sequence 54633, A
C 42	15.8	79.0	59554	6 US-10-052-482-202	Sequence 54634, A
C 43	15.4	77.0	25	5 US-09-396-196G-54634	Sequence 1291, Ap
C 44	15.4	77.0	25	5 US-09-396-196G-54634	
C 45	15.4	77.0	226	5 US-09-442-366A-1291	

ALIGNMENTS

RESULT 1
US-10-035-832-1262
; Sequence 1262, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Engelhard, David
; APPLICANT: Morris, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1262
; LENGTH: 45121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-832-1262

Query Match 100.0%; Score 20; DB 6; Length 45121;
Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 1 agagatgcccaactgtttt 20
|||||
Db 8037 agagatgcccaactgtttt 8056

RESULT 2
US-10-105-299-7482/C
; Sequence 7482, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; PRIOR APPLICATION removed
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7482
; LENGTH: 34547
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-105-299-7482

Query Match 85.0%; Score 17; DB 7; Length 34547;
Best Local Similarity 100.0%; Pred. No. 77;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 agatgcccacactgttt 19
|||||
DB 30417, AGATGCCCAACTGTTT 30401

RESULT 3

US-09-975-254-17065

Sequence 17065, Application US/09975254

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: Heck, Gregory R.

APPLICANT: La Rosa, Thomas J.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(15309)B

CURRENT APPLICATION NUMBER: US/09/975,254

PRIOR FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US/09/263,191

PRIOR FILING DATE: 1999-03-05

NUMBER OF SEQ ID NOS: 31255

SEQ ID NO 17065

LENGTH: 251

TYPE: DNA

ORGANISM: Glycine max

OTHER INFORMATION: Clone ID: 700953921H1

US-09-975-254-17065

Query Match 84.0%; Score 16.8; DB 5; Length 251;
Best Local Similarity 90.0%; Pred. No. 41;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agaatgcccacactgttt 20
|||||
DB 9 agaatgcccacactttt 28

RESULT 4

US-09-975-254-2234

Sequence 2234, Application US/09975254

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: Heck, Gregory R.

APPLICANT: La Rosa, Thomas J.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(15309)B

CURRENT APPLICATION NUMBER: US/09/975,254

PRIOR FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US/09/263,191

PRIOR FILING DATE: 1999-03-05

NUMBER OF SEQ ID NOS: 31255

SEQ ID NO 2234

LENGTH: 253

TYPE: DNA

ORGANISM: Glycine max

OTHER INFORMATION: Clone ID: 700733864H1

US-09-975-254-2234

Query Match 84.0%; Score 16.8; DB 5; Length 253;
Best Local Similarity 90.0%; Pred. No. 41;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agaatgcccacactgttt 20
|||||
11111111111111111111

DB 185 agaatgcccacactttt 204

RESULT 5

US-10-027-632-205156

Sequence 205156, Application US/10027632

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

POLYMORPHISMS IN THE HUMAN GENOME

FILE REFERENCE: 10827.129

CURRENT APPLICATION NUMBER: US/10/027,632

PRIOR FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

SOFTWARE: FASTSEQ for Windows Version 4.0

NUMBER OF SEQ ID NOS: 325720

SEQ ID NO 205156

LENGTH: 650

TYPE: DNA

ORGANISM: Human

US-10-027-632-205156

Query Match 84.0%; Score 16.8; DB 7; Length 650;
Best Local Similarity 90.0%; Pred. No. 49;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agaatgcccacactgttt 20
|||||
DB 70 agaatgcccacactgttt 89

RESULT 6

US-09-540-210B-20774/C

Sequence 20774, Application US/09540210B

GENERAL INFORMATION:

APPLICANT: Sellhammer, Jeffrey J.

APPLICANT: Deleage, Angelo M.

APPLICANT: Stuart, Susan G.

APPLICANT: Stuve, Laura L.

APPLICANT: Mullahy, Sara J.

TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE

FILE REFERENCE: PD-1037 CIP

CURRENT APPLICATION NUMBER: US/09/540,210B

PRIOR FILING DATE: 2002-04-03

PRIOR APPLICATION NUMBER: 08/972,899

PRIOR FILING DATE: November 18, 1997

PRIOR APPLICATION NUMBER: 08/395,244

PRIOR FILING DATE: February 27, 1995

PRIOR APPLICATION NUMBER: 08/722,922

PRIOR FILING DATE: September 27, 1996

PRIOR APPLICATION NUMBER: 60/005,526

PRIOR FILING DATE: September 29, 1995

PRIOR APPLICATION NUMBER: 08/824,029

PRIOR FILING DATE: March 25, 1997

PRIOR APPLICATION NUMBER: 60/014,010

PRIOR FILING DATE: March 25, 1996

PRIOR APPLICATION NUMBER: 08/826,847

PRIOR FILING DATE: April 10, 1997

PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/903,555
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/862,178
PRIOR FILING DATE: May 22, 1997
PRIOR APPLICATION NUMBER: 60/018,217
PRIOR FILING DATE: May 23, 1996
PRIOR APPLICATION NUMBER: 08/881,589
PRIOR FILING DATE: June 24, 1997
PRIOR APPLICATION NUMBER: 60/021,275
PRIOR FILING DATE: June 25, 1996
PRIOR APPLICATION NUMBER: 08/903,802
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/905,881
PRIOR FILING DATE: August 1, 1997
PRIOR APPLICATION NUMBER: 60/025,204
PRIOR FILING DATE: August 1, 1996
PRIOR APPLICATION NUMBER: 08/903,471
PRIOR FILING DATE: July 30, 1997
PRIOR APPLICATION NUMBER: 60/025,478
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/903,556
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/025,217
PRIOR FILING DATE: August 22, 1996
PRIOR APPLICATION NUMBER: 08/937,142
PRIOR FILING DATE: September 23, 1997
PRIOR APPLICATION NUMBER: 60/026,598
PRIOR FILING DATE: September 24, 1996
PRIOR APPLICATION NUMBER: 08/960,746
PRIOR FILING DATE: October 29, 1997
PRIOR APPLICATION NUMBER: 60/030,144
PRIOR FILING DATE: October 30, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/755,524
PRIOR FILING DATE: November 22, 1996
PRIOR APPLICATION NUMBER: 60/007,495
PRIOR FILING DATE: November 22, 1995
PRIOR APPLICATION NUMBER: 09/021,031
PRIOR FILING DATE: February 10, 1998
PRIOR APPLICATION NUMBER: 60/039,325
PRIOR FILING DATE: February 13, 1997
PRIOR APPLICATION NUMBER: 09/035,172
PRIOR FILING DATE: March 4, 1998
PRIOR APPLICATION NUMBER: 60/040,431
PRIOR FILING DATE: March 5, 1997
PRIOR APPLICATION NUMBER: 09/041,894
PRIOR FILING DATE: March 12, 1998
PRIOR APPLICATION NUMBER: 60/040,199
PRIOR FILING DATE: March 14, 1997
PRIOR APPLICATION NUMBER: 09/050,817
PRIOR FILING DATE: March 30, 1998
PRIOR APPLICATION NUMBER: 60/043,792
PRIOR FILING DATE: April 11, 1997
PRIOR APPLICATION NUMBER: 09/074,999
PRIOR FILING DATE: May 8, 1998
PRIOR APPLICATION NUMBER: 60/048,431
PRIOR FILING DATE: May 29, 1997
PRIOR APPLICATION NUMBER: 09/107,592
PRIOR FILING DATE: June 30, 1998
PRIOR APPLICATION NUMBER: 60/052,751
PRIOR FILING DATE: July 1, 1997
PRIOR APPLICATION NUMBER: 09/094,079
PRIOR FILING DATE: June 9, 1998
PRIOR APPLICATION NUMBER: 60/049,975

PRIOR FILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SOFTWARE: PERL Program
SEQ ID NO 20774
LENGTH: 289
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00473963
NAME/KEY: unsure
LOCATION: 31, 71, 74, 267
OTHER INFORMATION: a, t, c, g, or other
US-09-540-210B-20774

Query Match 79.0%; Score 15.8; DB 5; Length 289;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gagatgcccaactgttt 20
|||||
Db 101 GAGATGCCCACTGTGT 83

RESULT 7
US-09-785-276A-2716
Sequence 2716, Application US/09785276A
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 2716
LENGTH: 364
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 158, 166, 285
OTHER INFORMATION: n = A,T,C or G
US-09-785-276A-2716

Query Match 79.0%; Score 15.8; DB 5; Length 364;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gagatgcccaactgttt 20
|||||
Db 172 gagatgcccaactgttt 190

RESULT 8

```
US-09-785-276A-11885
; Sequence 11885, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11885
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-276A-11885
```

```
Query Match          79.0%; Score 15.8; DB 5; Length 416;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 2 gagatgcccaactgttt 20
    ||| ||||| ||||| |||
Db 137 gagagcccacactgtt 155

RESULT 9
US-09-785-276A-21743/c
; Sequence 21743, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21743
; TYPE: DNA
; ORGANISM: Homo sapiens
```

US-09-785-276A-21743

```
Query Match          79.0%; Score 15.8; DB 5; Length 440;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 2 gagatgcccaactgttt 20
    ||| ||||| ||||| |||
Db 308 GAGAGCCCAACTGCTTT 290
```

```
RESULT 10
US-09-785-276A-22947/c
; Sequence 22947, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22947
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-276A-22947
```

```
Query Match          79.0%; Score 15.8; DB 5; Length 440;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 2 gagatgcccaactgttt 20
    ||| ||||| ||||| |||
Db 308 GAGAGCCCAACTGCTTT 290
```

```
RESULT 11
US-09-785-276A-27588/c
; Sequence 27588, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
```

```

; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27588
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-276A-27588

Query Match          79.0%; Score 15.8; DB 5; Length 440;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gagatgcccaactgtttt 20
    ||| ||||| ||||| |||
Db 308 GAGAAGCCCAACTGCTTT 290

RESULT 12
US-09-785-276A-28808/C
; Sequence 28808, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28808
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-276A-28808

Query Match          79.0%; Score 15.8; DB 5; Length 440;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gagatgcccaactgtttt 20
    ||| ||||| ||||| |||
Db 308 GAGAAGCCCAACTGCTTT 290

RESULT 13
US-09-785-276A-33057
; Sequence 33057, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
```

```

; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41983
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-276A-41983

Query Match          79.0%; Score 15.8; DB 5; Length 451;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gagatgcccaactgtttt 20
    ||| ||||| ||||| |||
Db 174 gagaaGCCCAACTGCTT 192

RESULT 14
US-09-785-276A-41983
; Sequence 41983, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41983
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-276A-41983

Query Match          79.0%; Score 15.8; DB 5; Length 451;
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Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gagatgcccgaactgtttt 20
||| ||||| ||||| |||
Db 174 gagaagcccgaactgtttt 192

RESULT 15
US-09-785-276A-43780

; Sequence 43780, Application US/09785276A
; GENERAL INFORMATION:

; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007B

; CURRENT APPLICATION NUMBER: US/09/785,276A
; CURRENT FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17

; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16

; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09

; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18

; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13

; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 43780
; LENGTH: 451
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-785-276A-43780

Query Match 79.0%; Score 15.8; DB 5; Length 451;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gagatgcccgaactgtttt 20
||| ||||| ||||| |||
Db 174 gagaagcccgaactgtttt 192

Search completed: September 8, 2002, 01:09:18
Job time: 37036 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:30:49 ; Search time 13836.9 Seconds
(without alignments)
31.271 Million cell updates/sec

Title: US-09-834-291-1_COPY_44_63
Perfect score: 20
Sequence: 1 agagatgcccaactgtttt 20

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
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2	20	100.0	40	32	US-09-834-291-18
3	20	100.0	40	32	US-09-834-291-26
4	20	100.0	2827	32	US-09-834-291-4
5	20	100.0	3212	32	US-09-834-291-1
6	20	100.0	732	34	US-09-910-943-719
7	17.4	87.0	26460	19	US-09-528-2378-596
8	17.4	87.0	1230230	18	US-09-438-185-1
9	17.4	87.0	1230230	18	US-09-438-185-1
10	17.4	85.0	1501	31	US-09-815-264-56014
11	17	85.0	7865	24	US-09-620-392-50130
12	17	85.0	7865	28	US-09-702-134-2703
13	17	85.0	7865	31	US-09-815-264-82703
14	17	85.0	34547	35	US-09-950-083-5331
15	17	85.0	34547	35	US-60-248-505-361
16	17	85.0	176251	63	US-60-248-505-158
17	17	85.0	236630	63	US-09-834-291-13
18	16.8	84.0	20	32	US-09-244-000A-53774
19	16.8	84.0	201	16	US-09-978-703-53774
20	16.8	84.0	201	36	PCT-US02-03987-3905
21	16.8	84.0	234	31	US-10-072-851-3905
22	16.8	84.0	234	37	US-09-283-466-6288
23	16.8	84.0	250	16	US-09-263-191-17065
24	16.8	84.0	251	16	US-09-654-617-108604
25	16.8	84.0	251	27	US-09-684-016-108604
26	16.8	84.0	251	27	US-09-263-191-2234
27	16.8	84.0	253	16	US-09-283-466-6446
28	16.8	84.0	255	16	US-08-766-606-458
29	16.8	84.0	267	11	US-08-979-854A-458
30	16.8	84.0	267	13	Sequence 12, Appl
31	16.8	84.0	267	13	Sequence 18, Appl

32 16.8 84.0 267 21 US-09-540-229-21936 Sequence 21936, A
33 16.8 84.0 269 16 US-09-283-466-6496 Sequence 6496, A
34 16.8 84.0 293 51 US-60-125-818-6768 Sequence 6768, Ap
C 35 16.8 84.0 306 1 PCM-US02-03987-6707 Sequence 6707, Ap
C 36 16.8 84.0 306 31 US-09-815-242-6707 Sequence 6707, Ap
C 37 16.8 84.0 306 37 US-10-072-851-6707 Sequence 6707, Ap
C 38 16.8 84.0 312 8 US-08-438-571A-341 Sequence 341, Appl
C 39 16.8 84.0 320 17 US-09-342-216-311 Sequence 31, Appl
C 40 16.8 84.0 320 17 US-09-342-216A-31 Sequence 31, Appl
C 41 16.8 84.0 320 14 US-09-908-601-311 Sequence 31, Appl
C 42 16.8 84.0 320 34 US-09-912-292-1183 Sequence 1183, Ap
C 43 16.8 84.0 321 15 US-09-134-000-2304 Sequence 2304, Ap
C 44 16.8 84.0 366 36 US-09-574-300-1452 Sequence 1452, Ap
45 16.8 84.0 386 17 US-09-304-517A-249988 Sequence 249988,

ALIGNMENTS

RESULT 1
US-09-834-291-12
; Sequence 12, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-12

Query Match 100.0%; Score 20; DB 32; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 agagatgcccaactgtttt 20
Db 1 agagatgcccaactgtttt 20

RESULT 2
US-09-834-291-18
; Sequence 18, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-18

US-09-834-291-18

Query Match 100.0%; Score 20; DB 32; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
Db 11 agagatgcccaactgtttt 30

RESULT 3
US-09-834-291-26
; Sequence 26, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-26

Query Match 100.0%; Score 20; DB 32; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 agagatgcccaactgtttt 20
Db 11 agagatgcccaactgtttt 30

RESULT 4
US-09-834-291-4
; Sequence 4, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2827
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-4

Query Match 100.0%; Score 20; DB 32; Length 2827;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 agagatgcccaactgtttt 20
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Db 44 agagatgcccaactgtttt 63

RESULT 5
US-09-834-291-1
; Sequence 1, Application US/09834291
; GENERAL INFORMATION:

APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIORITY APPLICATION NUMBER: PCT/DE99/03343
PRIORITY FILING DATE: 1999-10-18
PRIORITY APPLICATION NUMBER: DE 198 47 779.1
PRIORITY FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1
LENGTH: 3212
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-834-291-1

Query Match 100.0%; Score 20; DB 32; Length 3212;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 agagatgcccaactgtttt 20
|||||
Db 44 agagatgcccaactgtttt 63

RESULT 6
US-09-997-722-10
; Sequence 10, Application US/09997722
; GENERAL INFORMATION:

APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71171/RMS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIORITY APPLICATION NUMBER: US 09/747,377
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: US 09/798,586
PRIORITY FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1

SEQ ID NO 10
LENGTH: 45121
TYPE: DNA
ORGANISM: Homo sapiens
US-09-997-722-10

Query Match 100.0%; Score 20; DB 36; Length 45121;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 agagatgcccaactgtttt 20
|||||
Db 8037 agagatgcccaactgtttt 8056

RESULT 7
US-09-910-943-719/C
; Sequence 719, Application US/09910943

GENERAL INFORMATION:
APPLICANT: Hemmati-Brivanlou, Ali

APPLICANT: Altman, Curtis
TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
FILE REFERENCE: 7529/1G1480S1
CURRENT APPLICATION NUMBER: US/09/910,943
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 742
SOFTWARE: PatentIn version 3.1
SEQ ID NO 719
LENGTH: 732
TYPE: DNA
ORGANISM: Xenopus laevis
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)-(732)
OTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-719

Query Match 87.0%; Score 17.4; DB 34; Length 732;
Best Local Similarity 94.7%; Pred. No. 3,1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gagatgcccaactgtttt 20
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Db 101 gagatgcccaactgtttt 83

RESULT 8
US-09-528-237A-596/C
; Sequence 596, Application US/09528237A
; GENERAL INFORMATION:

APPLICANT: Venter, J. Craig
TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
TITLE OF INVENTION: Sequences and Uses Thereof
FILE REFERENCE: CL000284
CURRENT APPLICATION NUMBER: US/09/528,237A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 2926
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 596
LENGTH: 26460
TYPE: DNA
ORGANISM: Drosophila
US-09-528-237A-596

Query Match 87.0%; Score 17.4; DB 19; Length 26460;
Best Local Similarity 94.7%; Pred. No. 6,4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 agagatgcccaactgtttt 19
|||||
Db 23498 agagatgcccaactgtttt 23480

RESULT 9
US-09-438-185-1/C
; Sequence 1, Application US/09438185
; GENERAL INFORMATION:

APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kaiman, Sue
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185
CURRENT FILING DATE: 1999-11-11
PRIORITY APPLICATION NUMBER: US 60/108,279
PRIORITY FILING DATE: 1998-11-12

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;; PRIOR APPLICATION NUMBER: US 60/128,606
;; PRIOR FILING DATE: 1999-04-08
;; NUMBER OF SEQ ID NOS: 1074
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 1
;; LENGTH: 1230230
;; TYPE: DNA
;; ORGANISM: Chlamydia pneumoniae
US-09-438-185-1
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Query Match
Best Local Similarity 94.7%; Score 17.4; DB 18; Length 1230230;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2 gagatgcccaactgtttt 20
Db 1024745 GAGATGCCCAAACTGTTT 1024727
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RESULT 10
US-09-438-185A-1/c
; Sequence 1, Application US/09438185A
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1230230
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-438-185A-1
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Query Match
Best Local Similarity 87.0%; Score 17.4; DB 18; Length 1230230;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2 gagatgcccaactgtttt 20
Db 1024745 GAGATGCCCAAACTGTTT 1024727
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RESULT 11
US-09-815-264-56014/c
; Sequence 56014, Application US/09815264
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Dolson, Stanton B.
; APPLICANT: Koshi, Jeffrey M.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51237)G
; CURRENT APPLICATION NUMBER: US/09/815,264
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
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;; PRIOR APPLICATION NUMBER: US 09/702,134
;; PRIOR FILING DATE: 2000-10-31
;; NUMBER OF SEQ ID NOS: 109669
;; SEQ ID NO 56014
;; LENGTH: 1501
;; TYPE: DNA
;; ORGANISM: Oryza sativa
US-09-815-264-56014
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Query Match
Best Local Similarity 85.0%; Score 17; DB 31; Length 1501;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 3 agatgcccaactgtttt 19
Db 926 AGATGCCCAAACTGTTT 910
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RESULT 12
US-09-620-392-50130/c
; Sequence 50130, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 50130
; LENGTH: 7865
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-620-392-50130
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Query Match
Best Local Similarity 85.0%; Score 17; DB 24; Length 7865;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 3 agatgcccaactgtttt 19
Db 1445 AGATGCCCAAACTGTTT 1429
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RESULT 13
US-09-702-134-2703/c
; Sequence 2703, Application US/09702134
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/702,134
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 52202
; SEQ ID NO 2703
; LENGTH: 7865
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-702-134-2703
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Query Match
Best Local Similarity 85.0%; Score 17; DB 28; Length 7865;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 3 agatgcccaactgttt 19
 |||||||
 DB 1445 AGATGCCCAACTGTTT 1429

RESULT 14
 US-09-815-264-82703/C
 : Sequence 82703, Application US/09815264
 : GENERAL INFORMATION:

APPLICANT: Boukharov, Andrey A.
 APPLICANT: Cao, Yongwei
 APPLICANT: Dotson, Stanton B.
 APPLICANT: Koshl, Jeffrey M.
 APPLICANT: Kovalic, David K.
 APPLICANT: Liu, Jingdong
 APPLICANT: McIninch, James
 APPLICANT: Mu, Wei
 TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
 FILE REFERENCE: 38-21(31237)G
 CURRENT APPLICATION NUMBER: US/09/815,264
 CURRENT FILING DATE: 2001-03-23
 PRIOR APPLICATION NUMBER: US 09/620,392
 PRIOR FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: US 09/702,134
 PRIOR FILING DATE: 2000-10-31
 NUMBER OF SEQ ID NOS: 109669
 SEQ ID NO 82703
 LENGTH: 7865
 TYPE: DNA
 ORGANISM: Oryza sativa
 US-09-815-264-82703

Query Match 85.0%; Score 17; DB 31; Length 7865;
 Best local Similarity 100.0%; Pred. No. 8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 agatgcccaactgttt 19
 |||||||
 DB 1445 AGATGCCCAACTGTTT 1429

RESULT 15
 US-09-950-083-5331/C
 : Sequence 5331, Application US/09950083
 : GENERAL INFORMATION:
 : APPLICANT: Rosen, et. al
 : TITLE OF INVENTION: Human Secreted Proteins
 : FILE REFERENCE: PS805
 : CURRENT APPLICATION NUMBER: US/09/950,083
 : CURRENT FILING DATE: 2001-09-12
 : PRIOR APPLICATION NUMBER: 60/278,650
 : PRIOR FILING DATE: 2001-03-27
 : PRIOR APPLICATION NUMBER: 09/833,245
 : PRIOR FILING DATE: 2001-04-12
 : PRIOR APPLICATION NUMBER: PCT/US01/11988
 : PRIOR FILING DATE: 2001-04-12
 : PRIOR APPLICATION NUMBER: PCT/US00/06043
 : PRIOR FILING DATE: 2000-03-09
 : PRIOR APPLICATION NUMBER: PCT/US00/06012
 : PRIOR FILING DATE: 2000-03-09
 : PRIOR APPLICATION NUMBER: PCT/US00/06058
 : PRIOR FILING DATE: 2000-03-09
 : PRIOR APPLICATION NUMBER: PCT/US00/06044
 : PRIOR FILING DATE: 2000-03-09
 : PRIOR APPLICATION NUMBER: PCT/US00/06059
 : PRIOR FILING DATE: 2000-03-09
 : PRIOR APPLICATION NUMBER: PCT/US00/06042
 : PRIOR FILING DATE: 2000-03-09
 : PRIOR APPLICATION NUMBER: PCT/US00/06014
 : PRIOR FILING DATE: 2000-03-09
 : PRIOR APPLICATION NUMBER: PCT/US00/06013

PRIOR FILING DATE: 2000-03-09
 PRIOR APPLICATION NUMBER: PCT/US00/06049
 PRIOR FILING DATE: 2000-03-09
 PRIOR APPLICATION NUMBER: PCT/US00/06057
 PRIOR FILING DATE: 2000-03-09
 PRIOR APPLICATION NUMBER: PCT/US00/06824
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 PRIOR APPLICATION NUMBER: PCT/US00/07677
 PRIOR FILING DATE: 2000-03-23
 PRIOR APPLICATION NUMBER: PCT/US00/07725
 PRIOR FILING DATE: 2000-03-23
 PRIOR APPLICATION NUMBER: PCT/US00/09070
 PRIOR FILING DATE: 2000-04-06
 PRIOR APPLICATION NUMBER: PCT/US00/08982
 PRIOR FILING DATE: 2000-04-06
 PRIOR APPLICATION NUMBER: PCT/US00/08983
 PRIOR FILING DATE: 2000-04-06
 PRIOR APPLICATION NUMBER: PCT/US00/09067
 PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: PCT/US00/09066
 PRIOR FILING DATE: 2000-04-06
 PRIOR APPLICATION NUMBER: PCT/US00/09068
 PRIOR FILING DATE: 2000-04-06
 PRIOR APPLICATION NUMBER: PCT/US00/08981
 PRIOR FILING DATE: 2000-04-06
 PRIOR APPLICATION NUMBER: PCT/US00/08980
 PRIOR FILING DATE: 2000-04-06
 PRIOR APPLICATION NUMBER: PCT/US00/09071
 PRIOR FILING DATE: 2000-04-06
 PRIOR APPLICATION NUMBER: PCT/US00/09069
 PRIOR FILING DATE: 2000-04-06
 PRIOR APPLICATION NUMBER: PCT/US00/15136
 PRIOR FILING DATE: 2000-06-01
 PRIOR APPLICATION NUMBER: PCT/US00/14926
 PRIOR FILING DATE: 2000-06-01
 PRIOR APPLICATION NUMBER: PCT/US00/14963
 PRIOR FILING DATE: 2000-06-01
 PRIOR APPLICATION NUMBER: PCT/US00/15135
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 PRIOR APPLICATION NUMBER: PCT/US00/14934
 PRIOR FILING DATE: 2000-06-01
 PRIOR APPLICATION NUMBER: PCT/US00/14933
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 PRIOR APPLICATION NUMBER: PCT/US00/26337
 PRIOR FILING DATE: 2000-09-26
 PRIOR APPLICATION NUMBER: PCT/US01/13318
 PRIOR FILING DATE: 2001-04-27
 PRIOR APPLICATION NUMBER: US 60/124,146
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: US 60/167,061
 PRIOR FILING DATE: 1999-11-23
 PRIOR APPLICATION NUMBER: US 60/124,093
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: US 60/166,989
 PRIOR FILING DATE: 1999-11-23
 PRIOR APPLICATION NUMBER: US 60/124,145
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 PRIOR APPLICATION NUMBER: US 60/168,654
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/124,099
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: US 60/168,661
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/124,096
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: US 60/168,622
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/124,143
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: US 60/168,663
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/124,095
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: US 60/138,598
 PRIOR FILING DATE: 1999-06-11
 PRIOR APPLICATION NUMBER: US 60/168,665

PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/125,360
 PRIOR FILING DATE: 1999-03-19
 PRIOR APPLICATION NUMBER: US 60/138,626
 PRIOR FILING DATE: 1999-06-11
 PRIOR APPLICATION NUMBER: US 60/168,662
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/124,144
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: US 60/138,574
 PRIOR FILING DATE: 1999-06-11
 PRIOR APPLICATION NUMBER: US 60/168,667
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/124,142
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: US 60/138,597
 PRIOR FILING DATE: 1999-06-11
 PRIOR APPLICATION NUMBER: US 60/168,666
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/125,359
 PRIOR FILING DATE: 1999-03-19
 PRIOR APPLICATION NUMBER: US 60/168,664
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/126,051
 PRIOR FILING DATE: 1999-03-23
 PRIOR APPLICATION NUMBER: US 60/169,906

Query Match 85.0%; Score 17; DB 35; Length 34547;
 Best Local Similarity 100.0%; Pred. No. 11e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 agatgccaaactgttt 19
 Db 30417 AGATGCCAAACTGTTT 30401

Search completed: September 7, 2002, 22:31:31
 Job time: 43785 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:21:05 ; Search time 212.3 Seconds
(without alignments)
23.140 Million cell updates/sec

Title: US-09-834-291-1_COPY_44_63
Perfect score: 20
Sequence: 1 agagatgcccaactgtttt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA:*
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCRNUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	16.8	84.0	661 3	US-08-578-634C-3
2	16.8	84.0	43795 3	US-08-742-185-101
3	15.8	79.0	1195 4	US-09-323-873A-1
4	15.8	79.0	3627 4	US-09-323-873A-6
5	15.4	77.0	1644 3	US-07-903-047-7
6	15.4	77.0	1644 3	US-09-111-752-13
7	15.4	77.0	1644 4	US-09-380-061B-15
8	15.4	77.0	1704 1	US-08-460-934-5
9	15.4	77.0	1704 2	US-08-782-118-5
10	15.4	77.0	1908 2	US-08-460-934-8
11	15.4	77.0	1908 2	US-08-782-118-8
12	15.2	76.0	668 3	US-08-578-634C-2
13	14.8	74.0	495 3	US-09-109-204-19
14	14.8	74.0	605 3	US-09-109-204-5
15	14.8	74.0	2125 3	US-09-109-204-5
16	14.8	74.0	26664 4	US-09-564-805-28
17	14.4	72.0	832 1	US-08-473-496-1
18	14.4	72.0	832 5	US-08-454-028-3
19	14.4	72.0	832 5	PCT-US94-05388-3
20	14.4	72.0	832 5	PCT-US95-09121-1
21	14.4	72.0	832 5	PCT-US95-07496-3
22	14.4	72.0	978 3	US-08-217-609A-4
23	14.4	72.0	978 4	US-08-873-235B-4
24	14.4	72.0	2364 2	US-08-981-690-1
25	14.4	72.0	2451 3	US-09-217-609A-21
26	14.4	72.0	2451 4	US-08-873-235B-21
27	14.4	72.0	9103 1	US-08-466-033-182

28	14.4	72.0	9103 1	US-08-444-733-182	Sequence 182, App
29	14.4	72.0	9103 2	US-08-464-134-182	Sequence 182, App
30	14.4	72.0	9103 2	US-08-461-361-182	Sequence 182, App
31	14.4	72.0	9103 2	US-08-485-910-182	Sequence 156, App
32	14.4	72.0	9103 2	PCT-US95-06266-156	Sequence 11, App
33	14.2	71.0	63 5	PCT-US96-03940-11	Sequence 64, App
34	14.2	71.0	612 4	US-09-385-982-64	Sequence 15, App
35	14.2	71.0	660 3	US-09-284-782-15	Sequence 104, App
36	14.2	71.0	756 5	PCT-US96-03940-2	Sequence 52, App
37	14.2	71.0	957 4	US-08-858-207A-104	Sequence 28, App
38	14.2	71.0	1067 4	US-09-058-368-6	Sequence 3, App
39	14.2	71.0	1255 4	US-09-227-357-52	Sequence 27, App
40	14.2	71.0	1284 5	PCT-US96-03940-28	Sequence 10, App
41	14.2	71.0	1407 5	PCT-US96-03940-3	Sequence 3, App
42	14.2	71.0	1461 5	PCT-US96-03940-27	Sequence 11, App
43	14.2	71.0	1492 5	US-09-657-042A-10	Sequence 3, App
44	14.2	71.0	1596 5	PCT-US94-11328A-3	Sequence 14, App
45	14.2	71.0	1757 2	US-08-453-848-14	

ALIGNMENTS

RESULT 1
US-08-578-634C-3/C
Sequence 3, Application US/08578634C
Patent No. 6025163
GENERAL INFORMATION:
APPLICANT: Vladimir Shamanin
APPLICANT: Ethel Michele De Villiers
APPLICANT: Zur Hausen
APPLICANT: Irene Leigh
APPLICANT: Harald Zur Hausen
TITLE OF INVENTION: DNA CODING FOR A PEPTIDE OF A PAPILLOMA
TITLE OF SEQUENCES: 9
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578, 634C
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B.
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8484-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 493-4935
TELEFAX: (650) 493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1... 660

US-08-578-634C-3

Query Match

Best Local Similarity 84.0%; Score 16.8; DB 3; Length 661;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 agagatgcccaactgtttt 20
Db 567 AGAGTGTGCCCAAGTGTTTT 548

RESULT 2

US-08-742-185-101
Sequence 101, Application US/08742185
Patent No. 6020476

GENERAL INFORMATION:

APPLICANT: Page, David C.
APPLICANT: Reijo, Renee
APPLICANT: Saxena, Richa
APPLICANT: Hawkins, Trevor
APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,734
FILING DATE: 31-JUL-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:

LENGTH: 43795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-742-185-101

Query Match

Best Local Similarity 90.0%; Score 16.8; DB 3; Length 43795;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 agagatgcccaactgtttt 20
Db 22516 AGAGTGTGCCCAAGTGTTTT 22535

RESULT 3

US-09-323-873A-1/c

Sequence 1, Application US/09323873A
Patent No. 6329503

GENERAL INFORMATION:

APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahon Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
FILE REFERENCE: 129,16US02
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-323-873A-1

Query Match

Best Local Similarity 79.0%; Score 15.8; DB 4; Length 1195;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gagatgcccaactgtttt 20
Db 566 GAGAAGCCCAACTGCTTT 548

RESULT 4

US-09-323-873A-6/c
Sequence 6, Application US/09323873A
Patent No. 6329503

GENERAL INFORMATION:

APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahon Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
FILE REFERENCE: 129,16US02
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 6
LENGTH: 3627
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-323-873A-6

Query Match

Best Local Similarity 79.0%; Score 15.8; DB 4; Length 3627;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gagatgcccaactgtttt 20
Db 596 GAGAAGCCCAACTGCTTT 578

RESULT 5
US-07-903-047-7/c
Sequence 7, Application US/07903047
Patent No. 5229285
GENERAL INFORMATION:
APPLICANT: Kajiya, Naoki
TITLE OF INVENTION: Thermostable luciferase of firefly,
TITLE OF INVENTION: Thermostable luciferase gene of firefly, No. 5229285el Recombi
TITLE OF INVENTION: DNA And Process For The Preparation Of Thermostable
TITLE OF INVENTION: Luciferase Of Firefly
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903.047
FILING DATE: 19920623
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1644 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA
US-07-903-047-7

Query Match 77.0%; Score 15.4; DB 1; Length 1644;
Best local Similarity 94.1%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 agagatgcccaactgt 17
|||||
Db 369 AGAGATGCTTAAGT 353

RESULT 6
US-09-111-752-13/c
Sequence 13, Application US/09111752
Patent No. 6074859
GENERAL INFORMATION:
APPLICANT: HIROKAWA, KOZO
APPLICANT: KAJIYAMA, NAOKI
APPLICANT: MURAKAMI, SEIJI
TITLE OF INVENTION: MUTANT-TYPE BIOLUMINESCENT PROTEIN, AND
TITLE OF INVENTION: PROCESS FOR PRODUCING MUTANT-TYPE LUMINESCENT PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON

STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,752
FILING DATE: 08-JUL-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126-0009-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1644 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Luciola lateralis
US-09-111-752-13

Query Match 77.0%; Score 15.4; DB 3; Length 1644;
Best local Similarity 94.1%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 agagatgcccaactgt 17
|||||
Db 369 AGAGATGCTTAAGT 353

RESULT 7
US-09-380-061B-15/c
Sequence 15, Application US/09380061B
Patent No. 6265177
GENERAL INFORMATION:
APPLICANT: SQUIRELL, DAVID JAMES
WHITE, PETER JOHN
LOWE, CHRISTOPHER ROBIN
MURRAY, JAMES AUGUSTUS HENRY
TITLE OF INVENTION: ENZYME ASSAY FOR MUTANT FIREFLY LUCIFERASE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,061B
FILING DATE: 25-AUG-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01026
FILING DATE: 7-APR-1998
APPLICATION NUMBER: GB 9707468.8
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 124-725
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1644 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1644
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-380-061B-15

Query Match 77.0%; Score 15.4; DB 4; Length 1644;
Best Local Similarity 94.1%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agagatgcccaactgt 17
|||||||
Db 369 AGAGATGCCCTAACTGT 353

RESULT 8
US-08-460-934-5/c
Sequence 5, Application US/08460934
Patent No. 5814465
GENERAL INFORMATION:
APPLICANT: TATSUMI, HIROKI
APPLICANT: FUKUDA, SATOSHI
APPLICANT: KIKUCHI, MAMORU
APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA,
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINYLATED AND A BIOLUMINESCENT
TITLE OF INVENTION: ANALYSIS METHOD
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,934
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 98857/1995
FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126-001-0

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
NAME/KEY: misc feature
LOCATION: 1..1704
OTHER INFORMATION: /note="Nucleotide sequence of the
OTHER INFORMATION: biotinylated firefly luciferase gene contained in recombin
OTHER INFORMATION: plasmid pHLf203 DNA"
US-08-460-934-5

Query Match 77.0%; Score 15.4; DB 1; Length 1704;
Best Local Similarity 94.1%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agagatgcccaactgt 17
|||||||
Db 429 AGAGATGCCCTAACTGT 413

RESULT 9
US-08-782-118-5/c
Sequence 5, Application US/08782118
Patent No. 5843746
GENERAL INFORMATION:
APPLICANT: TATSUMI, HIROKI
APPLICANT: FUKUDA, SATOSHI
APPLICANT: KIKUCHI, MAMORU
APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA,
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINYLATED AND A BIOLUMINESCENT
TITLE OF INVENTION: ANALYSIS METHOD
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/782,118
FILING DATE: 13-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/460,934
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 98857/1995
FILING DATE: 24-APR-1995

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126-001-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..1704 /note= "Nucleotide sequence of the
OTHER INFORMATION: the biotinylated firefly luciferase gene contained in recombinant
OTHER INFORMATION: biotinylated firefly luciferase gene contained in recombinant
OTHER INFORMATION: plasmid pHLf203 DNA"
US-08-782-118-5

Query Match 77.0%; Score 15.4; DB 2; Length 1704;
Best Local Similarity 94.1%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agagatgcccaactgt 17
|||||
DB 429 AGAGATGCTAACTGT 413

RESULT 10
US-08-460-934-8/C
Sequence 8, Application US/08460934
Patent No. 5814465
GENERAL INFORMATION:
APPLICANT: TATSUMI, HIROKI
APPLICANT: FUKUDA, SATOSHI
APPLICANT: KIKUCHI, MAMORU
APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
TITLE OF INVENTION: ANALYSIS METHOD
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,934
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 98857/1995
FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126-001-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1908 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..1908 /note= "The nucleotide sequence of
OTHER INFORMATION: the biotinylated firefly luciferase gene contained in
OTHER INFORMATION: recombinant plasmid pHLf248 DNA"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1908
US-08-460-934-8

Query Match 77.0%; Score 15.4; DB 1; Length 1908;
Best Local Similarity 94.1%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agagatgcccaactgt 17
|||||
DB 369 AGAGATGCTAACTGT 353

RESULT 11
US-08-782-118-8/C
Sequence 8, Application US/08782118
Patent No. 5843746
GENERAL INFORMATION:
APPLICANT: TATSUMI, HIROKI
APPLICANT: FUKUDA, SATOSHI
APPLICANT: KIKUCHI, MAMORU
APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
TITLE OF INVENTION: ANALYSIS METHOD
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/782,118
FILING DATE: 13-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/460,934
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 54625/1995

FILING DATE: 14-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 98857/1995

FILING DATE: 24-APR-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 7126-001-0

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1908 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: misc-feature

LOCATION: 1..1908

OTHER INFORMATION: /note="The nucleotide sequence of

OTHER INFORMATION: the biotinylated firefly luciferase gene contained in

FEATURE: recombinant plasmid pHLf248 DNA"

NAME/KEY: CDS

LOCATION: 1..1908

US-08-782-118-8

Query Match Best Local Similarity 77.0%; Score 15.4; DB 2; Length 1908;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtt 17

Db 369 AGAGATGCCCTAAGTGT 353

RESULT 12

US-08-578-634C-2/c

Sequence 2, Application US/08578634C

Patent No. 6025163

GENERAL INFORMATION:

APPLICANT: Vladimir Shamanin

APPLICANT: Ethel Michele De Villiers

APPLICANT: Irene Leigh

APPLICANT: Harald Zur Hausen

TITLE OF INVENTION: DNA CODING FOR A PEPTIDE OF A PAPILLOMA

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESS: Penite & Edmonds LLP

CITY: 1155 Avenue of The Americas

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

OPERATING SYSTEM: IBM PC Compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/578,634C

FILING DATE: 26-JAN-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: Abrams, Samuel B.

REGISTRATION NUMBER: 30,605

REFERENCE/DOCKET NUMBER: 8484-007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 493-4935

TELEFAX: (650) 493-5556

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 668 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..666

US-08-578-634C-2

Query Match Best Local Similarity 76.0%; Score 15.2; DB 3; Length 668;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 agagatgcccaactgttt 20

Db 567 AGAGTACCCCAAGTGT 548

RESULT 13

US-09-109-204-20/c

Sequence 20, Application US/09109204

Patent No. 6060250

GENERAL INFORMATION:

APPLICANT: Lal, Preethi

APPLICANT: Bandman, Olga

APPLICANT: Hillman, Jennifer L.

APPLICANT: Guegler, Karl J.

APPLICANT: Gorgone, Gina A.

APPLICANT: Corley, Neil C.

APPLICANT: Patterson, Chandra

TITLE OF INVENTION: HUMAN TRANSFERASES

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESS: Inocyte Pharmaceuticals, Inc.

CITY: 3174 Porter Drive

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/109,204

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Cerrone, Michael C

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0546 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-855-0572

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 495 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTNOT04
CLONE: 301251r6
US-09-109-204-20

Query Match 74.0%; Score 14.8; DB 3; Length 495;
Best Local Similarity 88.9%; Pred. No. 51;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 agatgcccaactgtttt 20
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Db 345 AGATGCCCAACTGTATT 328

RESULT 14

US-09-109-204-19
Sequence 19, Application US/09109204
Patent No. 6060250

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,204
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
FILING DATE:
APPLICATION NUMBER:

NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0546 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-855-0572

TELEX:
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 605 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: N/A
CLONE: SAGA01614F1
US-09-109-204-19

Query Match 74.0%; Score 14.8; DB 3; Length 605;

Best Local Similarity 88.9%; Pred. No. 53;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 agatgcccaactgtttt 20
||||| ||||| ||||| ||
Db 537 AGATGCCCAACTGTATT 554

RESULT 15

US-09-109-204-5
Sequence 5, Application US/09109204
Patent No. 6060250

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,204
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
FILING DATE:
APPLICATION NUMBER:

NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0546 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-855-0572

TELEX:
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 2125 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAINOT09
CLONE: 2150892
US-09-109-204-5

Query Match 74.0%; Score 14.8; DB 3; Length 2125;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 agatgcccaactgtttt 20
||||| ||||| ||||| ||
Db 1780 AGATGCCCAACTGTATT 1797

Search completed: September 7, 2002, 18:21:07
Job time: 28761 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:39:36 : Search time 1139.19 Seconds
(without alignments)
30.143 Million cell updates/sec

Title: US-09-834-291-1_COPY_44_63
Perfect score: 20
Sequence: 1 agagatgcccaactgtttt 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.*
4:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1983.DAT.*
5:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1984.DAT.*
6:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1985.DAT.*
7:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1986.DAT.*
8:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1987.DAT.*
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13:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1992.DAT.*
14:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1993.DAT.*
15:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1994.DAT.*
16:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1995.DAT.*
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24:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	AAZ88701	Human CD95 recepto
2	16.8	84.0	234	AAS51323	Enterococcus faeca
3	16.8	84.0	306	AAS53070	Enterococcus faeca
4	16.8	84.0	338	AACT18125	Human secreted pro
5	16.8	84.0	661	AAV39501	Papilloma virus ma
6	16.8	84.0	2008	AAV39297	Human RAD54 nuclei
7	16.8	84.0	3001	AAH51750	Chromosome 13q31-q
8	16.8	84.0	9821	AAI03245	Human reproductive
9	16.8	84.0	9824	AAI03246	Human reproductive

10	16.8	84.0	20072	20	AAI13026
11	16.8	84.0	43795	21	AAZ92583
12	16.8	84.0	349980	22	AAH41226
13	16.4	82.0	396	22	AAH9123
14	15.8	79.0	1157	22	AAH63808
15	15.8	79.0	1193	21	AAZ49395
16	15.8	79.0	1193	22	AAH07067
17	15.8	79.0	1195	22	AAH3924
18	15.8	79.0	1195	22	AAH3924
19	15.8	79.0	1227	23	AAH3924
20	15.8	79.0	1229	22	AAH3924
21	15.8	79.0	1294	22	AAH3924
22	15.8	79.0	2005	22	AAH3924
23	15.8	79.0	2108	24	ABA90868
24	15.8	79.0	2516	23	AAH3924
25	15.8	79.0	2757	24	AAH3924
26	15.8	79.0	3123	23	ABL16463
27	15.8	79.0	3627	21	AAZ49396
28	15.8	79.0	4005	23	ABL13428
29	15.8	79.0	4005	23	ABL13428
30	15.8	79.0	16989	23	ABL13428
31	15.8	79.0	16989	23	ABL13428
32	15.8	79.0	32172	22	AAH3924
33	15.4	77.0	150	21	AAH3924
34	15.4	77.0	496	22	AAH3924
35	15.4	77.0	1644	11	AAH3924
36	15.4	77.0	1644	14	AAH3924
37	15.4	77.0	1644	20	AAH3924
38	15.4	77.0	1644	20	AAH3924
39	15.4	77.0	1644	20	AAH3924
40	15.4	77.0	1656	20	AAH3924
41	15.4	77.0	1704	18	AAH3924
42	15.4	77.0	1704	19	AAH3924
43	15.4	77.0	1920	18	AAH3924
44	15.4	77.0	1920	19	AAH3924
45	15.4	77.0	1920	17	AAH3924

ALIGNMENTS

RESULT 1
ID AAZ88701 standard; DNA; 20 BP.
AC AAZ88701;
DT 11-MAY-2000 (first entry)
XX Human CD95 receptor promoter DNA p53 binding fragment #1.
DE Human CD95 receptor; human; screening; apoptosis-modulation;
KW p53; CD95 receptor; human; screening; apoptosis-modulation;
KW cancer chemotherapy; ss.
XX Homo sapiens.
OS
XX DE19847779-C1.
XX 03-FEB-2000.
XX 16-OCT-1998; 98DE-1047779.
XX 16-OCT-1998; 98DE-1047779.
XX 16-OCT-1998; 98DE-1047779.
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX Krammer P, Mueller-Schilling M, Oren M;
XX WPI: 2000-162245/15.
XX Novel receptor DNA useful for identifying apoptosis-modulating
XX substances potentially useful for cancer chemotherapy

PS Claim 2; Fig 5; 12pp; German.

CC This invention describes a novel p53-binding region of a human CD95
 CC receptor DNA molecule. The p53-binding region, or a vector containing
 CC it, can be used to screen for apoptosis-modulating substances
 CC potentially useful for cancer chemotherapy. This sequence represents a
 CC fragment of the human CD95 receptor promoter which is capable of
 CC binding p53.

XX Sequence 20 BP; 6 A; 4 C; 4 G; 6 T; 0 other;

Query Match Best Local Similarity 100.0%; Score 20; DB 21; Length 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
 Db 1 agagatgcccaactgtttt 20

RESULT 2

AA551323/c ID AA551323 standard; DNA: 234 BP.

AC AA551323;

DT 13-FEB-2002 (first entry)

DE Enterococcus faecalis DNA for cellular proliferation protein #100.

KW Antisense; ds; prokaryotic cellular proliferation gene;
 KW antibiotic; antibacterial; drug design.

OS Enterococcus faecalis.

PN WO200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2001; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

PA (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

DR P-PSDB; AAU33464.

DR P-PSDB; AAU33464.

XX New polynucleotides for the identification and development of

XX antibiotics, comprise sequences of antisense nucleic acids -

XX Claim 27; Seq ID No 3905; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to

XX prokaryotic cellular proliferation, their use in identifying the

XX genes themselves and the encoded proteins. The prokaryotes used are

XX *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*

XX *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The

XX invention is also useful for the identification of potential new targets

XX for antibiotic development. The antisense nucleic acids can also be used

XX and to obtain antibodies capable of binding to the expressed proteins.

CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence encodes an
 CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 234 BP; 84 A; 33 C; 46 G; 71 T; 0 other;

Query Match Best Local Similarity 84.0%; Score 16.8; DB 23; Length 234;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
 Db 87 AGAATGCACCAACTGTTT 68

RESULT 3

AA553070/c ID AA553070 standard; DNA: 306 BP.

AC AA553070;

DT 13-FEB-2002 (first entry)

DE Enterococcus faecalis DNA for cellular proliferation protein #498.

KW Antisense; ds; prokaryotic cellular proliferation gene;
 KW antibiotic; antibacterial; drug design.

OS Enterococcus faecalis.

PN WO200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2001; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

PA (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

DR P-PSDB; AAU35211.

DR P-PSDB; AAU35211.

XX New polynucleotides for the identification and development of

XX antibiotics, comprise sequences of antisense nucleic acids -

XX Claim 27; Seq ID No 6707; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to

XX prokaryotic cellular proliferation, their use in identifying the

XX genes themselves and the encoded proteins. The prokaryotes used are

XX *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*

XX *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The

XX invention is also useful for the identification of potential new targets

XX for antibiotic development. The antisense nucleic acids can also be used

XX and to obtain antibodies capable of binding to the expressed proteins.

CC expression and secretion vectors

RESULT
AAV39297

ID AAV39297 standard; CDNA; 2008 BP.
XX
AC AAV39297;
XX
DT 16-SEP-1998 (first entry)
XX
DE Human RAD54 nucleic acid sequence comprising exons 5-8.
XX
KW Human; RAD54; hRAD54; cancer; xeroderma pigmentosum; Bloom syndrome;
KW Werner's syndrome; ATR-X; diagnosis; detection; SNF2 superfamily;
KW X-linked mental retardation with alpha-thalassemia syndrome; tumour;
KW gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP844305-A2.
XX
PD 27-MAY-1998.
XX
PF 10-NOV-1997; 97EP-0308998.
XX
PR 13-NOV-1996; 96US-0030676.
XX
PA (SMR) SMITHKLINE BEECHAM CORP.
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Croce CM, Fishel RA, Rasio D, Robbins DJ;
PI WPI; 1998-274189/25.
XX
DR Human hRAD54 DNA and polypeptide - and agonists, antibodies,
XX antagonists, etc.
XX
PS Claim 1; Page 27-28; 64pp; English.
XX
CC The present sequence represents a specifically claimed partial nucleic
CC acid sequence encoding human RAD54 (hRAD54). A method for analysing a
CC sample for mutation of DNA encoding hRAD54 has been developed using a
CC DNA sequence of at least 15 and no more than 30 consecutive bases of
CC the DNA sequence encoding hRAD54. hRAD54 is a gene thought to be present
CC in tumours that display allelic imbalance at 1p32, the chromosomal band
CC identified as one of four minimal regions of chromosome 1 deletion in
CC breast carcinomas. hRAD54 is useful for production of proteins, inter
CC alia, that have been identified as novel hRAD54 by homology between the
CC amino acid sequence given in AAM62186 and known amino acid sequences
CC such as yeast RAD54. hRAD54 proteins are used in the treatment of
CC cancer, including Xeroderma pigmentosum and Bloom syndrome, Werner's
CC syndrome and X-linked mental retardation with alpha-thalassemia
CC detecting complementary nucleotides for use as a diagnostic agent, for
CC especially useful for diagnosis of disease or susceptibility to diseases.
CC hRAD54 polynucleotide, proteins, agonists and antagonists which are
CC proteins are useful in gene therapy.
XX
SQ Sequence 2008 BP; 489 A; 419 C; 570 G; 526 T; 4 other;

Query Match 84.0%; Score 16.8; DB 19; Length 2008;
Best Local Similarity 90.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agagatgcccaactgttt 20
DB 139 agagatgcccaactgagtt 158

RESULT 7
AAH51750/c
ID AAH51750 standard; DNA; 3001 BP.
XX
AC AAH51750;
XX
DT 29-AUG-2001 (first entry)

XX
XX Chromosome 13q31-q33 biallelic marker containing amplicon SEQ ID 162.
XX
XX sbg1; g34665; sbg2; g35017; g35018; chromosome 13q31-q33; haplotype;
XX biallelic marker; polymorphism; schizophrenia; bipolar disorder; ds.
XX
XX Homo sapiens.
XX
PN WO200058510-A2.
XX
PD 05-OCT-2000.
XX
PF 30-MAR-2000; 2000WO-IB00435.
XX
PR 30-MAR-1999; 99US-0126903.
PR 30-APR-1999; 99US-0131971.
PR 30-APR-1999; 99US-0132065.
PR 14-JUL-1999; 99US-0143928.
PR 27-JUL-1999; 99US-0145915.
PR 29-JUL-1999; 99US-0146452.
PR 29-JUL-1999; 99US-0146453.
PR 28-OCT-1999; 99US-0162288.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I, Bougueleret L, Bihain B;
PI Essioux L;
XX
DR WPI; 2000-619082/59.
XX
PT Polynucleotides comprising sequences from sbg1 and g35018 biallelic
PT markers are used for genotyping and detecting schizophrenia or bipolar
PT disorder and predisposition to these disorders -
XX
PS Claim 2; Page 643-644; 737pp; English.
XX
CC AAH51601 represents a human genomic nucleotide sequence comprising sbg1,
CC g34665, sbg2, g35017 and g35018 nucleic acid sequences located on the
CC human chromosome 13q31-q33 locus. The nucleotide sequences contain
CC biallelic markers and polymorphisms. Sequences AAH51602 - AAH51626 and
CC AAB62907 - AAB62915 represent cDNA human sbg1 cDNA sequences and protein
CC products. AAH51627 - AAH51631 and AAB62916 - AAB62918 represent g35018
CC cDNA sequences and protein products. Primers AAH51632 - AAH51699 are used
CC to isolate sbg1 cDNAs, while sbg1 exons from different primates are
CC represented by sequences AAH51642 - AAH51699. Nucleotide sequences of
CC amplicons which comprise biallelic markers located on the chromosome
CC 13q31-q33 locus are represented in AAH51700 - AAH51817. Biallelic markers
CC are represented in the sequences by degenerate/undefined base codes. PCR
CC primers AAH51818 and AAH51819 are used in the isolation of sequences of
CC the invention. The biallelic marker containing nucleotide sequences are
CC used to determine the identity of the nucleotide at a biallelic marker in
CC a sample DNA sequence. The nucleotide sequences may be labelled and used
CC for genotyping by determining the identity of a nucleotide at a region
CC D-related biallelic marker in a biological sample from single or multiple
CC subjects. By determining the frequency of a biallelic marker in a
CC population an association between a genotype and a trait, a haplotype and
CC a trait and a phenotype and a trait can be detected. The sequences can be
CC used to determine a predisposition to or early onset of schizophrenia or
CC bipolar disorder or a beneficial response to or side effects related to
CC treatment against schizophrenia or bipolar disorder.
XX
SQ Sequence 3001 BP; 842 A; 608 C; 584 G; 966 T; 1 other;

Query Match 84.0%; Score 16.8; DB 21; Length 3001;
Best Local Similarity 90.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agagatgcccaactgttt 20
DB 427 AGAGCTGCCCAACTGCTTT 408

RESULT 8
AAL03245/C
ID AAL03245 standard; DNA: 9821 BP.
XX
AAL03245;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 5933.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN W0200155320-A2.
PD 02-AUG-2001.
PE 17-JAN-2001; 2001WO-US01339.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-022547.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 14-AUG-2000; 2000US-0226279.
PR 18-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227709.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231966.

PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235835.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 29-SEP-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 02-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 13-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0244617.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.

PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMAN-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-465570/50.
 XX
 PT Isolated nucleic acid molecule encoding a reproductive system antigen
 XX is used in preventing, treating or ameliorating a medical condition -
 PS Disclosure; SEQ ID NO 5933; 1297bp + Sequence Listing; English.
 CC
 CC The present invention provides the protein and coding sequences of a
 CC number of human reproductive system related antigens. These can be used
 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a genomic sequence encoding a
 CC protein of the invention.
 XX
 SO Sequence 9821 BP; 3056 A; 1735 C; 1689 G; 3341 T; 0 other;

Query Match 84.0%; Score 16.8; DB 22; Length 9821;
 Best Local Similarity 90.0%; Pred. No. 74;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 agagatgcccaactgtttt 20
 |||||
 DB 2800 AGAGCTGCCCAACTGCTTT 2781

RESULT 9
 AAL03246/C
 ID AAL03246 standard; DNA; 9824 BP.
 XX
 AC AAL03246;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE Human reproductive system related antigen DNA SEQ ID NO: 5934.
 XX
 KW Human; reproductive system related antigen; reproductive system disorder;
 XX cancer; gene therapy; ds.
 OS Homo sapiens.
 XX
 OS
 PN WO200155320-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01339.
 XX
 PF 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 14-AUG-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225477.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 18-AUG-2000; 2000US-0225759.
 PR 22-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226688.
 PR 23-AUG-2000; 2000US-0227182.
 PR 30-AUG-2000; 2000US-0227009.
 PR 01-SEP-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 05-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 12-SEP-2000; 2000US-0232081.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234224.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 13-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 20-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.

PR	20-OCT-2000	2000US-0241808	
PR	20-OCT-2000	2000US-0241809	
PR	20-OCT-2000	2000US-0241826	
PR	01-NOV-2000	2000US-0246167	
PR	08-NOV-2000	2000US-0246474	
PR	08-NOV-2000	2000US-0246475	
PR	08-NOV-2000	2000US-0246476	
PR	08-NOV-2000	2000US-0246477	
PR	08-NOV-2000	2000US-0246478	
PR	08-NOV-2000	2000US-0246523	
PR	08-NOV-2000	2000US-0246524	
PR	08-NOV-2000	2000US-0246525	
PR	08-NOV-2000	2000US-0246526	
PR	08-NOV-2000	2000US-0246527	
PR	08-NOV-2000	2000US-0246528	
PR	08-NOV-2000	2000US-0246532	
PR	08-NOV-2000	2000US-0246609	
PR	08-NOV-2000	2000US-0246610	
PR	08-NOV-2000	2000US-0246611	
PR	08-NOV-2000	2000US-0246613	
PR	17-NOV-2000	2000US-0249207	
PR	17-NOV-2000	2000US-0249208	
PR	17-NOV-2000	2000US-0249209	
PR	17-NOV-2000	2000US-0249210	
PR	17-NOV-2000	2000US-0249211	
PR	17-NOV-2000	2000US-0249212	
PR	17-NOV-2000	2000US-0249213	
PR	17-NOV-2000	2000US-0249214	
PR	17-NOV-2000	2000US-0249215	
PR	17-NOV-2000	2000US-0249216	
PR	17-NOV-2000	2000US-0249217	
PR	17-NOV-2000	2000US-0249218	
PR	17-NOV-2000	2000US-0249244	
PR	17-NOV-2000	2000US-0249245	
PR	17-NOV-2000	2000US-0249264	
PR	17-NOV-2000	2000US-0249265	
PR	17-NOV-2000	2000US-0249267	
PR	17-NOV-2000	2000US-0249269	
PR	17-NOV-2000	2000US-0249300	
PR	01-DEC-2000	2000US-0250160	
PR	01-DEC-2000	2000US-0250391	
PR	05-DEC-2000	2000US-0251030	
PR	05-DEC-2000	2000US-0251988	
PR	05-DEC-2000	2000US-0256719	
PR	06-DEC-2000	2000US-0251479	
PR	06-DEC-2000	2000US-0251856	
PR	08-DEC-2000	2000US-0251868	
PR	08-DEC-2000	2000US-0251869	
PR	08-DEC-2000	2000US-0251989	
PR	08-DEC-2000	2000US-0251990	
PR	11-DEC-2000	2000US-0254097	
PR	05-JAN-2001	2001US-02559678	
XX			
PA	(HUMAN)	HUMAN GENOME SCI INC.	
XX			
PI	Rosen CA, Barash SC, Ruben SM.		
XX			
XX	WPI: 2001-46570/50.		
DR			
XX			
XX			
PT	Isolated nucleic acid molecule encoding a reproductive system antigen		
PT	is used in preventing, treating or ameliorating a medical condition		
XX			
PS	Disclosure: SEQ ID NO 5934; 1297bp + Sequence Listing; English.		
XX			
CC	The present invention provides the protein and coding sequences of a		
CC	number of human reproductive system related antigens. These can be used		
CC	in the prevention and treatment of reproductive system disorders,		
CC	including cancer. The present sequence is a genomic sequence encoding a		
CC	protein of the invention.		
XX			
XX	Sequence 9824 BP; 3057 A; 1735 C; 1689 G; 3343 T; 0 other;		

Query Match	84.0%;	Score 16.8;	DB 22;	Length 9824;
Best Local Similarity	90.0%;	Pred. No. 74;		
Matches 18;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
1 agaatgcccgaactgtttt 20				
Db 2800 AGAGCTGCCCAAACTGCTT 2781				
RESULT 10				
ID AAX13026				
AXA13026 standard; DNA: 20072 BP.				
XX AAX13026;				
AC				
XX 19-MAR-1999 (first entry)				
DT				
XX Enterococcus faecalis genome contig SEQ ID NO:89.				
DE				
XX Enterococcus faecalis; contig; detection; Enterococcal infection;				
XX vaccine; attenuation; computer readable medium; ds.				
KW				
XX Enterococcus faecalis.				
OS				
XX WO9850555-A2.				
PN				
XX 12-NOV-1998.				
PD				
XX 04-MAY-1998; 98WO-US08985.				
PF				
XX 14-NOV-1997; 97US-0066009.				
PR 06-MAY-1997; 97US-0044031.				
PR 16-MAY-1997; 97US-0046655.				
XX				
PA (HUMA-) HUMAN GENOME SCI INC.				
XX				
PI Barash SC, Dillon PJ, Kunsch CA;				
XX WPI: 1999-045171/04.				
DR				
XX New isolated Enterococcus faecalis polynucleotides and polypeptides				
PT - used to develop products for the detection of Enterococcus and for				
PT use in vaccines for prevention or attenuation of Enterococcus				
PT infection.				
XX Claim 1; Page 596-606; 2084pp; English.				
XX				
PS A computer readable medium has been developed which has recorded on it				
CC 992 nucleotide sequences isolated from the Enterococcus faecalis genome.				
CC AAX12938 to AAX13319 represent these nucleotide sequences which are				
CC primary nucleotide sequences, also known as contigs. The computer-based				
CC system can identify fragments of the Enterococcus faecalis genome with				
CC commercial importance. The products can be used to detect the presence				
CC of Enterococcus faecalis in samples. They can also be used for				
CC diagnosing Enterococcal infection in an animal and monitoring				
CC progression of disease, and for identifying agents which can be used to				
CC modulate the growth or pathogenicity of Enterococcus faecalis, or				
CC another related organism, in vivo or in vitro. In particular the				
CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences				
CC can be used in vaccines to prevent or attenuate an Enterococcal				
CC infection.				
CC				
XX Sequence 20072 BP; 5846 A; 4288 C; 3266 G; 6628 T; 44 other;				
XX				
Query Match	84.0%;	Score 16.8;	DB 20;	Length 20072;
Best Local Similarity	90.0%;	Pred. No. 84;		
Matches 18;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
1 agaatgcccgaactgtttt 20				
Db 7383 agaatgcccgaactgtttt 7402				

RESULT 11

AAZ92583
ID AAZ92583 standard; DNA; 43795 BP.

XX
AC AAZ92583;

XX
DT 05-JUN-2000 (first entry)

XX
DE Human DAZ genomic sequence, SEQ ID NO:101.

XX
KW DAZ gene; chromosome Yq; male infertility; sperm count; diagnosis;
treatment; gene therapy; ss.

XX
OS Homo sapiens.

XX
PN US6020476-A.

XX
PD 01-FEB-2000.

XX
PF 30-OCT-1996; 96US-0742185.

XX
PR 22-SEP-1994; 94US-0310429.

XX
PR 31-JUL-1996; 96US-0690734.

XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX
PI Hawkins T, Reeve MP, Saxena R, Page DC, Reljo R;
WPI; 2000-181393/16.

XX
PT New nucleic acid, useful for diagnosis and treatment of reduced sperm
count, is derived from the human DAZ or DAZH genes .

XX
PS Claim 6; Fig 11A-L; 110pp; English.

XX
CC The invention relates to a family of human genes referred to as the
CC DAZ gene family, and to a functional DAZ homologue, DAZH. Members of the
CC DAZ gene family are clustered in the same region of the Y chromosome.
CC In particular, the invention relates to an isolated DAZ gene (AAZ92499)
CC present in interval 6D and/or 6E of the distal portion of Yq, mutations
CC in which are associated with reduced sperm count. The DAZH gene
CC (AAZ92580) is located on chromosome 3; however, the entire DAZH gene
CC family, including DAZH is expressed in germ cells. DAZ and DAZH
CC nucleotide sequences may be used as a source of primers and probes for
CC the diagnosis of cases of reduced sperm count associated with alteration
CC or deletion of the DAZ gene. They are also used as human chromosome Y
CC markers. Functional DAZ genes can be used in gene therapy for treating
CC reduced sperm counts. Sequence AAZ92499 represents human DAZ cDNA, and
CC sequences AAZ92583-92584 are genomic DAZ sequences. Sequences
CC AAZ92491-92492 are partial DNA sequences of DAZ gene family members.

XX
SQ Sequence 43795 BP; 12175 A; 8166 C; 8183 G; 15271 T; 0 other;

Query Match 84.0%; Score 16.8; DB 21; Length 43795;
Best Local Similarity 90.0%; Pred. No. 95;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
||||| |||||||||
DB 22516 agagatgcccaactgtttt 22535

RESULT 12

AAH41226
ID AAH41226 standard; DNA; 349980 BP.

XX
AC AAH41226;

XX
DT 29-OCT-2001 (first entry)

XX
DE Pyrococcus abyssi genomic fragment #5.

XX
KW Hyperthermophilic archaeon; hyperthermophilic protein; ds.
XX
OS Pyrococcus abyssi.

XX
EH Key Location/Qualifiers
FT misc-feature 1..49980

FT /tag= a
FT /note= "this sequence overlaps with the 3' end of
AAH41225"

FT misc-feature 300001..349980

FT /tag= b
FT /note= "This sequence overlaps with the 5' end of
AAH41227"

XX
PN FR2792651-A1.

XX
PD 27-OCT-2000.

XX
PF 21-APR-1999; 99FR-0005034.

XX
PR 21-APR-1999; 99FR-0005034.

XX
PA (CNRS) CNRS CENT NAT RECH SCI
PA (IFRE-) IFREMER INST FR RECH EXPL MER.

XX
PI Forterre P, Thierry JC, Priour D, Dietrich J, Lecompte O;
PI Querellou J, Weissenbach J, Saurin W, Hellig R;

XX
PI WPI; 2001-126236/14.

XX
PT New nucleotide sequences isolated from Pyrococcus abyssi encode
PT proteins useful in industry .

XX
PS Claim 1; Page 511-606; 1657pp; French.

XX
CC The present invention relates to the genomic sequence of Pyrococcus
CC abyssi and P. abyssi proteins (see AAB96053-AAB96842). P. abyssi is a
CC hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal
CC vents. The present sequence is a fragment of the genomic sequence of P.
CC abyssi. The 5' end of this sequence overlaps with the 3' end of AAH41225
CC and the 3' end of this sequence overlaps with the 5' end of AAH41227. The
CC proteins of the present invention have various potential industrial uses,
CC since the proteins are stable at very high temperatures, some up to 110
CC degrees centigrade.
CC Note: This patent is in the same patent family as WO2000065062, which
CC contains additional sequences as shown in AAB99132-AAB99143,
CC AAH75903-AAH75920 and AAG66436.

XX
SQ Sequence 349980 BP; 98084 A; 80447 C; 77665 G; 93784 T; 0 other;

Query Match 84.0%; Score 16.8; DB 22; Length 349980;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
||||| |||||||||
DB 53995 aaagatcccaactgtttt 54014

RESULT 13

AAH99123
ID AAH99123 standard; cDNA; 396 BP.

XX
AC AAH99123;

XX
DT 12-OCT-2001 (first entry)

XX
DE Human EST-derived coding sequence SEQ ID NO: 980.

XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX Homo sapiens.
XX MO200154477-A2.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001MO-US02687.
XX 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Dirmannac RA, Zhang J, Werlman T;
XX WPI: 2001-476164/51.
DR P-PSDB: AAM24464.
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
PS Claim 1: Page 766; 1275pp; English.
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC for forensic, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a CDNA
CC of the invention.
XX Sequence 396 BP; 80 A; 115 C; 86 G; 115 T; 0 other;
QY 1 agagatgcccaactgtt 18
DB 122 agaatgcccactgtt 139
RESULT 14
AAAF63808/c
ID AAF63808 standard; CDNA: 1157 BP.
XX AAF63808;
AC
XX 03-APR-2001 (first entry)
DT
XX Human secreted protein gene 20 SEQ ID NO:30.
DE
XX Human; immunosuppressive; antiarthritic; antirheumatic; nootropic;
KW antiproliferative; cytoskeletal; cardiant; vasotropic; cerebroprotective;
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
KW vulnary; autoimmune disease; hyperproliferative disorder; cancer;
KW cardiovascular disorder; cerebrovascular disorder; infection;
KW nervous system disorder; ocular disorder; chemotaxis; food additive;
KW secreted protein; ss.
XX
XX Homo sapiens.
XX OS
XX MO200077021-A1.
XX 21-DEC-2000.

XX 01-JUN-2000; 2000MO-US15135.
PF
XX 11-JUN-1999; 99US-0138632.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
XX Rosen CA, Ruben SM, Komatsoulis GA;
PI
XX WPI: 2001-071257/08.
DR P-PSDB: AAB75259.
XX Nucleic acid molecules encoding human secreted proteins, used in
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT Parkinson's diseases and cancers -
XX
XX Claim 1: Page 451; 530pp; English.
XX This invention relates to polynucleotide sequences AAF63789 - AAF63836
CC which encode human secreted proteins AAB75260 - AAB75287. Included in the
CC invention are protein sequences AAB75288 - AAB75341 which are fragments
CC of the secreted proteins and amino acid sequences with which these
CC fragments share homology. Examples of the activities of the proteins and
CC polynucleotides and the activities of their agonists and antagonists
CC include, immunosuppressive; antiarthritic; antirheumatic;
CC antiproliferative; cytoskeletal; cardiant; vasotropic; fungicide;
CC nootropic; neuroprotective; antibacterial; virucide; fungicide;
CC ophthalmological; and vulnary activity. The protein and polynucleotide
CC sequences, their agonists and antagonists may be useful for treating,
CC preventing and diagnosing diseases and disorders such as autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders
CC e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities. Included in the invention are
CC oligonucleotides AAF63780 - AAF63788 and peptide AAB75239 which are used
CC in the identification and characterisation of the DNA and protein
CC sequences of the invention.
XX Sequence 1157 BP; 326 A; 223 C; 269 G; 339 T; 0 other;
QY 2 gagatgcccaactgttt 20
DB 138 GAGAAAGCCCAACTGCTTT 120
RESULT 15
AAZ49395/c
ID AAZ49395 standard; CDNA: 1193 BP.
XX AAZ49395;
AC
XX 14-MAR-2000 (first entry)
DT
XX Human STRAP-1 cDNA.
DE
XX Serpentine transmembrane antigen of the prostate; STRAP-1; prostate;
KW transmembrane domain; type IIIa membrane protein; expression; cancer;
KW prostate cancer; bladder cancer; colon cancer; pancreatic cancer;
KW ovarian cancer; tumor antigen; immunisation; immune response;
KW cellular; humoral; anticancer vaccine; antibody; detection; diagnosis;

prognosis; monitoring; susceptibility; therapeutic inhibitor;
drug targeting; recombinant protein; ds.

Homo sapiens.

Key Location/Qualifiers
CDS 64..1083
FT /tag=a
FT /product="Human STRAP-1 (serpentine transmembrane
antigen of the prostate)"

WO9962941-A2.

09-DEC-1999.

01-JUN-1999; 99WO-US12157.

01-JUN-1998; 98US-0087520.
30-JUN-1998; 98US-0091183.

(UROC-) UROGENESYS INC.

(AFAR/) AFAR D E.

(HUBE/) HUBERT R S.

(LEON/) LEONG K.

(RAIT/) RAITANO A B.

(SAFE/) SAFFRAN D C.

Afar DE, Hubert RS, Leong K, Raitano AB, Safran DC;

WPI; 2000-072832/06.

P-PSDB; AAY58194.

Novel proteins useful as diagnostic markers and therapeutic targets,
particularly for prostatic cancer

Claim 4; Fig 1A; 83pp; English.

This sequence represents cDNA encoding a novel human protein, STRAP-1 (serpentine transmembrane antigen of the prostate). STRAP-1 is the prototype member of the STRAP family of proteins (AAY58194-Y58197) which exhibit a high degree of structural conservation, but which show no significant structural homology to known human proteins. The STRAP-1 gene has been localised to chromosome 7p22. STRAP-1 is thought to be a type IIIa membrane protein and is expressed predominantly in prostate cells in normal human tissues. Structurally, STRAP-1 is a 339 amino acid protein characterised by six transmembrane domains and intracellular N- and C-termini, suggesting that it folds in a "serpentine" manner into three extracellular and two intracellular loops. STRAP-1 mRNA and protein expression is maintained at high levels and throughout all stages of prostate cancer. STRAP-1 mRNA and/or protein is also overexpressed in certain other cancers, including bladder, colon, pancreatic and ovarian cancer. The function of the STRAP proteins is not known. They may be ion channels (from the presence of six transmembrane domains, a feature which is shared by certain ion channels) or gap-junction proteins (from immunohistochemical staining). STRAP-1 and STRAP-2 are cell-surface tumour antigens. Immunisation with a STRAP protein induces cellular and humoral immune responses against STRAP-expressing cells. STRAP proteins may be used to identify specific-binding agents, to produce anticancer vaccines and to generate specific antibodies. The antibodies may be used for detection, prognosis, and monitoring of cancers (or susceptibility to cancer), as therapeutic inhibitors or to target therapeutic agents to their site of action. STRAP nucleic acids may be used for recombinant protein production, as diagnostic and prognostic reagents, for identifying STRAP-expressing cells for screening inhibitors of STRAP expression and for therapeutic modulation/inhibition of STRAP expression. Since high levels of STRAP proteins are exposed on the cell surface, they are easily targeted by systemically administered agents, and because they are expressed mainly on prostatic epithelial cells, agents targeted to them should have minimal side effects on other tissues.

Sequence 1193 BP; 382 A; 219 C; 233 G; 359 T; 0 other;

Query Match 79.0%; Score 15.8; DB 21; Length 1193;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gagatgccccacgtttt 20
||| ||||| ||||| |||
Db 564 GAGAAAGCCCAACTGCTTT 546

Search completed: September 7, 2002, 18:39:44
Job time: 29878 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:21:38 ; Search time 12179.2 Seconds
(without alignments)
34.364 Million cell updates/sec

Title: US-09-834-291-1_COPY_44_63
Perfect score: 1 agagatgcccaactgtttt 20
Sequence: 1

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Genem1:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pal:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_inv:

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
------------	-------	-------	--------	-------	-------------

1	20	100.0	20	6	AX026100	Sequence
2	20	100.0	40	6	AX026106	Sequence
3	20	100.0	40	6	AX026114	Sequence
4	20	100.0	2344	6	HSCD955FR	Sequence
5	20	100.0	2837	6	AX026092	Sequence
6	20	100.0	3212	6	AX026089	Sequence
7	20	100.0	187313	9	AL157394	Human DNA
8	18.4	92.0	74951	9	AL151364	Human DNA
9	18.4	92.0	90478	2	AL365355	Homo sapi
10	18.4	92.0	168522	2	AC024302	Homo sapi
11	18.4	92.0	181497	2	AC099561	Homo sapi
12	18.4	92.0	236685	2	AC084744	Mus muscu
13	17.4	87.0	16157	1	AE001670	Chlamydia
14	17.4	87.0	17395	1	AE002255	Chlamydia
15	17.4	87.0	20563	2	AC015202	Drosophila
16	17.4	87.0	121249	5	AL591593	Drosophila
17	17.4	87.0	128969	2	AC018486	Homo sapi
18	17.4	87.0	156136	2	AC079160	Homo sapi
19	17.4	87.0	181053	3	AC022346	Rattus no
20	17.4	87.0	241213	2	AC103322	Rattus no
21	17.4	87.0	325865	1	AC002548	Chlamydia
22	17.4	85.0	34200	8	AB022785	Homo sapi
23	17	85.0	37068	8	AC067938	Homo sapi
24	17	85.0	43556	8	AC067937	Neurospor
25	17	85.0	96376	2	AC007626	Homo sapi
26	17	85.0	100000	9	AP000065	Homo sapi
27	17	85.0	134086	2	AC084024	Homo sapi
28	17	85.0	154671	2	AC021680	Homo sapi
29	17	85.0	162925	2	AP004461	Homo sapi
30	17	85.0	196951	2	AC091962	Homo sapi
31	17	85.0	199080	2	AL671173	Mus muscu
32	17	85.0	216188	2	AL627345	Mus muscu
33	16.8	84.0	20	6	AX026101	Sequence
34	16.8	84.0	661	14	HPV8407	Sequence
35	16.8	84.0	661	14	HPV8407	Sequence
36	16.8	84.0	1876	3	AF363304	Bairdico
37	16.8	84.0	3006	9	HS181913	Homo sapi
38	16.8	84.0	7537	14	HPV15173	Homo sapi
39	16.8	84.0	17518	2	AC110307	Rattus no
40	16.8	84.0	28006	2	AC109534	Rattus no
41	16.8	84.0	37906	9	HS015704	Human DNA
42	16.8	84.0	42303	9	AL355133	Human DNA
43	16.8	84.0	43795	9	AC000022	Genomic s
44	16.8	84.0	54207	2	AP002024	Homo sapi
45	16.8	84.0	54554	9	AC009500	Homo sapi

ALIGNMENTS

RESULT 1
AX026100 20 bp DNA Linear PAT 16-SEP-2000
Sequence 12 from Patent DE19847779.
AX026100
AX026100.1 GI:10187531

SOURCE
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
Mueller-Schilling, M., Krammer, P. and Oren, M.
TITLE
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
JOURNAL
DEUTSCHES KREBSFORSCH (DE)
Patent: DE 19847779-C 12 03-FEB-2000;
Location/Qualifiers
FEATURES
source
1..20
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT
6 a 4 c 4 g 6 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
Db 1 AGAGATGCCCAACTGTGTTT 20

RESULT 2
AX026106
LOCUS AX026106 40 bp DNA Linear PAT 16-SEP-2000
DEFINITION Sequence 18 from Patent DE19847779.
ACCESSION AX026106
VERSION AX026106.1 GI:10187537
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Mueller-Schilling, M., Krammer, P. and Oren, M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
JOURNAL Patent: DE 1984779-C 18 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
FEATURES
source location/Qualifiers
1..40
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 14 a 11 c 5 g 10 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
Db 11 AGAGATGCCCAACTGTGTTT 30

RESULT 3
AX026114
LOCUS AX026114 40 bp DNA Linear PAT 16-SEP-2000
DEFINITION Sequence 26 from Patent DE19847779.
ACCESSION AX026114
VERSION AX026114.1 GI:10187545
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Mueller-Schilling, M., Krammer, P. and Oren, M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
JOURNAL Patent: DE 1984779-C 26 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
FEATURES
source location/Qualifiers
1..40
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 14 a 11 c 5 g 10 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
Db 11 AGAGATGCCCAACTGTGTTT 30

RESULT 4
HSCD955FR 2344 bp DNA Linear PRI 05-FEB-1997
LOCUS HSCD955FR
DEFINITION H.sapiens CD95 gene 5' flanking region.
ACCESSION X87625
VERSION X87625.1 GI:902311
KEYWORDS beta.interferon; CD95 gene; silencer.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2344)
AUTHORS Rudert, F., Visser, E., Forbes, L., Lindridge, E., Wang, Y. and
Watson, V.
TITLE Identification of a silencer, enhancer, and basal promoter region
JOURNAL DNA Cell Biol. 14 (11), 931-937 (1995)
MEDLINE 96069539
REFERENCE 2 (bases 1 to 2344)
AUTHORS Rudert, F.H.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-1995) F.H. Rudert, Genesis Research &
Development, Corporation Ltd., PO Box 50, Auckland, NEW ZEALAND
OVERLAPS with X81335, & X82279-X82286.
COMMENT
FEATURES
source location/Qualifiers
1..2344
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/germline
/tissue_type="Placenta"
/map="q24.1"
564..1337
/note="silencer"
717..801
/note="beta interferon silencer B motifs"
complement(1237..1244)
/note="Lysozyme silencer 1"
1338..1919
1920..2344
/note="Basal promoter"

BASE COUNT 637 a 546 c 511 g 650 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 2344;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
Db 161 AGAGATGCCCAACTGTGTTT 180

RESULT 5
AX026092 2827 bp DNA Linear PAT 16-SEP-2000
LOCUS AX026092
DEFINITION Sequence 4 from Patent DE19847779.
ACCESSION AX026092
VERSION AX026092.1 GI:10187523
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2827)
AUTHORS Mueller-Schilling, M., Krammer, P. and Oren, M.

TITLE Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy
JOURNAL Patent: DE 1984779-C 4 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
FEATURES Location/Qualifiers
SOURCE 1..2827
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 728 a 676 c 657 g 766 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2827;
Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

OY 1 agagatgcccaactgtttt 20
|||||
Db 44 AGAGATGCCCAACTGTTT 63

RESULT 6
AX026089 3212 bp DNA linear PAT 16-SEP-2000
LOCUS AX026089
DEFINITION Sequence 1 from Patent DE1984779.
ACCESSION AX026089
VERSION AX026089.1 GI:10187520
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3212)
Muller-Schilling, M., Krammer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy
Patent: DE 1984779-C 1 03-FEB-2000;
JOURNAL DEUTSCHES KREBSFORSCH (DE)
FEATURES Location/Qualifiers
SOURCE 1..3212
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 778 a 784 c 809 g 841 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3212;
Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

OY 1 agagatgcccaactgtttt 20
|||||
Db 44 AGAGATGCCCAACTGTTT 63

RESULT 7
AL157394 187313 bp DNA linear PRI 22-AUG-2001
LOCUS AL157394
DEFINITION Human DNA sequence from clone Rpl1-399019 on chromosome 10, complete sequence.
ACCESSION AL157394
VERSION AL157394.15 GI:15384622
KEYWORDS HMG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 187313)
Blakey, S.
Direct Submission
Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk

COMMENT
On Aug 31, 2001 this sequence version replaced g1:14161146.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL, Sw, SWISSPROT, Tr, TrEMBL, Wp, WORMPEP. Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr10
Rpl1-399019 is from the library RPl1-11.2 constructed by the group of Pieter de Jong. For further details see
http://www.chori.org/hacpac/home.htm
VECTOR: pACE3.6
This sequence is the entire insert of clone Rpl1-399019 The true left end of clone Rpl1-496H23 is at 166408 in this sequence. The true right end of clone Rpl1-30415 is at 18704 in this sequence.

FEATURES
SOURCE Location/Qualifiers
1..187313
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="Rpl1-399019"
/clone_1lb="RPl1-11.2"
100119..100156
/note="Sequence confirmed by AC015461 sequenced by WIBR."
100157..100198
/note="Sequence confirmed by WIBR."
105808..105972
/note="Sequence confirmed by WIBR."
105973..105989
/note="Sequence confirmed by AC015461 sequenced by WIBR."
misc_feature
BASE COUNT 5569 a 36398 c 36888 g 58358 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 187313;
Best Local Similarity 100.0%; Pred. No. 2.2; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

OY 1 agagatgcccaactgtttt 20
|||||
Db 142012 AGAGATGCCCAACTGTTT 142031

RESULT 8
AL513364 74951 bp DNA linear PRI 15-NOV-2001
LOCUS AL513364
DEFINITION Human DNA sequence from clone Rpl1-480N10 on chromosome 1, complete sequence.
ACCESSION AL513364
VERSION AL513364.10 GI:16973038
KEYWORDS HMG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 74951)
Almeida, J.
Direct Submission

JOURNAL

COMMENT

Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk On Nov 16, 2001 this sequence version replaced gi:16944088. Where difference assembly data is compared from overlapping clones, together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; information on the WormPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1> RP11-480N10 is from the library RP11-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/Bacpac/home.htm> VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-480N10. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-480N10 is at 74951 in this sequence. The true left end of clone RP11-7768 is at 42605 in this sequence. The true right end of clone RP11-541J2 is at 2000 in this sequence.

FEATURES

source

1. 74951

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="1"

/clone="RP11-480N10"

/clone_1lb="RP11-11.2"

misc_feature

14860..14861

misc_feature

/note="Single clone region. Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."

misc_feature

48431..48432

/note="Tandem repeat. Forced join. Gap size estimated to be approximately 300bp by restriction digest data."

misc_feature

/note="Single clone region. Assembly consistent with restriction digest data."

BASE COUNT 25517 a 14184 c 13984 g 21266 t
ORIGIN

Query Match 92.0%; Score 18.4; DB 9; Length 74951;
Best Local Similarity 95.0%; Pred. No. 18;

Mismatches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 agagatcccccaattgtttt 20
|||||

DB 51780 AGAATGCCCAACTGTTT 51799

RESULT

9

AL365355

LOCUS

DEFINITION

Homo sapiens chromosome 1 clone RP4-722L13 map p22.3-31.2, ***

SEQUENCING IN PROGRESS ***; 9 unordered pieces.

ACCESSION AL365355

5

VERSION AL365355.3 GI:9798268
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 90478)
Pavitt, R.

AUTHORS

Direct Submission

TITLE

Submitted (19-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,

JOURNAL

requests: clonerequests@sanger.ac.uk

COMMENT

On Aug 12, 2001 this sequence version replaced gi:9187428.

JOURNAL

Center: Sanger Centre

AUTHORS

Center code: SC

TITLE

Web site: <http://www.sanger.ac.uk>

JOURNAL

Contact: humquerry@sanger.ac.uk

AUTHORS

Project Information

TITLE

Center project name: dj722L13

----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 5% of reads
Quality: 86233 bases at least Q40
Consensus quality: 87417 bases at least Q30
Insert size: 96678; sum-of-contigs
Quality coverage: 4.75x in Q20 bases; sum-of-contigs quality coverage: 4.78x in Q20 bases; agarose-fp

----- NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 12389: contig of 12389 bp in length
12390 12489: gap of 100 bp
12490 17235: contig of 4746 bp in length
17236 17335: gap of 100 bp
17336 21293: contig of 3958 bp in length
21294 21393: gap of 100 bp
21394 37557: contig of 16164 bp in length
37558 37657: gap of 100 bp
37658 54929: contig of 17272 bp in length
54930 55029: gap of 100 bp
55030 62839: contig of 7810 bp in length
62840 62939: gap of 100 bp
62940 74511: contig of 11572 bp in length
74512 74611: gap of 100 bp
74612 83633: contig of 9022 bp in length
83634 83733: gap of 100 bp
83734 90478: contig of 6745 bp in length.

FEATURES

source

1. 90478

misc_feature

/organism="Homo sapiens"

misc_feature

/db_xref="taxon:9606"

misc_feature

/chromosome="1"

misc_feature

/map="p22.3-31.2"

misc_feature

/clone="RP4-722L13"

misc_feature

/clone_1lb="RP11-11.2"

misc_feature

/note="assembly-fragment:00957"

misc_feature

fragment_chain:1"

misc_feature

/note="assembly-fragment:00528"

misc_feature

fragment_chain:1"

misc_feature

17336..21293

misc_feature /note="assembly_fragment:00064
fragment_chain:1"
21394..37557
/note="assembly_fragment:01038
fragment_chain:1"
37658..54929
/note="assembly_fragment:00052.0"
55030..62839
/note="assembly_fragment:00124"
62940..74511
/note="assembly_fragment:00131.0"
74612..83633
/note="assembly_fragment:00870"
83734..90478
/note="assembly_fragment:01225"
27811 a 16881 c 16980 g 28004 t 802 others

Query Match 92.0%; Score 18.4; DB 2; Length 90478;
Best Local Similarity 95.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 agagatgcccaactgttt 20
Db 43021 AGAATGCGCAACTGTTT 43040

RESULT 10
AC024302/c 168522 bp DNA linear HTG 14-MAR-2000
LOCUS Homo sapiens clone RP11-23123, WORKING DRAFT SEQUENCE, 18 unordered
DEFINITION pieces.
AC024302.2 GI:7239599
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 168522)
Birken, B., Linton, L., Nusbaum, C. and Lander, E.
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 168522)
Birken, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavsky, L.,
Bouhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Choepe, L., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Deatellano, K., Dewar, K., Diaz, J.S., Dodge, S., Dominko, M., Doyle, M.,
Festor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hages, B., Heaford, A., Horton, L.,
Howard, J.C., Iliev, I., Johnson, R., Lehoczy, J., Levine, R.,
Klein, J., Landers, T., Laroque, K., Lehoucq, P., Marquis, N., McCarthy, M.,
Lieu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N., McCarthy, M.,
McEwan, P., McGurk, A., McKernan, K., McPherson, R., Meldrum, J.,
Menens, L., Mihova, T., Miranda, C., Mienga, W., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Olyar, T.M.,
Peterson, K., Pierre, N., Pisanic, C., Pollara, V., Raymond, C.,
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Subramanian, A., Talamas, J., Testa, S., Theodore, J., Tirrell, A.,
Travers, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,
Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
Zody, M. Submission

TITLE Direct Submission
JOURNAL Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Mar 14, 2000 this sequence version replaced g1:7108032.
All repeats were identified using RepeatMasker:
Smt, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4376
Center clone name: 23-1-23
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 155724 bases at least Q40
Consensus quality: 162423 bases at least Q30
Consensus quality: 164971 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 166822; sum-of-coverage
Quality coverage: 4.0 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1007: contig of 1007 bp in length
* 1008 1107: gap of 100 bp
* 1108 2229: contig of 1122 bp in length
* 2230 2329: gap of 100 bp
* 2330 4120: contig of 1791 bp in length
* 4121 4220: gap of 100 bp
* 4221 6093: contig of 1873 bp in length
* 6094 6193: gap of 100 bp
* 6194 12656: contig of 6463 bp in length
* 12657 12756: gap of 100 bp
* 12757 19311: contig of 6555 bp in length
* 19312 19411: gap of 100 bp
* 19412 24024: contig of 4613 bp in length
* 24025 24124: gap of 100 bp
* 24125 30616: contig of 6492 bp in length
* 30617 30716: gap of 100 bp
* 30717 35830: contig of 5114 bp in length
* 35831 35930: gap of 100 bp
* 35931 45340: contig of 9410 bp in length
* 45341 45440: gap of 100 bp
* 45441 55960: contig of 10520 bp in length
* 55961 56060: gap of 100 bp
* 56061 67711: contig of 11651 bp in length
* 67712 67811: gap of 100 bp
* 67812 78627: contig of 10816 bp in length
* 78628 78727: gap of 100 bp
* 78728 91285: contig of 12558 bp in length
* 91286 91385: gap of 100 bp
* 91386 106039: contig of 14654 bp in length
* 106040 106139: gap of 100 bp
* 106140 123134: contig of 16995 bp in length
* 123135 123234: gap of 100 bp
* 123235 140131: contig of 16897 bp in length
* 140132 140231: gap of 100 bp
* 140232 168522: contig of 28291 bp in length.
Location/Qualifiers
1. 168522
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="RP11-23123"
/clone_lib="RP11-23123"
1. 1007
/note="assembly_fragment"
1108..2229
/note="assembly_fragment"

FEATURES
SOURCE
misc_feature
misc_feature
misc_feature
/note="assembly_fragment"

Center: University of Washington Genome Center

Location	Qualifiers	bp in length
1	2355: contig of 2355 bp in length	
2356	2455: gap of unknown length	
2456	4455: contig of 2040 bp in length	
4456	4505: gap of unknown length	
4506	7640: contig of 3045 bp in length	
7641	7740: gap of unknown length	
7741	12455: contig of 4685 bp in length	
12426	12525: gap of unknown length	
12526	17111: contig of 4646 bp in length	
17112	17271: gap of unknown length	
17272	26889: contig of 9618 bp in length	
26890	62181: gap of unknown length	
26990	62181: contig of 35192 bp in length	
62182	109708: gap of unknown length	
62282	109708: contig of 47427 bp in length	
109709	181497: gap of unknown length	
109809	181497: contig of 71689 bp in length	

BASE COUNT	ORIGIN	note-assembly_name:Config107"
58138	a	34626 c 32770 g 55026 t 937 others

1000 JOURNAL OF CLIMATE

100

1

DEFINITION Chlamydia pneumoniae section 86 of 103 of the complete genome.
ACCESSION AE001670 AE001363
VERSION AE001670.1 GI:4377212
KEYWORDS Chlamydia pneumoniae CML029.
ORGANISM Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE 1 (bases 1 to 16157)
AUTHORS Kaiman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L., Olinger, L., Grimwood, J., Davis, R. W., and Stephens, R. S., Comparative genomes of Chlamydia pneumoniae and C. trachomatis
JOURNAL Nat. Genet. 21 (4), 385-389 (1999)
MEDLINE 99206606
PUBMED 10192388
REFERENCE 2 (bases 1 to 16157)
AUTHORS Kaiman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L., Grimwood, J., Davis, R. W., and Stephens, R. S., Direct Submission
JOURNAL Submitted (01-DEC-1998) Program in Infectious Diseases, University of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
FEATURES
source 1. 16157
/organism="Chlamydia pneumoniae CML029"
/strain="CML029"
/db_xref="taxon:115713"
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AUTHORS
1 (bases 1 to 17395)
Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F.,
White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Uterback,T.,
Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B.,
Bowman,C., Dodson,R., Gwinn,M., Nelson,W., Deboy,R., Kolonay,J.,
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Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
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Nucleic Acids Res. 28 (6), 1397-1406 (2000)
JOURNAL
MEDLINE
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10684935
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AUTHORS
2 (bases 1 to 17395)
Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F.,
White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Uterback,T.,
Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B.,
Bowman,C., Dodson,R., Gwinn,M., Nelson,W., Deboy,R., Kolonay,J.,
McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
Direct Submission
Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
On Jun 1, 2000 this sequence version replaced gi:7189881.
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/product="uroporphyrinogen decarboxylase"
/protein_id="AAF38756.1"
/db_xref="GI:7189889"
/translation="MSAPDPLKSTASHPPTMLRQVGRYPPYQELKSGSLTFF
HTEPILVATLIGSLHLVADAILPADLILSDGVAVYDFAPRIQFSPQPTFF
SDPOTITSYILBETLTKOKLPVLIYVAAASFETLACYLIDGASAKDSKTSFLYV
PERFDOLSTIIEGTATYILKQMDGAAGAALFESSSLRSLPRTVTEENRRIA
KLKQALPVSLEFCRFEENFYTLQATQDTPHDPVHVLHRLKRLMSLQCNLPAT
FLPQERKLHYVEAFVLPVLPYPRNIFNSGHILPEPYLENVQLVVSIVQRL"
12020. .13396
/gene="CP0977"
12020. .13396
/gene="CP0977"
Query Match 87.0%; Score 17.4; DB 1; Length 17395;
Best Local Similarity 94.7%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 gagatgcccaactgcttt 20
Db 4110 GAGATGCCCAACTGCTTT 4128
RESULT 15
AC015202
LOCUS 20563 bp DNA linear HTG 16-NOV-1999
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
pieces.
AC015202
VERSION AC015202.1 GI:6436133
KEYWORDS HTG; HTGS_PHASE2.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 20563)
AUTHORS Adams, M. and Venter, J.C.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,

COMMENT

Rockville, MD, USA
This sequence was identified as CDM:10213741 by the submitter.
For further information on this sequence e-mail to flyce@elera.com
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES

Source

```
1. .20563
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
4000 5000 +
1148
```

BASE COUNT

6416 a 4099 c 4148 g 5900 t

ORIGIN

Query Match	87.0%;	Score 17.4;	DB 2;	Length 20563;
Best Local Similarity	94.7%;	Pred. No. 62;		
Matches 18; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

1 agatgccaactgtt 19

Db 2966 AGAGATGCCCAACTGATT 2984

Search completed: September 7, 2002, 18:21:55
Job time: 28814 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 14:51:20 ; Search time 8462.63 seconds
(without alignments)
191.387 Million cell updates/sec

Title: US-09-834-291-1_COPY_337_456
Perfect score: 120
Sequence: 1 taagggaaggggtatggca.....aatgttgcttaagctttttt 120

Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43.2	36.0	716	10	BG256799 602371024
2	42.4	35.3	488	12	AG019885 Homo sapi
3	42.4	35.3	756	12	AG019562 Homo sapi
4	40.6	33.8	469	9	AA279976 AA279976
5	40.2	33.5	421	12	AG033226 AG033226
6	39.9	32.5	698	12	AG093829 Pan trogl
7	38.8	32.3	530	12	AG070826 HS-5571_A
8	38.8	31.7	691	12	AG040694 CIT-HSP-2
9	37.4	31.2	367	9	AA376998 EST89574
10	37.4	31.2	437	12	AG049848 HS-5088_B
11	36.8	30.7	605	12	AG054706 CIT-HSP-2
12	36.6	30.5	686	12	A2590942 IM0400K14
13	35.8	29.8	482	12	AG0603697 HS-2126_A
14	35.8	29.8	640	12	AG040377 Pan trogl
15	35.8	29.8	719	12	AG089826 HS-3100_A
16	35.8	29.8	750	12	AG089097 HS-3100_A
17	35.6	29.7	497	12	AQ375661 RPI11-15

C 18	35.6	29.7	590	12	AQ375699 RPI11-15
C 19	35.6	29.7	718	12	AQ108019 CIT-HSP-2
C 20	35.2	29.3	220	9	AW903211 CM4-NN102
C 21	35.2	29.3	268	10	C17241 C17241
C 22	35.2	29.3	270	10	C16982 C16982
C 23	35.2	29.3	301	9	AA350574 AA350574
C 24	35.2	29.3	346	9	AV694681 AV694681
C 25	35.2	29.3	353	9	AA362251 AA362251
C 26	35.2	29.3	377	9	AV692265 AV692265
C 27	35.2	29.3	394	10	BG897243 BG897243
C 28	35.2	29.3	474	12	AQ146371 AQ146371
C 29	35.2	29.3	688	12	AQ420313 AQ420313
C 30	35.2	29.3	740	12	AQ420267 AQ420267
C 31	35.2	29.2	444	12	B35593 B35593
C 32	35.2	29.2	448	12	B36994 B36994
C 33	35.2	29.2	585	12	AQ056850 AQ056850
C 34	35.2	29.2	642	12	AG125770 AG125770
C 35	34.8	29.0	387	12	AQ021233 AQ021233
C 36	34.8	29.0	399	10	BG011412 BG011412
C 37	34.8	29.0	497	12	B39893 B39893
C 38	34.8	29.0	527	9	AW297626 AW297626
C 39	34.8	29.0	696	12	B10814 B10814
C 40	34.6	28.8	384	9	AV743395 AV743395
C 41	34.6	28.8	397	9	A1244275 A1244275
C 42	34.6	28.8	414	9	A1469365 A1469365
C 43	34.6	28.8	429	12	AQ170644 AQ170644
C 44	34.6	28.8	441	12	B95491 B95491
C 45	34.6	28.8	466	9	A1635956 A1635956

ALIGNMENTS

RESULT 1
BG256799 716 bp mRNA EST 13-FEB-2001
LOCUS 602371024F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4479221 5',
DEFINITION mRNA sequence.
ACCESSION BG256799.1 GI:12766615
VERSION BG256799.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 716)
NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@rsf@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10310 row: p column: 06
High quality sequence stop: 708.
location/qualifiers
1. 716
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4479221"
/clone_lib="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORE6; Site: 1; NCI;
Site: 2; Salt: Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

FEATURES

source


```

/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/Note="Vector: pTR73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD+),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-GTGTACCAATCGAGTGGAGCGCCCTGCTTATTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pTR73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT      123 a      99 c      107 g      140 t
ORIGIN

Query Match      33.8%; Score 40.6; DB 9; Length 469;
Best Local Similarity 64.2%; Pred. No. 0.096;
Matches 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Oy 25 aagagcaggaccttgggagcaagaatcttaagttatctctgctgctattatata 84
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 31 AAGAGCACAATTTTGTGACCACTTCTCGTGAGCTCAAACTTACTATTACCA 90
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Oy 85 actaacacatttgcacatgttcttaagctttt 119
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 91 ACGAGGTGGCCTTGATCAAGTACTTAACCTTTT 125
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 5
LOCUS      A0033226      421 bp      DNA      linear      GSS 02-JUL-1998
DEFINITION HS_2226.A2.D01.MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2226 Col=2 Row=G, DNA sequence.
ACCESSION  A0033226
VERSION     A0033226.1  GI:3285414
KEYWORDS    GSS.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 421)
Mahaits,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,D., Young,D., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahaits GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2226 row: G column: 2
Class: BAC ends
High quality sequence stop: 421.
Location/Qualifiers
1. 421
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Plate=2226 Col=2 Row=G"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/Note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"

```

```

BASE COUNT      143 a      85 c      58 g      129 t      6 others
ORIGIN

Query Match      33.5%; Score 40.2; DB 12; Length 421;
Best Local Similarity 63.2%; Pred. No. 0.12;
Matches 60; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Oy 25 aagagcaggaccttgggagcaagaatcttaagttatctctgctgctattatata 84
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 202 AAGATGATGACCTTGAAGCCAAACCACTAAACATGATGACTGCTGCTACTACTA 261
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Oy 85 actaacacatttgcacatgttcttaagctttt 119
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 262 ACTTCAGACCTTGNGCAAGTATTATTTT 296
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 6
LOCUS      AG093829      698 bp      DNA      linear      GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-094G15.F, genomic survey sequence.
ACCESSION  AG093829
VERSION     AG093829.1  GI:16645631
KEYWORDS    GSS: GSS (genome survey sequence).
SOURCE      Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-094G15.F.
ORGANISM    Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
1 (sites)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 698)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suenho-chou,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbess@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1. 698
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-094G15.F"
/sex="male"
/cell_type="Lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT      197 a      165 c      134 g      198 t      4 others
ORIGIN

Query Match      32.5%; Score 39; DB 12; Length 698;
Best Local Similarity 63.2%; Pred. No. 0.3;
Matches 60; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Oy 25 aagagcaggaccttgggagcaagaatcttaagttatctctgctgctattatata 84
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 180 AAGAGCCAGACTTGAAGCCAGACTGCTTGAATCTGCTGCTGCTGCTACTATA 239
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Oy 85 actaacacatttgcacatgttcttaagctttt 119
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

Db 240 GTTATATGACCTTGAGCATATTACTTAACCTCTCT 274

RESULT	7
LOCUS	A0708262
DEFINITION	A0708262 530 bp DNA linear GSS 07-JUL-1999
ACCESSION	HS_571.1A1.F11.T7A.RPCI-11 Human Male BAC Library Homo sapiens
VERSION	A0708262
KEYWORDS	A0708262.1 GI:5417688
SOURCE	GSS.
ORGANISM	human.
	Homo sapiens

REFERENCE	TITLE
Mammalia; Eutheria; Chiroptera; Euteleostomi; 1 (basses 1 to 530)	
Mahatras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Koller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)	
99380589	Contact: Mahatras GG, Wallace JC, Hood L

```

sequence stop: 530
Location/Qualifiers
1. .530

```

DEFINITION	CIT-HSP-2386K22.TF.1 CIT-HSP Homo sapiens genomic clone 2386K22 DNA sequence.
ACCESSION	AQ240694
VERSION	AQ240694.1
KEYWORDS	GI:3672892
SCOPED	GSS.
human	human

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 691)
REFERENCE AUTHORS	Adams,M.D., Kounstley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE	Use of a random human BAC End sequence Database for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other_GSSs: CIT-HSP-2386K22.FR.1

BASE COUNT	263 a	103 g	225 t	1 others
ORIGIN	99 c			

RESULT	9
AA376998	
LOCUS	AA376998
DEFINITION	367 bp mRNA
ACCESSION	EST898974 Small intestine I Homo sapiens cDNA 5' end, linear
VERSION	AA376998
KEYWORDS	AA376998.1 GI:2029388
SOURCE	EST.
	human,

REFERENCE
AUTHORS
Ekmalyola, Melacota; Chordata; Carnivora; Vertebrates; Euteleostomi;
Kamatala; Euthera; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 367)
Adams, M.D., Kertavage, A.R., Fleischmann, R.D., Fuidner, R.A., Bult
C.M., Sutton, R.H., Kirkness, E.F., Weisrock, K.G., Gocayne, J.D., White
O., Sulten, C., Blake, J.A., Brandon, R.C., Man-Wal, C., Clayton, R.A.,
Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
L.M., Fitzhugh, W.N., Fleischmann, J.T., Geoghegan, N.S., Glodek, A.

Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,L.J., Saudé,D.M., Shirley,R., Small,K.V., Springs,T.A., Uterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dumke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A., He,W.M., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungnig,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

66026280

COMMENT

Contact: Kerlavage, AR

Bioinformatics for Genomic Research

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tldb/hgi/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1..367

/organism="Homo sapiens"

/db_xref="ATCC (inhost):181474"

/db_xref="taxon:9606"

/clone_lib="Small intestine I"

/dev_stage="adult"

/note="Organ: small intestine; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

Site_1: EcoRI; Site_2: XhoI

BASE COUNT 110 a 58 c 64 g 134 t 1 others

ORIGIN

Query Match 31.2%; Score 37.4; DB 9; length 367;

Best local Similarity 74.6%; Pred. No. 0.79; 16; Indels 0; Gaps 0;

Matches 47; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 25 aagagcagccttggagcaagatactaaatttaattcctgactctgattatla 84

DB 77 AAAGCCTGAACCTTAGAGTAAATACTACGTATTAAAGTCTGCTCTATATTA 136

OY 85 act 87

DB 137 ACT 139

RESULT 10

AQ498448 437 bp DNA linear GSS 28-APR-1999

LOCUS HS.5088.B1.F12.SP6E.RPCT-11 Human Male BAC Library Homo sapiens

DEFINITION genomic clone Plate-664 COL-23 Row-L, DNA sequence.

ACCESSION AQ498448

VERSION AQ498448.1 GI:4698571

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 437)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

MEDLINE 99380589

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCT-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (inforesgen.com). BAC end web Server: <http://www.hnsc.washington.edu>

Plate: 664 row: L column: 23

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 437.

Location/Qualifiers

1..437

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate-664 COL-23 Row-L"

/clone_lib="RPCT-11 Human Male BAC Library"

/sex="male"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

BASE COUNT 138 a 72 c 71 g 155 t 1 others

ORIGIN

Query Match 31.2%; Score 37.4; DB 12; length 437;

Best local Similarity 74.6%; Pred. No. 0.81; 16; Indels 0; Gaps 0;

Matches 47; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 25 aagagcagccttggagcaagatactaaatttaattcctgactctgattatla 84

DB 96 AAAGCCTGAACCTTAGAGTAAATACTACGTATTAAAGTCTGCTCTATATTA 155

OY 85 act 87

DB 156 ACT 158

RESULT 11

AQ054706 605 bp DNA linear GSS 30-JUL-1998

LOCUS CIT-HSP-2343H11.TF CIT-HSP Homo sapiens genomic clone 2343H11, DNA

DEFINITION sequence.

ACCESSION AQ054706

VERSION AQ054706.1 GI:3351312

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 605)

Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.

Building of a random BAC End Sequence Database for Sequence-Ready Map Use of a random BAC End Sequence Database for Sequence-Ready Map

Unpublished (1998)

Other GSSs: CIT-HSP-2343H11.TF

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES

Source Location/Qualifiers
1. 605
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2343H11"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2: HindIII"
BASE COUNT 221 a 102 c 104 g 178 t
ORIGIN

Query Match 30.7%; Score 36.8; DB 12; Length 605;
Best local Similarity 61.5%; Pred. No. 1.3;
Matches 59; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 25 aagagcagcagccttgagcagaatatactgaatttaattcctgactctgctattatta 84
Db 501 AAGAGCCTGTGCTTGAGACAGACTATTGGGTTCAACCCCTGCTGCTACTCTGTAT 442
Qy 85 actaacatccttgccaatgttgcttaagcttttt 120
Db 441 ACTGTGTGACTTTGGCGCAAGTGTCTTAACCTCTTGT 406

RESULT 12
A2590942 686 bp DNA linear GSS 13-DEC-2000
LOCUS Jm0400K14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0400K14 R, DNA sequence.
ACCESSION A2590942
VERSION A2590942.1 GI:11713132
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 686)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0400 row: K column: 14
Seq primer: CACACAGGAAGACGCTATGACC
Class: plasmid ends
High quality sequence stop: 686.

TITLE Location/Qualifiers
1. 686
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0400K14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"

FEATURES

Source Location/Qualifiers
1. 686
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0400K14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"

BASE COUNT 222 a 98 c 96 g 268 t 2 others
ORIGIN

Query Match 30.5%; Score 36.6; DB 12; Length 686;
Best local Similarity 60.0%; Pred. No. 1.5;
Matches 60; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 21 tagaagagcagcagccttgagcagaatatactgaatttaattcctgactctgctatt 80
Db 219 TATTAGGAGCAGAGAGCTGCTGAAATTTATGCTTAATTCACCTCTTATTCAGTATTT 278
Qy 81 attaacatcctcttgcacatgttgcttaagcttttt 120
Db 279 ATAAATTTACCATAGTTTAAATTTTATGAGGAATCTTT 318

RESULT 13
A0603697 482 bp DNA linear GSS 10-JUN-1999
LOCUS HS-2126-A1-B05-MR CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=2126 Col=9 Row=C, DNA sequence.
ACCESSION A0603697
VERSION A0603697.1 GI:5063691
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 482)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Hood,L., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
CONTACT: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.hsc.washington.edu>
Plate: 2126 row: C column: 9
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 482.

TITLE Location/Qualifiers
1. 482
/organism="Homo sapiens"

FEATURES
Source Location/Qualifiers
1. 482
/organism="Homo sapiens"

FEATURES
Source Location/Qualifiers
1. 482
/organism="Homo sapiens"

Query Match	29.8%	Score 35.8;	DB 12;	Length 640;
Best Local Similarity	61.1%;	Pred. No. 2.5;		
Matches	58;	Conservative	0;	Mismatches 37; Indels 0; Gaps 0

Query Match	29.8 %	Score 35.8	DB 12	Length 719
Best Local Similarity	61.1 %	Pred. No. 2.6		
Matches	58	Conservative	0	Mismatches 37
				Indels 0
				Gaps 0
Qy	25	aaagagagagaccttggagagaagaatataatgaatttaattcctcgaactcgcgtattatca	84	
Db	559	aaacacacagacctctggagacacagatggcctgaacctcaaaatccgtgtctgcacactatg	500	
Qy	85	actaacacatcttgcacatggttgcttaagctttt	119	
Db	499	gctgtgttaattcttgagcaaaatttacttaagattctt	465	

Search completed: September 7, 2002, 14:51:24
Job time: 16183 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 8, 2002, 01:09:18 ; Search time 1826.34 Seconds
(without alignments)
200.099 Million cell updates/sec

Title: US-09-834-291-1_COPY_337_456
Perfect score: 120
Sequence: 1 tagggggaagggtatgca.....aatgttgaagctttttt 120

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2036664 seqs, 1522705736 residues

Total number of hits satisfying chosen parameters: 4073328

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	45121	6	US-10-035-832-1262
2	38	31.7	633	7	US-10-027-632-281585
3	36.4	30.3	860	7	US-10-027-632-129548
4	36.2	30.2	637	7	US-10-027-632-248649
5	35.8	29.8	471	7	US-10-027-632-295053
6	35.8	29.8	595	7	US-10-027-632-57014
7	35.8	29.8	604	7	US-10-027-632-4265
8	35.8	29.8	604	7	US-10-027-632-4266
9	35.8	29.8	13046	7	US-10-125-540-595
10	35.6	29.7	657	7	US-10-027-632-265257
11	35.4	29.5	162450	5	US-09-345-882-1
12	35.4	29.5	162450	5	US-09-345-882-1
13	35.4	29.5	162450	7	US-10-126-704-1
14	35.2	29.3	606	7	US-10-027-632-231146
15	35.2	29.3	7379	5	US-09-984-827-14
16	35	29.2	825	7	US-10-027-632-167773
17	35	29.2	825	7	US-10-027-632-167774
18	35	29.2	834	7	US-10-027-632-152436
19	35	29.2	834	7	US-10-027-632-152437
20	35	29.2	834	7	US-10-027-632-152438
21	35	29.2	240000	1	PCT-US02-17382-31
22	34.8	29.0	448	5	US-09-918-995-14451
23	34.8	29.0	561	7	US-10-027-632-163012
24	34.8	29.0	611	7	US-10-027-632-174901
25	34.8	29.0	620	6	US-10-198-846-4515

C 26	34.8	29.0	17597	6	US-10-206-664-2409	Sequence 2409, Ap
C 27	34.8	29.0	17597	6	US-10-212-054-2144	Sequence 2144, Ap
C 28	34.8	29.0	378361	1	PCT-US02-21669-3	Sequence 3, Appl
C 29	34.6	28.8	456	5	US-09-918-995-12552	Sequence 12552, A
C 30	34.6	28.8	467	5	US-09-918-995-10146	Sequence 10146, A
C 31	34.6	28.8	496	7	US-10-027-632-333053	Sequence 333053, A
C 32	34.4	28.7	663	7	US-10-137-757-619	Sequence 619, App
C 33	34.4	28.7	2281	7	US-10-027-632-102247	Sequence 102247, A
C 34	34.4	28.7	2281	7	US-10-027-632-102248	Sequence 102248, A
C 35	34.4	28.7	6803	7	PCT-US02-25766-1885	Sequence 1885, Ap
C 36	34.2	28.5	277	6	US-10-198-846-12340	Sequence 12340, A
C 37	34.2	28.5	603	7	US-10-027-632-177	Sequence 177, App
C 38	34.2	28.5	1335	7	US-10-126-103-273	Sequence 177, App
C 39	34.2	28.5	25550	7	US-10-105-298-14994	Sequence 14994, A
C 40	34	28.3	619	7	US-10-027-632-277529	Sequence 277529, A
C 41	33.8	28.2	519	7	US-10-027-632-185527	Sequence 185527, A
C 42	33.8	28.2	623	7	US-10-027-632-190488	Sequence 190488, A
C 43	33.8	28.2	623	7	US-10-027-632-190489	Sequence 190489, A
C 44	33.8	28.2	623	7	US-10-027-632-190490	Sequence 190490, A
C 45	33.8	28.2	1029	7	US-10-027-632-30428	Sequence 30428, A

ALIGNMENTS

RESULT 1
US-10-035-832-1262
; Sequence 1262, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Engelhard, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035, 832
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1262
; LENGTH: 45121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-832-1262

Query Match 100.0%; Score 120; DB 6; Length 45121;
Best Local Similarity 100.0%; Pred. No. 2.7e-26;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taggggaagggtatgcatagaagcagccttggtggaagaatattctagttt 60
|||||
Db 8330 taggggaagggtatgcatagaagcagccttggtggaagaatattctagttt 8389
QY 61 aattccgacttgccttattatcaaccatcttgcacatgttgtaagctttt 120
|||||
Db 8390 aattccgacttgccttattatcaaccatcttgcacatgttgtaagctttt 8449

RESULT 2
US-10-027-632-281585/C
; Sequence 281585, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12


```
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 295053
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-295053
```

```
Query Match          29.8%; Score 35.8; DB 7; Length 471;
Best Local Similarity 61.1%; Pred. No. 0.32;
Matches 58; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
```

```
Oy 25 aagagcagaccttggagcagaataatcgaattcaatccgcgactcgtctattt 84
    ||||| || || || || || || || || || || || || || || || ||
Db 316 AAGACATGAACTCTGAAACCGACAGCTGTATGTCTGAATCCCACTTCACTTACTA 257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 85 actaacacatttgcacatgttgccttaagctttt 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 256 GCTACATGACCTTGGACAAATTAATTAACTCTCT 222
```

RESULT 6

```
US-10-027-632-57014/c
; Sequence 57014, Application US/10027632
; GENERAL INFORMATION:
```

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57014
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-57014
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Query Match          29.8%; Score 35.8; DB 7; Length 595;
Best Local Similarity 61.1%; Pred. No. 0.34;
Matches 58; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
```

```
Oy 25 aagagcagaccttggagcagaataatcgaattcaatccgcgactcgtctattt 84
    ||||| || || || || || || || || || || || || || || || ||
Db 316 AAGACATGAACTCTGAAACCGACAGCTGTATGTCTGAATCCCACTTCACTTACTA 257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 85 actaacacatttgcacatgttgccttaagctttt 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 256 GCTACATGACCTTGGACAAATTAATTAACTCTCT 222
```

RESULT 7

```
US-10-027-632-4265/c
; Sequence 4265, Application US/10027632
; GENERAL INFORMATION:
```

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4265
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-4265
```

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Query Match          29.8%; Score 35.8; DB 7; Length 604;
Best Local Similarity 61.1%; Pred. No. 0.34;
Matches 58; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
```

```
Oy 25 aagagcagaccttggagcagaataatcgaattcaatccgcgactcgtctattt 84
    ||||| || || || || || || || || || || || || || || || ||
Db 325 AAGACATGAACTCTGAAACCGACAGCTGTATGTCTGAATCCCACTTCACTTACTA 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 85 actaacacatttgcacatgttgccttaagctttt 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 265 GCTACATGACCTTGGACAAATTAATTAACTCTCT 231
```

RESULT 8

```
US-10-027-632-4266/c
; Sequence 4266, Application US/10027632
; GENERAL INFORMATION:
```

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4266
; LENGTH: 604
```

```
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-4266

Query Match          29.8%; Score 35.8; DB 7; Length 604;
Best Local Similarity 61.1%; Pred. No. 0.34;
Matches 58; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 25 aaggagcagacctggggagcaagaatatctaagtttaattcccgacctgctatttata 84
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 325 AAGACATGACCTCTGACACCGACGCTGATCTGATCTGCAATCCCAACTTCATTGCTTACTA 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 85 actaacactcttgccaatgttgcttaagctttt 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 265 GCTACATGACCTTGACACAAATTACTTAACCTCTCT 231
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
US-10-125-540-595/c
; Sequence 595, Application US/10125540
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 595
; LENGTH: 13046
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-125-540-595

Query Match          29.8%; Score 35.8; DB 7; Length 13046;
Best Local Similarity 61.1%; Pred. No. 0.7;
Matches 58; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 25 aaggagcagacctggggagcaagaatatctaagtttaattcccgacctgctatttata 84
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8107 AAAAGCAGGACCTCTGACACCGACGCTGCTGATTTGAATCCCTAGCTCTGCCAATTACTA 8048
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 85 actaacactcttgccaatgttgcttaagctttt 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8047 ACTGTGACCTTGCGCAAGTACTTACCTTCTCT 8013
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
US-10-027-632-265257
; Sequence 265257, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
```

```
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 265257
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-265257

Query Match          29.7%; Score 35.6; DB 7; Length 657;
Best Local Similarity 71.2%; Pred. No. 0.4;
Matches 47; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 23 gaagagcagacctggggagcaagaatatctaagtttaattcccgacctgctatttata 82
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 368 gaagacacagcctgtgtaaccagtaatacttaagtttaattccctgctatttata 427
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 83 taacta 88
    |||||
Db 428 taacta 433
    |||||

RESULT 11
US-09-345-882-1
; Sequence 1, Application US/09345882
; GENERAL INFORMATION:
; APPLICANT: Bouguetelret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-
; FILE REFERENCE: GENSET.031A
; CURRENT APPLICATION NUMBER: US/09/345,882
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72794
; OTHER INFORMATION: 5-124-273 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 88073
; OTHER INFORMATION: 5-127-261 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90842
; OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 93714
; OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97122
; OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97152
; OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99098
; OTHER INFORMATION: 5-130-257 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
```

LOCATION: 99117 : polymorphic base A or G
OTHER INFORMATION: 5-130-276 : polymorphic base A or G
FEATURE: NAME/KEY: allele
LOCATION: 103806 : polymorphic base A or T
OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE: NAME/KEY: allele
LOCATION: 106940 : polymorphic base insertion of A
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE: NAME/KEY: allele
LOCATION: 108106 : polymorphic base insertion of A
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE: NAME/KEY: allele
LOCATION: 108149 : polymorphic base insertion of GTTT
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
FEATURE: NAME/KEY: allele
LOCATION: 108308 : polymorphic base A or G
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE: NAME/KEY: allele
LOCATION: 108471 : polymorphic base C or T
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE: NAME/KEY: allele
LOCATION: 134134 : polymorphic base C or T
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE: NAME/KEY: allele
LOCATION: 134362 : polymorphic base insertion of A
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE: NAME/KEY: allele
LOCATION: 134374 : polymorphic base insertion of CA
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE: NAME/KEY: allele
LOCATION: 146328 : polymorphic base A or G
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE: NAME/KEY: allele
LOCATION: 146345 : polymorphic base A or C
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE: NAME/KEY: allele
LOCATION: 150329 : polymorphic base A or G
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE: NAME/KEY: allele
LOCATION: 160031 : polymorphic base G or T
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE: NAME/KEY: allele
LOCATION: 72771..72817 : polymorphic fragment 5-124-273 SEQ ID30
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE: NAME/KEY: allele
LOCATION: 72771..72817 : polymorphic fragment 5-124-273 SEQ ID51
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
FEATURE: NAME/KEY: allele
LOCATION: 88050..88096 : polymorphic fragment 5-127-261 SEQ ID31
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE: NAME/KEY: allele
LOCATION: 88050..88096 : polymorphic fragment 5-127-261 SEQ ID52
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
FEATURE: NAME/KEY: allele
LOCATION: 90819..90865 : polymorphic fragment 5-135-198 SEQ ID39
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39

OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE: NAME/KEY: allele
LOCATION: 90819..90865 : complement polymorphic fragment 99-1437-325 SEQ ID70
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE: NAME/KEY: allele
LOCATION: 93690..93736 : polymorphic fragment 5-128-60 SEQ ID32
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE: NAME/KEY: allele
LOCATION: 93690..93736 : polymorphic fragment 5-128-60 SEQ ID53
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE: NAME/KEY: allele
LOCATION: 97099..97145 : polymorphic fragment 99-1442-224 SEQ ID50
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE: NAME/KEY: allele
LOCATION: 97099..97145 : polymorphic fragment 99-1442-224 SEQ ID71
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE: NAME/KEY: allele
LOCATION: 97130..97177 : polymorphic fragment 5-129-144 SEQ ID33
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE: NAME/KEY: allele
LOCATION: 97130..97177 : polymorphic fragment 5-129-144 SEQ ID54
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE: NAME/KEY: allele
LOCATION: 99075..99121 : polymorphic fragment 5-130-257 SEQ ID34
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE: NAME/KEY: allele
LOCATION: 99075..99121 : polymorphic fragment 5-130-257 SEQ ID55
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE: NAME/KEY: allele
LOCATION: 99094..99140 : polymorphic fragment 5-130-276 SEQ ID35
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE: NAME/KEY: allele
LOCATION: 99094..99140 : polymorphic fragment 5-130-276 SEQ ID56
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE: NAME/KEY: allele
LOCATION: 103783..103828 : polymorphic fragment 5-131-395 SEQ ID36
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE: NAME/KEY: allele
LOCATION: 103783..103828 : polymorphic fragment 5-131-395 SEQ ID57
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE: NAME/KEY: allele
LOCATION: 106918..106966 : polymorphic fragment 5-133-375 SEQ ID37
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE: NAME/KEY: allele
LOCATION: 106918..106966 : polymorphic fragment 5-133-375 SEQ ID58
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE: NAME/KEY: allele
LOCATION: 108084..108130 : polymorphic fragment 5-135-155 SEQ ID38
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE: NAME/KEY: allele
LOCATION: 108084..108130 : polymorphic fragment 5-135-155 SEQ ID59
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE: NAME/KEY: allele
LOCATION: 108127..108177 : polymorphic fragment 5-135-198 SEQ ID39
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39

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FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
NAME/KEY: allele

Query Match          29.5%; Score 35.4; DB 5; Length 162450;
Best Local Similarity 61.3%; Pred. No. 1.7;
Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 26 agagcagccttgaggagcagaataaatttaattctgactgctattatataa 85
DB 82403 atagatgaacttgaggcagctgtgtgtgtgaactcctgctgcacactcctg 82462
QY 86 ctaccactcttgccactgtgtgtaaccttt 118
DB 82463 ctgtgtgactctggagtggttaacttaactcttt 82495

RESULT 12
US-09-345-882-1
; Sequence 1, Application US/09345882
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; FILE REFERENCE: GENSET.031A
; CURRENT APPLICATION NUMBER: US/09/345,882
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72794
; OTHER INFORMATION: 5-124-273 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 88073
; OTHER INFORMATION: 5-127-261 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90842
; OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 93714
; OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97122
; OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97152
; OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99098
; OTHER INFORMATION: 5-130-257 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99117
; OTHER INFORMATION: 5-130-276 : polymorphic base A or G
; FEATURE:

NAME/KEY: allele
LOCATION: 103806
OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTT
FEATURE:
NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134362
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE:
NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
```

LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177

OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
NAME/KEY: allele
Query Match 29.5%; Score 35.4; DB 5; Length 162450;
Best Local Similarity 61.3%; Pred No. 1.7;
Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
Oy 26 agacgagacctggggaagaatactaaatttaactctgactgctattttaa 85
Db 82403 atagatgaactgctggagcagctgtgctgttggaatccctgctgcaactcttg 82462
Oy 86 ctaccatcttgccaatgctcttaagctttt 118
Db 82463 ctgtgtgactctggatggttacttaactttt 82495
RESULT 13
US-10-126-704-1
; Sequence 1, Application US/10126704
; GENERAL INFORMATION:
; APPLICANT: Bouguetere, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-
; TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
; FILE REFERENCE: 44,US,DIY
; CURRENT FILING DATE: 2002-04-20
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72794
; OTHER INFORMATION: 5-124-273 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 88073
; OTHER INFORMATION: 5-127-261 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90842
; OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 93714
; OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97122
; OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97152
; OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99098
; OTHER INFORMATION: 5-130-257 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99117
; OTHER INFORMATION: 5-130-276 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 103806
; OTHER INFORMATION: 5-131-395 : polymorphic base A or T

FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
FEATURE:
NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134362
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE:
NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE:

NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
NAME/KEY: allele

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Query Match          29.5%; Score 35.4; DB 7; Length 162450;
Best Local Similarity 61.3%; Pred. No. 1.7;
Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 26 agagcagagccttgaggaagaatacctaagtttaattcctgaactgtattattaa 85
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 82403 atagatgaactcgttgagcgaagtgtctgggtttgaatccctggtccactcttg 82462
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 86 ctaccacattgccaatgttgcctaagcttt 118
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 82463 ctgtgtgatcttgagatggttaacttaattt 82495
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-10-027-632-231146
; Sequence 231146, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US/10/027, 632
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231146
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231146

Query Match          29.3%; Score 35.2; DB 7; Length 606;
Best Local Similarity 58.7%; Pred. No. 0.52;
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 9 ggggtatgcatagaagagcagacctggagcaagaatatctaagtttaattcctg 68
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 500 ggtgttaataatagtgtaagcagcagactctgagccaactgcctaggttaactta 559
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 69 acctgcatttaactaactaacattcttgccaatgttgcttaa 112
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 560 gctctattacttctaactctgtgacttggtggccaatgacttaa 603
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-09-984-827-14
; Sequence 14, Application US/09984827
; GENERAL INFORMATION:
; APPLICANT: DENERLE, PATRICE
; APPLICANT: ROSTIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984, 827
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; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 7379
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-827-14
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Query Match          29.3%; Score 35.2; DB 5; Length 7379;
Best Local Similarity 62.5%; Pred. No. 0.94;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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Db 1376 gggagtttggagcatacagagctcaagtgaatccctgaacttgaactatttgctatat 1435
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 92 atcttgccaatgttgcttaagctttt 119
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1436 gaccttgggcaagcgtcttaagctctct 1463
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Search completed: September 8, 2002, 01:09:44
Job time: 37062 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:31:31 ; Search time 13836.9 Seconds
(without alignments)
187.627 Million cell updates/sec

Title: US-09-834-291-1_COPY_337_456
Sequence: 1 taggggaaggggtagtggca.....aatgtgttaagcttttt 120

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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2	120	100.0	3212	32	US-09-834-291-1
3	120	100.0	45121	36	US-09-997-722-10
4	45.8	38.2	17974	63	US-60-245-224-9
5	43.2	36.0	443	17	US-09-353-690-10171
6	43.2	36.0	443	34	US-09-922-340-10171
7	43.2	36.0	443	34	US-09-922-340A-10171
8	43.2	36.0	518	29	US-09-726-803-609
9	43.2	36.0	684	29	US-09-726-803-1202
10	43.2	36.0	11532	59	US-60-205-418-135
11	42.8	35.7	396	31	US-09-824-559-1394
12	41.6	34.7	32768	52	US-60-207-583-151
13	41.6	34.7	32768	52	US-60-230-445-984
14	41.6	34.7	143899	36	US-09-972-546-15
15	40.6	33.8	4041	61	US-60-212-358-85
16	40.6	33.8	136163	61	US-60-226-176-1053
17	40.6	33.8	136163	62	US-60-233-468-1053
18	40.6	33.8	136163	70	US-60-313-371-1053
19	40.6	33.8	151471	61	US-60-226-176-239
20	40.6	33.8	151471	62	US-60-233-468-239
21	40.6	33.8	151471	70	US-60-313-371-239
22	40.4	33.7	79312	63	US-60-242-679-393
23	39	32.5	262	1	PCT-US01-15674A-99
24	39	32.5	262	16	US-09-234-119A-145
25	39	32.5	262	16	US-09-573-080A-99
26	39	32.5	359	18	US-09-428-151A-2422
27	39	32.5	359	23	US-09-614-387-1897
28	39	32.5	13964	62	US-60-230-445-917
29	39	32.5	32659	59	US-60-206-020-98
30	39	32.5	216504	63	US-60-242-679-316
31	38.8	32.3	32768	60	US-60-213-177-302

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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32 38.8 32.3 32768 62 US-60-230-445-490 Sequence 490, App
33 38.8 32.3 32768 62 US-60-233-937-211 Sequence 211, App
34 38.4 32.0 9613 1 PCT-US01-01334-8121 Sequence 8121, App
35 38.4 32.0 9613 30 US-09-764-874-8121 Sequence 8121, App
36 38.4 32.0 9613 37 US-10-092-400-8121 Sequence 8121, App
37 38.4 32.0 9614 1 PCT-US01-01334-8123 Sequence 8123, App
38 38.4 32.0 9614 30 US-09-764-874-8123 Sequence 8123, App
39 38.4 32.0 9614 37 US-10-092-400-8123 Sequence 8123, App
40 38.4 32.0 112392 63 US-60-245-228-209 Sequence 209, App
41 38.4 32.0 112392 64 US-60-258-272-83 Sequence 83, App
42 38.2 31.8 576 24 US-09-637-889-5424 Sequence 5424, App
43 38 31.7 633 24 US-09-634-306B-281585 Sequence 281585, App
44 38 31.7 32768 59 US-60-208-084-23 Sequence 23, App
45 38 31.7 32768 59 US-60-208-596-27 Sequence 27, App
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ALIGNMENTS

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RESULT 1
US-09-834-291-4
; Sequence 4, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2827
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-4
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Best Local Similarity 100.0%; Pred. No. 1.9e-26;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taggggaagggtatggtacatagaagagcagaccttgggaagaagaataatcttaagttt 60
Db 337 taggggaagggtatggtacatagaagagcagaccttgggaagaagaataatcttaagttt 396
QY 61 aattcctgactctgctattatttaactaacacatcttggccaatgttgccttaagctttt 120
Db 397 aattcctgactctgctattatttaactaacacatcttggccaatgttgccttaagctttt 456
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RESULT 2
US-09-834-291-1
; Sequence 1, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.1
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; SEQ ID NO 1
; LENGTH: 3212
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-1
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Query Match 100.0%; Score 120; DB 32; Length 3212;
Best Local Similarity 100.0%; Pred. No. 1.9e-26;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 337 taggggaagggtatggtacatagaagagcagaccttgggaagaagaataatcttaagttt 396
QY 61 aattcctgactctgctattatttaactaacacatcttggccaatgttgccttaagctttt 120
Db 397 aattcctgactctgctattatttaactaacacatcttggccaatgttgccttaagctttt 456
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RESULT 3
US-09-997-722-10
; Sequence 10, Application US/09997722
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCP
; CURRENT APPLICATION NUMBER: US/09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 10
; LENGTH: 45121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-997-722-10
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Best Local Similarity 100.0%; Pred. No. 4.3e-26;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taggggaagggtatggtacatagaagagcagaccttgggaagaagaataatcttaagttt 60
Db 8330 taggggaagggtatggtacatagaagagcagaccttgggaagaagaataatcttaagttt 8389
QY 61 aattcctgactctgctattatttaactaacacatcttggccaatgttgccttaagctttt 120
Db 8390 aattcctgactctgctattatttaactaacacatcttggccaatgttgccttaagctttt 8449
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```
RESULT 4
US-60-245-224-9/C
; Sequence 9, Application US/60245224
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: C1000887
; CURRENT APPLICATION NUMBER: US/60/245,224
; CURRENT FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 17974
; TYPE: DNA
; ORGANISM: HUMAN
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US-60-245-224-9

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Best Local Similarity 64.8%; Pred. No. 0.0034;
Matches 68; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 15 atggcctagaagaagagacgttgggagcaagaatataaagttaattccgtactg 74
DB 14562 ATGTGTAGAAACACATTAACCTGTGGCGCAGACATAGCTCAATCTATTG 14503

QY 75 ctaatttaacacacattcttgccaatgttgcttaagctttt 119
DB 14502 CTAATTCTCAAGCTGTGTAACCTGAAATAATGCTTAACCTCTCT 14458

RESULT 5
US-09-353-690-10171/C
Sequence 10171, Application US/09353690
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FILE REFERENCE: 20411-726CON2
CURRENT APPLICATION NUMBER: US/09/353,690
CURRENT FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: US 09/217,517
EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 12181
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10171
LENGTH: 443
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(443)
OTHER INFORMATION: n = A,T,C or G
US-09-353-690-10171

Query Match 36.0%; Score 43.2; DB 17; Length 443;
Best Local Similarity 60.0%; Pred. No. 0.0071;
Matches 72; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 taggggaagggtatgcatagaaagagcagacgttgggagcaagaatacttaagtt 60
DB 146 TGGAGGAAATGAAAGGCATATCGAGAGCCTGGGCTGTGCATGCAATGCTGAGTTC 87

QY 61 aatccctgactctctatttataactaacatttgcgaatgttgcttaagctttt 120
DB 86 AAACCTGTCTCTCTTTTGTGTAACCTGTGACCTTTGGGCAAGTCCCTTAACCTCTCT 27

RESULT 6
US-09-922-340-10171/C
Sequence 10171, Application US/09922340
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FILE REFERENCE: 20411-726CON2
CURRENT APPLICATION NUMBER: US/09/922,340
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US/09/353,690
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR FILING DATE: 1998-01-07
NUMBER OF SEQ ID NOS: 12181
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10171

LENGTH: 443
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(443)
OTHER INFORMATION: n = A,T,C or G
US-09-922-340-10171

Query Match 36.0%; Score 43.2; DB 34; Length 443;
Best Local Similarity 60.0%; Pred. No. 0.0071;
Matches 72; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 taggggaagggtatgcatagaaagagcagacgttgggagcaagaatacttaagtt 60
DB 146 TGGAGGAAATGAAAGGCATATCGAGAGCCTGGGCTGTGCATGCAATGCTGAGTTC 87

QY 61 aatccctgactctctatttataactaacatttgcgaatgttgcttaagctttt 120
DB 86 AAACCTGTCTCTCTTTTGTGTAACCTGTGACCTTTGGGCAAGTCCCTTAACCTCTCT 27

RESULT 7
US-09-922-340A-10171/C
Sequence 10171, Application US/09922340A
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FILE REFERENCE: 20411-726CON2
CURRENT APPLICATION NUMBER: US/09/922,340A
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US/09/353,690
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/217,517
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 12181
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10171
LENGTH: 443
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(443)
OTHER INFORMATION: n = A,T,C or G
US-09-922-340A-10171

Query Match 36.0%; Score 43.2; DB 34; Length 443;
Best Local Similarity 60.0%; Pred. No. 0.0071;
Matches 72; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 taggggaagggtatgcatagaaagagcagacgttgggagcaagaatacttaagtt 60
DB 146 TGGAGGAAATGAAAGGCATATCGAGAGCCTGGGCTGTGCATGCAATGCTGAGTTC 87

QY 61 aatccctgactctctatttataactaacatttgcgaatgttgcttaagctttt 120
DB 86 AAACCTGTCTCTCTTTTGTGTAACCTGTGACCTTTGGGCAAGTCCCTTAACCTCTCT 27

RESULT 8
US-09-726-803-609
Sequence 609, Application US/09726803
GENERAL INFORMATION:
APPLICANT: Geating, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Kingsbury, Gillian A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

```
;; TITLE OF INVENTION: THEREFOR
;; FILE REFERENCE: 1600.2050-001
;; CURRENT APPLICATION NUMBER: US/09/726,803
;; CURRENT FILING DATE: 2000-11-30
;; PRIOR APPLICATION NUMBER: 60/168,085
;; PRIOR FILING DATE: 1999-11-30
;; NUMBER OF SEQ ID NOS: 1769
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 609
;; LENGTH: 518
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(518)
;; OTHER INFORMATION: n = A,T,C or G
US-09-726-803-609
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```
Query Match          36.0%; Score 43.2; DB 29; Length 518;
Best Local Similarity 65.6%; Pred. No. 0.0075;
Matches 63; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
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```
QY 24 aaagacgagccttgggagcaagaatacttaattcctgactctgtctatttt 83
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 389 aagagacgtgacttgcagctagactgctgcttagaatacctgctctgcatgtatt 448
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 84 aactaacatcttgcgaatgttgccttaagctttt 119
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 449 agtcatgtgcttgcgtgcatgttacttaacctttc 484
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 9
US-09-726-803-1202
; Sequence 1202, Application US/09726803
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Kingsbury, Gillian A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2050-001
; CURRENT APPLICATION NUMBER: US/09/726,803
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/168,085
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 1769
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1202
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-726-803-1202
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Query Match          36.0%; Score 43.2; DB 29; Length 684;
Best Local Similarity 65.6%; Pred. No. 0.0081;
Matches 63; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
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```
QY 24 aaagacgagccttgggagcaagaatacttaattcctgactctgtctatttt 83
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 526 aagagacgtgacttgcagctagactgctgcttagaatacctgctctgcatgtatt 585
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 84 aactaacatcttgcgaatgttgccttaagctttt 119
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 586 agtcatgtgcttgcgtgcatgttacttaacctttc 621
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 10
US-60-205-418-135
; Sequence 135, Application US/60205418
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
```

```
;; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
;; FILE REFERENCE: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;; TITLE OF INVENTION: USES THEREOF
;; FILE REFERENCE: C1000556
;; CURRENT APPLICATION NUMBER: US/60/205,418
;; CURRENT FILING DATE: 2000-05-19
;; NUMBER OF SEQ ID NOS: 536
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 135
;; LENGTH: 11532
;; TYPE: DNA
;; ORGANISM: HUMAN
US-60-205-418-135
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Query Match          36.0%; Score 43.2; DB 59; Length 11532;
Best Local Similarity 60.0%; Pred. No. 0.019;
Matches 72; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
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QY 1 taggggaaggaggatgcatagaagaagcagaccctgggagcaagaatacttaatt 60
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6451 tggaggaaatgaaagcaatactgagcctgtgctctgcatcagaatgctgattc 6510
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 aatccgtactgtctatttacttaactaacatcttgcgaatgttgccttaagctttt 120
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6511 aaacctgtctctgtcttcttcttgccttgccttgccttgccttgccttgcctt 6570
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 11
US-09-824-559-1994
; Sequence 1994, Application US/09824559
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Jakubowski, Joseph A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2077-001
; CURRENT APPLICATION NUMBER: US/09/824,559
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/193,437
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 9929
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1994
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-824-559-1994
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Query Match          35.7%; Score 42.8; DB 31; Length 396;
Best Local Similarity 66.0%; Pred. No. 0.0092;
Matches 62; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
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QY 25 aagagacgagccttgggagcaagaatacttaattcctgactctgtctatttt 84
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 151 aagagcgtgaagtgtggaaacagacgctcgtgaatttaactcactaccactatla 210
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 85 aactaacatcttgcgaatgttgccttaagctttt 118
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 211 gctgtgtgactttagaagaagttaacttaaccttt 244
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 12
US-60-207-583-151/c
; Sequence 151, Application US/60207583
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: C1000598
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RESULT 15
US-60-212-358-85
; Sequence 85, Application US/60212358

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: GENERAL INFORMATION:
: APPLICANT: Beasley, Ellen
: TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
: TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR
: TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEREOF
: FILE REFERENCE: CL000684
: CURRENT APPLICATION NUMBER: US/60/212,358
: CURRENT FILING DATE: 2000-06-19
: NUMBER OF SEQ ID NOS: 324
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 85
: LENGTH: 4041
: TYPE: DNA
: ORGANISM: HUMAN
: US-60-212-358-85

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	Query	33.8%; Score 40.6; DB 60; Length 4041; Best Local Similarity 64.2%; Pred. No. 0.089; Matches 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY	25 aagagcagacctgggagcaagaatctacttaagttaattctctagctgcgattatata 84 	
Db	2183 aagagcatgagccctgaagacagatcatcctaagctcaaatccgattctgccaattaca 2242 	
QY	85 actaacctctcttgccaatgttgcttaagctttt 119 	
Db	2243 actgtgtaacctcgagcacttacttaactctctc 2277 	

Search completed: September 7, 2002, 22:31:46
Job time: 43800 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:21:07 ; Search time 212.3 Seconds
(without alignments)
138.841 Million cell updates/sec

Title: US-09-834-291-1_COPY_337_456
Perfect score: 120
Sequence: 1 taagggaaggggtatgcga.....aatgttctaagcttttt 120

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/Packfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	32.2	26.8	10564	1 US-08-206-176-5	Sequence 5, Appli
C 2	30.6	25.5	1980	2 US-08-766-858A-4	Sequence 4, Appli
C 3	28.6	23.8	2369	1 US-07-797-556-1	Sequence 1, Appli
C 4	28.6	23.8	2369	1 US-08-308-881-1	Sequence 1, Appli
C 5	28.6	23.8	2369	2 US-09-058-263-1	Sequence 1, Appli
C 6	28.6	23.8	2369	2 US-09-059-099-1	Sequence 1, Appli
C 7	28.6	23.8	2369	3 US-09-058-264-1	Sequence 1, Appli
C 8	28.6	23.8	2369	5 PCT-US95-06530-1	Sequence 1, Appli
C 9	28.6	23.8	3085	4 US-08-795-473B-4	Sequence 4, Appli
C 10	28.2	23.5	87350	3 US-08-781-891-79	Sequence 79, Appli
C 11	28	23.3	2517	3 US-08-733-360A-4	Sequence 4, Appli
C 12	28	23.3	2517	3 US-08-987-743-16	Sequence 16, Appli
C 13	28	23.3	2517	4 US-08-916-935-4	Sequence 4, Appli
C 14	28	23.3	5873	1 US-07-928-464-4	Sequence 4, Appli
C 15	28	23.3	5873	5 PCT-US93-07347-4	Sequence 4, Appli
C 16	28	23.3	5890	1 US-07-928-464-3	Sequence 3, Appli
C 17	28	23.3	5890	1 US-07-928-464-5	Sequence 5, Appli
C 18	28	23.3	5890	1 US-07-928-464-6	Sequence 6, Appli
C 19	28	23.3	5890	5 PCT-US93-07347-3	Sequence 3, Appli
C 20	28	23.3	5890	5 PCT-US93-07347-5	Sequence 5, Appli
C 21	28	23.3	5890	5 PCT-US93-07347-6	Sequence 6, Appli
C 22	28	23.3	6295	1 US-08-003-311B-4	Sequence 4, Appli
C 23	28	23.3	6295	1 US-08-261-432-4	Sequence 4, Appli
C 24	28	23.3	6312	1 US-08-003-311B-3	Sequence 3, Appli
C 25	28	23.3	6312	1 US-08-003-311B-5	Sequence 5, Appli
C 26	28	23.3	6312	1 US-08-003-311B-6	Sequence 6, Appli
C 27	28	23.3	6312	1 US-08-003-311B-7	Sequence 7, Appli

C 28	28	23.3	6312	1 US-08-261-432-3	Sequence 3, Appli
C 29	28	23.3	6312	1 US-08-261-432-5	Sequence 5, Appli
C 30	28	23.3	6312	1 US-08-261-432-6	Sequence 6, Appli
C 31	28	23.3	6312	1 US-08-261-432-7	Sequence 7, Appli
C 32	27.8	23.2	1679	1 US-08-202-056-6	Sequence 6, Appli
C 33	27.8	23.2	1679	1 US-08-076-093A-5	Sequence 5, Appli
C 34	27.8	23.2	1679	1 US-08-701-265-5	Sequence 5, Appli
C 35	27.8	23.2	1679	2 US-08-284-586-5	Sequence 5, Appli
C 36	27.8	23.2	1679	2 US-08-805-478-5	Sequence 5, Appli
C 37	27.8	23.2	1679	2 US-08-802-627A-5	Sequence 5, Appli
C 38	27.8	23.2	1679	2 US-08-801-238-5	Sequence 5, Appli
C 39	27.8	23.2	1679	2 US-08-801-238-5	Sequence 5, Appli
C 40	27.8	23.2	1679	3 US-09-104-296-5	Sequence 5, Appli
C 41	27.8	23.2	1679	5 PCT-US94-06380-3	Sequence 3, Appli
C 42	27.6	23.0	59065	4 US-09-813-817-3	Sequence 3, Appli
C 43	27.2	22.7	867	4 US-09-273-839A-7	Sequence 7, Appli
C 44	27.2	22.7	2160	1 US-08-082-849B-30	Sequence 30, Appli
C 45	27.2	22.7	2160	5 PCT-US94-01624-30	Sequence 30, Appli

ALIGNMENTS

RESULT 1
US-08-206-176-5/C
Sequence 5, Application US/08206176
Patent No. 5639940
GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Dairymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Zymogenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: human fibrinogen gamma chain
FEATURE:
NAME/KEY: CDS
LOCATION: join(1799..1876, 1973..2017, 2207..2390, 2510
..2603, 4211..4541, 4645..4778, 5758..5942, 7426
LOCATION: ..7703, 9342..9571)
US-08-206-176-5

RESULT 4
US-08-308-881-1
Sequence 1, Application US/08308881
Patent No. 5783672
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10G/PDC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 310..2369
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 244..309
US-08-308-881-1

Query Match 23.8%; Score 28.6; DB 1; Length 2369;
Best Local Similarity 55.6%; Pred. No. 1.2;
Matches 55; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Db 20 atagaagaagcagccttgaggagcaagaatatcctaagtttaattcctgactgctatt 79
150 ATGGAAGAAAGCATGACATTAGAGAGTAGAGCTTAGCTCAATCCCTACTCTTCACT 209

Qy 80 tattaactaacatcttgcgaatgttgcttaagctttt 118
210 TACTAATTTTGTGATTGTGAATATCCGCCCAAGATGTT 248

RESULT 5
US-09-058-263-1
Sequence 1, Application US/09058263
Patent No. 5891997
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10G/PDC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 310..2369
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 244..309
US-09-058-263-1

Query Match 23.8%; Score 28.6; DB 2; Length 2369;
Best Local Similarity 55.6%; Pred. No. 1.2;
Matches 55; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Db 20 atagaagaagcagccttgaggagcaagaatatcctaagtttaattcctgactgctatt 79
150 ATGGAAGAAAGCATGACATTAGAGAGTAGAGCTTAGCTCAATCCCTACTCTTCACT 209

Dy 80 tattaactaaccaaccttgcgaatgttgcttaagcttt 118
|| || | || | || || ||
Db 210 TACTAATTTTGTGATTGGAAATATCCGCCCAAGATGT 248

RESULT 6

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US-09-059-099-1
? Sequence ID: Application US/09059099
? Patent No. 5925740
? GENERAL INFORMATION:
? APPLICANT: Mosley, Bruce
? APPLICANT: Cosman, David J.
? TITLE OF INVENTION: Receptor for Oncostatin M
? NUMBER OF SEQUENCES: 11
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Immunex Corporation
? STREET: 51 University Street
? CITY: Seattle
? STATE: WA
? COUNTRY: USA
? ZIP: 98101
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: Apple Macintosh
? OPERATING SYSTEM: Apple 7.1
? SOFTWARE: Microsoft Word, Version 5.1a
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/059,099
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/308,881
? FILING DATE: 12-SEP-1994
? APPLICATION NUMBER: US 08/249,553
? FILING DATE: 26-MAY-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Seeee, Kathryn A.
? REGISTRATION NUMBER: 32,172
? REFERENCE/DOCKET NUMBER: 2614-A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 587-0430
? TELEFAX: (206) 233-0644
? TELEX: 7568822
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2369 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: N-terminal
? ORIGINAL SOURCE:
? TISSUE TYPE: human placenta
? IMMEDIATE SOURCE:
? CLONE: B10G/pDC303
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 244..2369
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 310..2369
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: 244..309
? US-09-059-099-1

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Query Match	23.8%	Score 28.6;	DB 2;	Length 2369;
Best Local Similarity	55.6%;	Pred. No. 1.2;		
Matches 55;	Conservative 0;	Mismatches 44;	Indels 0;	Gaps 0

DY 20 atggaagcagcaggaccttgaggcaagaataatctaagttaattctgtactgtctatt 79
|| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 150 ATGGA AAAAGCATGACATTTAGAAGTAGAAGACTTACCTCAAAATCCCTACTCCTTCAC T 209

Db 211

```

RESULT 7
US-09-058-264-1
; Sequence 1, Application US/09058264
; Patent No. 6010886
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,264
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; TISSUE TYPE: human placenta
; IMMEDIATE SOURCE:
; CLONE: B10G/pDC303
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 244..2369
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 310..2369
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 244..309
; US-09-058-264-1

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RESULT 10
US-08-781-891-79/c
; Sequence 79, Application US/08781891
; Patent No. 6090620
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Oshima, Junko
; APPLICANT: Mulligan, John T.
; APPLICANT: Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,891
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090620tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 240052.419
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-781-891-79
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Query Match 23.5%; Score 28.2; DB 3; Length 87350;
Best Local Similarity 54.3%; Pred. No. 5.5;
Matches 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 3 ggggaaggggtatgcatagaagagcagaccttggagcaagaatatcttaagttaa 62
Db 7618 gttgaagccatnccacagatgcacatgctatagagatccctcagctgggttga 76559
QY 63 ttcctactctgctattataaaccatcttgcgaatgttg 107
Db 76558 atcctgctctcccgcttactaataatagcaatctaggaattatng 76514
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RESULT 11
US-08-733-360A-4/c
; Sequence 4, Application US/08733360A
; Patent No. 6103525
; GENERAL INFORMATION:
; APPLICANT: Stern, Robert
; APPLICANT: Frost, Gregory
; APPLICANT: Csoka, Anthony
; APPLICANT: Wong, Tim M.
; TITLE OF INVENTION: Human Plasma Hyaluronidase
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol L. Francis, Ph.D.
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
```

```
STAMP: CA
COUNTRY: USA
ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,360A
; FILING DATE: 17-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Francis, Carol L.
; REGISTRATION NUMBER: 36,513
; REFERENCE/DOCKET NUMBER: 06510/063001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 327-3400
; TELEFAX: (650) 327-3231
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-733-360A-4
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Query Match 23.3%; Score 28; DB 3; Length 2517;
Best Local Similarity 55.0%; Pred. No. 2;
Matches 55; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 16 tggcataagaagcagaccccttggagcaagaatatcttaagttaactctgactctgc 75
Db 2432 tagcagtgcaaggcctgtaccccgacgtagacagcctgggttgatctcaactctgc 2373
QY 76 tattataactaacacatcttggccaatgttgcttaagt 115
Db 2372 cctttctgtctgicacacttgggcaactgtcttactct 2333
```

```
RESULT 12
US-08-987-743-16/c
; Sequence 16, Application US/08987743
; Patent No. 6123938
; GENERAL INFORMATION:
; APPLICANT: Stern, Robert
; APPLICANT: Csoka, Anthony
; APPLICANT: Frost, Gregory I.
; APPLICANT: Wong, Tim M.
; TITLE OF INVENTION: Purification and Microsequencing of
; FILE REFERENCE: 9076/088CIP2
; CURRENT APPLICATION NUMBER: US/08/987,743
; EARLIER FILING DATE: 1997-12-09
; EARLIER APPLICATION NUMBER: 08/733,360
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 2517
; TYPE: DNA
; ORGANISM: H. sapiens
; US-08-987-743-16
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RESULT 13

US-08-916-935-4/c

Sequence 4, Application US/08916935

Patent No. 6193963

GENERAL INFORMATION:

APPLICANT: Stern, Robert

APPLICANT: Frost, Gregory I.

APPLICANT: Csoka, Anthony

APPLICANT: Wong, Tim. M.

TITLE OF INVENTION: Human Plasma Hyaluronidase

FILE REFERENCE: 9076-088CIP

CURRENT APPLICATION NUMBER: US/08/916,935

EARLIER FILING DATE: 1997-08-21

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 2517

TYPE: DNA

ORGANISM: Homo sapiens

US-08-916-935-4

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Db 2372 CCTTTCTGTGCTGTGCAACCTTGGCAACGTCGTTACTCT 2333

RESULT 14

US-07-928-464-4/c

Sequence 4, Application US/07928464

Patent No. 5367065

GENERAL INFORMATION:

APPLICANT: Ecker, Joseph R.

APPLICANT: Kieber, Joseph J.

TITLE OF INVENTION: Constitutive Triple Response Gene and

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/928,464

FILING DATE: 19920810

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Miller, Suzanne E.

REGISTRATION NUMBER: 32,279

REFERENCE/DOCKET NUMBER: UPN-1086

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 5873 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-07-928-464-4

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RESULT 15

PCT-US93-07347-4/c

Sequence 4, Application PC/TUS9307347

GENERAL INFORMATION:

APPLICANT: Ecker, Joseph R.

APPLICANT: Kieber, Joseph J.

TITLE OF INVENTION: Constitutive Triple Response Gene and

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07347

FILING DATE: 19930805

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Miller, Suzanne E.

REGISTRATION NUMBER: 32,279

REFERENCE/DOCKET NUMBER: UPN-1086

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 5873 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US93-07347-4

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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- 24: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	35.8	29.8	160755	23	AAH88704
7	35.4	29.5	162450	21	AAH69147
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C	10	35.2	29.3	14537	22	AAH46356	Tumour suppressor
C	11	35.2	29.3	56632	22	AAK65581	Human immune/haema
C	12	35.2	29.3	183999	22	AAH92831	Human ABC1 genomic
C	13	34.8	29.0	267	22	AAI13265	Human breast cancer
C	14	34.2	28.5	305	22	AAI22135	Human breast cancer
C	15	34.2	28.5	4171	22	AAI36300	Human breast cancer
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C	18	34.2	28.5	15944	22	ABAI5399	Human breast cancer
C	19	34	28.3	615	22	AAK57137	Human breast cancer
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C	25	33.4	27.8	19301	21	AAH21245	Human low adenosin
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ALIGNMENTS

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DT	23-JAN-2002	(first entry)
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KW	immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnerrary;	
KW	antiparkinsonian; antistickling; antianaemic; antiarthritic; cancer;	
KW	antithematic; hepatotropic; cerebroprotective; antinflammatory;	
KW	antiallergic; antidiabetic; antiliver; anticonvulsant; antitungal;	
KW	antiparasitic; cardiant; immune disorder; cardiovascular disorder;	
KW	neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.	
OS	Homo sapiens.	
XX		
PN	WO200159063-A2.	
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PD	16-AUG-2001.	
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PF	17-JAN-2001; 2001WO-US01334.	
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 PR 28-JUN-2000; 2000US-0214886.
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 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM:
 WPI: 2001-541565/60.
 Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 useful for preventing, diagnosing and/or treating nervous system
 cancers and metastases -
 Disclosure: SEQ ID NO 8121; 1701pp + Sequence Listing; English.
 The invention relates to novel genes (ABA11004-ABA21534) and proteins
 (AB14678-AB18001) useful for preventing, treating or ameliorating
 medical conditions e.g. by protein or gene therapy. The genes are

isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (anti)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from wipo.int/pub/published.pat.sequences.

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AC ABA15792;

DT 23-JAN-2002 (first entry)

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706	

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OS Homo sapiens.

PN W0200159063-A2

PD 16-AUG-2001.

PF 17-JAN-2001; 2001WO-US01334.

PR 31-JAN-2000; 2000US-0179065.

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PR	14-SEP-2000	2000US-0233064
PR	14-SEP-2000	2000US-0234223
PR	21-SEP-2000	2000US-0234225
PR	21-SEP-2000	2000US-0234274
PR	25-SEP-2000	2000US-0234997
PR	25-SEP-2000	2000US-0234998
PR	26-SEP-2000	2000US-0235334
PR	27-SEP-2000	2000US-0235344
PR	27-SEP-2000	2000US-0235363
PR	27-SEP-2000	2000US-0235366
PR	29-SEP-2000	2000US-0235327
PR	29-SEP-2000	2000US-0235657
PR	29-SEP-2000	2000US-0236358
PR	29-SEP-2000	2000US-0236359
PR	29-SEP-2000	2000US-0236370
PR	02-OCT-2000	2000US-0237037
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PR	02-OCT-2000	2000US-0237039
PR	02-OCT-2000	2000US-0237040
PR	13-OCT-2000	2000US-0239335
PR	13-OCT-2000	2000US-0239337
PR	20-OCT-2000	2000US-0240960
PR	20-OCT-2000	2000US-0241785
PR	20-OCT-2000	2000US-0241786
PR	20-OCT-2000	2000US-0241808
PR	20-OCT-2000	2000US-0241808
PR	20-OCT-2000	2000US-0241826
PR	01-NOV-2000	2000US-0244617

[illegible]

Query Match	32.0%	Score 38.4	DB 22	Length 9614
Best Local Similarity	62.5%	Pred. 0.016		
Matches 60: Conservative	0	Mismatches 36	Indels 0	Gaps 0
<p>(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.</p> <p>Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.</p>				
Sequence 9614 BP	3040 A	1582 C	1732 G	3260 T; 0 other;
OY	22	agaagagagagacctgggagcagaatactaagttatctcctgaactgctattra	81	
DB	5977	agaacaacaataagctacacgtttaaataacttgatggtcaaatcctaacccttcaatca	6036	
OY	82	ttacttaaccalccttgcacatgtgtgcthaactt	117	
DB	6037	ctagcaaatatgattggatgttcttctaactgt	6072	
RESULT 3				
ID	AAK85994	standard; DNA; 59060 BP.		
XX	AAK85994			
AC	AAK85994			
XX	AAK85994			
DT	07-NOV-2001	(first entry)		
XX				
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40806.			
XX				
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cyostatic; gene therapy; vaccine; metastasis; ds.			
XX				
OS	Homo sapiens.			
XX				
PN	WO200157182-A2.			
XX				
PD	09-AUG-2001.			
XX				
PF	17-JAN-2001; 2001WO-US01354.			
XX				
PR	31-JAN-2000; 2000US-0179065.			
PR	04-FEB-2000; 2000US-0180628.			
PR	24-FEB-2000; 2000US-0184664.			
PR	02-MAR-2000; 2000US-0186350.			
PR	16-MAR-2000; 2000US-0189874.			
PR	17-MAR-2000; 2000US-0190076.			
PR	18-APR-2000; 2000US-0198123.			
PR	19-MAY-2000; 2000US-0205515.			
PR	07-JUN-2000; 2000US-0209467.			
PR	28-JUN-2000; 2000US-0214886.			
PR	30-JUN-2000; 2000US-0215135.			
PR	07-JUL-2000; 2000US-0216647.			
PR	07-JUL-2000; 2000US-0216880.			
PR	11-JUL-2000; 2000US-0217487.			
PR	11-JUL-2000; 2000US-0217496.			
PR	14-JUL-2000; 2000US-0218290.			
PR	26-JUL-2000; 2000US-0220963.			
PR	26-JUL-2000; 2000US-0220964.			
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PR	14-AUG-2000; 2000US-0224519.			
PR	14-AUG-2000; 2000US-0225213.			
PR	14-AUG-2000; 2000US-0225214.			
PR	14-AUG-2000; 2000US-0225266.			
PR	14-AUG-2000; 2000US-0225267.			
PR	14-AUG-2000; 2000US-0225268.			
PR	14-AUG-2000; 2000US-0225270.			
PR	14-AUG-2000; 2000US-0225447.			
PR	14-AUG-2000; 2000US-0225757.			
PR	14-AUG-2000; 2000US-0225758.			

PR	14-AUG-2000	2000US-0225575
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PR	22-AUG-2000	2000US-0226686
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PR	30-AUG-2000	2000US-0228924
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PR	14-SEP-2000	2000US-0233064
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PR	20-OCT-2000	2000US-0241787
PR	20-OCT-2000	2000US-0241808
PR	20-OCT-2000	2000US-0241809
PR	01-NOV-2000	2000US-0244617
PR	08-NOV-2000	2000US-0244674
PR	08-NOV-2000	2000US-0244675
PR	08-NOV-2000	2000US-0244676
PR	08-NOV-2000	2000US-0244677
PR	08-NOV-2000	2000US-0245226
PR	08-NOV-2000	2000US-0245227
PR	08-NOV-2000	2000US-0245528
PR	08-NOV-2000	2000US-0245532
PR	08-NOV-2000	2000US-0246609
PR	08-NOV-2000	2000US-0246610

08-NOV-2000; 20000US-0246611.
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PR 17-NOV-2000; 20000US-0249209.
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PR 17-NOV-2000; 20000US-0249211.
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PR 17-NOV-2000; 20000US-0249214.
PR 17-NOV-2000; 20000US-0249215.
PR 17-NOV-2000; 20000US-0249216.
PR 17-NOV-2000; 20000US-0249217.
PR 17-NOV-2000; 20000US-0249218.
PR 17-NOV-2000; 20000US-0249244.
PR 17-NOV-2000; 20000US-0249245.
PR 17-NOV-2000; 20000US-0249264.
PR 17-NOV-2000; 20000US-0249265.
PR 17-NOV-2000; 20000US-0249297.
PR 17-NOV-2000; 20000US-0249299.
PR 17-NOV-2000; 20000US-0249300.
PR 01-DEC-2000; 20000US-0250160.
PR 01-DEC-2000; 20000US-0250391.
PR 05-DEC-2000; 20000US-0251030.
PR 05-DEC-2000; 20000US-0251188.
PR 05-DEC-2000; 20000US-0256719.
PR 06-DEC-2000; 20000US-0251479.
PR 08-DEC-2000; 20000US-0251856.
PR 08-DEC-2000; 20000US-0251868.
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PR 08-DEC-2000; 20000US-0251989.
PR 08-DEC-2000; 20000US-0251990.
PR 11-DEC-2000; 20000US-0254097.
PR 05-JAN-2001; 20010US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
PI Rosen CA, Barash SC, Ruben SM;
DR WPI; 2001-483426/52.
XX
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX
PS Disclosure; SEQ ID NO 40806; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 59060 BP; 14758 A; 13705 C; 13620 G; 16977 T; 0 other;

Query Match	30.0%;	Score 36;	DB 22;	Length 59060;
Best Local Similarity	58.3%;	Pred. No. 0.17;		
Matches 63; Conservative	0;	Mismatches 45;	Indels 0;	Gaps 0

Db 10088 gtcagagaaaaaggccctgagctcgagcaggaatgtaattcagtcctgattc 10147
QY 73 tgcatttattacacatcttggccaatgtgtgctaagcttttt 120
Db 10148 tgccttcattcccccagtggtcgtgaacaagctgtccctctctt 10195

RESULT 4
ID AAL03250
AC AAL03250; standard; DNA; 13046 BP.
XX
XX AAL03250;
XX
XX 21-NOV-2001 (first entry)
XX
XX Human reproductive system related antigen DNA SEQ ID NO: 5938.
DE Human reproductive system related antigen; reproductive system disorder;
XX
XX Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX
XX Homo sapiens.
OS
XX
XX W0200155320-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01339.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
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PR 18-APR-2000; 2000US-0198122.
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PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
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PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
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PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
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PR 08-SEP-2000; 2000US-0231242.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
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PR 29-SEP-2000; 2000US-0236369.
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PR 02-OCT-2000; 2000US-0236802.
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PR 02-OCT-2000; 2000US-0237038.
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PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
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PR 17-NOV-2000; 2000US-0249210.
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PR 17-NOV-2000; 2000US-0249245.
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PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
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PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465570/50.
XX Isolated nucleic acid molecule encoding a reproductive system antigen
XX is used in preventing, treating or ameliorating a medical condition -
PS Disclosure; SEQ ID NO 5938; 1297bp + Sequence Listing; English.
XX The present invention provides the protein and coding sequences of a
XX number of human reproductive system related antigens. These can be used
XX in the prevention and treatment of reproductive system disorders,
XX including cancer. The present sequence is a genomic sequence encoding a
XX protein of the invention.
SQ Sequence 13046 BP; 3599 A; 2614 C; 2885 G; 3948 T; 0 other;
Query Match 29.8%; Score 35.8; DB 22; Length 13046;
Best Local Similarity 61.1%; Pred. No. 0.12; Mismatches 0; Gaps 0;
Matches 58; Conservative 0; Indels 37;
QY 25 aagacgacgacgttggaagaataatcgaattacccctgctgtattatata 84
DB 4940 aaaaagcgcgacctggaaccagcgtctgaattgacatcctagctcgaactacta 4999
QY 85 actaacatcttgcgaatgttgccttaagctttt 119
DB 5000 actgtgaccttggaagtaactactgtctct 5034
RESULT 5
ID AAS31516/c
AC AAS31516; DNA; 13046 BP.
XX
XX
DT 04-DEC-2001 (first entry)
XX
XX Human DNA for a novel extracellular matrix protein, Seq ID No 595.
DE
XX Human: secreted extracellular matrix protein; ds; immunomodulatory;
KW Anti-HIV; anti-anemic; antirheumatic; antileukemic; cardiant; vascular;
KW cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic;
KW antialzheimers; immune/autoimmune disease; HIV infection; anaemia;
KW human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
KW cancers; hyperproliferative disorder; breast neoplasia; melanoma;
KW Sezary syndrome; Gaucher's disease; neurological diseases;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
KW cardiac arrest; tachycardia; angina; infection; corneal infections;
KW wound healing; immunogen; gene therapy; antisense; food additive.

XX OS Homo sapiens.
XX XX WO200155368-A1.
XX
XX PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01348.
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XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
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PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
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PR 25-SEP-2000; 2000US-0234998.

PR 26-SEP-2000; 2000US-0235484.
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PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236370.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 17-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251988.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465572/50.
DR
XX
PT Nucleic acid molecules encoding human secreted extracellular matrix
PT proteins, used in preventing, treating or ameliorating a disorder, e.g.
PT Alzheimer's and Parkinson's diseases and cancers -
XX
PS Claim 1; SEQ ID No 595; 577bp; English.
XX
XX The invention relates to isolated nucleic acid molecules encoding
CC novel human secreted extracellular matrix proteins (SPs). The
CC polynucleotides and proteins are used to prevent, treat a medical
CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
CC chickens or sheep. For example, disorders associated with decreased
CC expression of SPs. The SP polynucleotide or a vector expressing them may
CC be administered to treat diseases by gene therapy. Antisense molecules
CC may be administered to down regulate expression of SPs by binding with
CC the cells own genes and preventing their expression. The polynucleotides
CC may also be used as DNA probes in diagnostic assays. The SPs may also be
CC used as antigens to produce antibodies and to identify modulators
CC (agonists and antagonists) of the SPs. The anti-(SP) antibodies and
CC antagonists may also be used to down regulate expression and activity of
CC SP and as diagnostic agents for detecting the presence of SPs in samples.
CC The disorders include for example: immune/autoimmune diseases (e.g. HIV
CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
CC and multiple sclerosis), cancers and hyperproliferative disorders (e.g.
CC melanomas, neoplasms of the breast or liver, Sezary syndrome and
CC Parkinson's disease), neurological diseases (e.g. Alzheimer's disease,
CC arrest, tachycardia and angina), infections caused by bacteria, viruses
CC and fungi and ocular disorders (e.g. corneal infections). Other uses
CC include wound healing, maintenance of organs before transplantation,
CC support of cell culture of primary tissues, modulation of for example

Query Match 29.8%; Score 35.8; DB 22; Length 13046;
Best Local Similarity 61.1%; Pred. No. 0.12;
Matches 58; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 25 aagagcagaccttggagcaagataatcagtttaattcctgactgctatattat 84
Db 8107 AAAAGCAGCGACTGCGAACCAAGTCTGTGATTTGAATCCTACTCTGCCAATTAC 8048
QY 85 actaacatcttgcacatgttgccttaagctttt 119
Db 8047 ACTGTGTGACCTTGCGCAACTTACTTACTTCTCT 8013

RESULT 6
AAH88704/C
ID AAH88704 standard; DNA; 160755 BP.
XX
XX AAH88704;
AC
XX
DT 26-FEB-2002 (first entry)
XX
DE Human DNA sequence SEQ ID 544.
XX
KW Single nucleotide polymorphism; SNP; diallelic marker; human;
KW central nervous system disorder; CNS; ds.
OS Homo sapiens.
XX
PN WO200151659-A2.
XX
PD 19-JUL-2001.
XX
PF 11-JAN-2001; 2001MO-IB00116.
XX
PR 13-JAN-2000; 2000US-0175854.
XX

SQ Sequence 160755 BP; 43057 A; 36601 C; 38189 G; 42727 T; 181 other;

Matches	64;	Conservative	0;	Mismatches	47;	Indels	0;	Gaps	0;
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Db 144773 GTGATGTTGCTAAGATAGAGCATGGACTTTGAACACAGATTAACTGCATCTGAAGCCTG 144714

Db 144713 GCTCTGCTACTTACTGGCTGGGAGTTTCACCTGTTTGGGCCCTCAGTTTCT 144663

ID	AAZ86967	standard; DNA; 162450 BP.

AC AAZ86967;

DT 16-MAY-2000 (first entry)

Retinoblastoma binding protein-7 genomic DNA sequence

KW	lymphoma; ds.		
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100			

OS Homo sapiens

PN WO200000607-A1

PD 06-JAN-2000.

PF 30-JUN-1999; 99WO-IB01242.

PR	30-JUN-1998;	98US-00913.15.
PR	10-DEC-1998;	98US-01119.09.

XX
DA (CEEM) CENECT

XX Bouquet d'arcs et T.

XX
DP
WPT: 2000-117170/10

PT differentiation -

PS Claim 1; Page 118-163; 223pp; English.

CC Lymphomas. RBP-7 antibodies are useful as diagnostic agents.

Sequence 162450 BP; 45465 A; 30661 C; 32637 G; 53673 T; 14 other;

Matches	57;	Conservative	0;	Mismatches	36;	Indels	0;	Gaps	0;
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Db 82403 atagtatactgtggagccagttgtgtctgtggtttgaatcctgctgcaccattcctg 82462

Db 82463 ctgtgtatcttggaagtgtactaatctt 82495

ID AAC69140 standard; DNA; 7052 BP

AAC69140; AC

DT 29-JAN-2001 (first entry)

Human ABC1 gene exons 23-28

KM Human ABC1 cholesterol transporter; chromosome 9q31

KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;

KW cerebrovascular disease; peripheral vascular disease;

KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;

XX

[illegible]

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XX
15 MAR 2000 2000R0-TD00E33

XX 15-MAR-1999. 0905-0124702

PR	08-JUN-1999;	99US-0138048
PR	17-JUN-1999;	99US-0139600

PR 01-SEP-1999; 99US-0151977

PA	(UYBR-)	UNIV BRITISH COLUMBIA
PA	(YENO-)	XENON BIORESEARCH INC

XX	Hayden	MB	Wilson	AB	Pimstone	SN:
PI						

DR WPI; 2000-587528/55.

PT New ABC1 polypeptide is useful for treating diseases associated with
PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
XX disease and cancer -
XX
PS

XX Disclosure; Fig 12; 229pp; English.

CC The invention relates to the human ABC1 cholesterol transporter protein
CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC a member of the ATP-binding cassette (ABC transporter) superfamily of
CC proteins, and plays a crucial role in cholesterol transport, particularly
CC intracellular cholesterol trafficking in monocytes and fibroblasts. Being
CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC located on chromosome 9q31, and mutations in this gene are associated
CC with two genetic HDL (high density lipoprotein) deficiency disorders,
CC Tangier disease (TD) and familial HDL deficiency (FHD). These diseases
CC are distinguishable in that TD is an autosomal recessive disorder, while
CC FHD is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC cholesterol") in the blood correlate with a high risk of cardiovascular
CC disease, particularly coronary artery disease, but also cerebrovascular
CC disease, coronary restenosis, and peripheral vascular disease.
CC Conversely, a high level of HDL has protective effects against
CC cardiovascular disease. The invention provides genetic constructs and
CC transgenic cells and non-human animals comprising human ABC1 nucleic
CC acids, and methods of gene therapy for the treatment or prevention of
CC cardiovascular disease comprising the administration of an expression
CC vector encoding ABC1 or an active fragment thereof. The invention also
CC encompasses compounds which mimic ABC1 activity, compounds which
CC stimulate ABC1 expression and methods of screening for such compounds.
CC It further relates to methods for determining whether a patient has an
CC increased risk for cardiovascular disease due to polymorphisms in the
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
CC or prevent cardiovascular disease, especially coronary artery disease,
CC cerebrovascular disease, coronary restenosis or peripheral vascular
CC disease. They may also be used in the treatment of diseases associated
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC The invention specifically excludes proteins with the exact amino acid
CC sequences of Genbank Accession No. CAA10005.1 and X75926, and the nucleic
CC acid with the exact sequence as Genbank Accession No. AJ012376.1.
CC The present sequence represents a fragment of the human ABC1 gene
CC comprising exonic sequences.
XX
XX

XX Sequence 7052 BP; 1816 A; 1465 C; 1725 G; 2045 T; 1 other;

Query Match 29.3%; Score 35.2; DB 21; Length 7052;
Best Local Similarity 62.5%; Pred. No. 0.16;

Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

YY 32 ggaacttgagagcaagaataatcctaattcctgactctgactatttaactaac 91

DB 5846 gggaggttgagcagcatagcagctgaactcctgactctgactattgcatat 5905

YY 92 atcttgccaatgttgccttaagctttt 119

DB 5906 gaccttgagcaagctgttgcctctc 5933

RESULT 9

AAAL37169 standard; DNA; 9519 BP.

XX AAAL37169;

XX 08-JAN-2002 (first entry)

XX Human musculoskeletal system related polynucleotide SEQ ID NO 3534.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX anti-allergic; hepatotropic; antidiabetic; antiinflammatory; anticancer;
XX vulnerrary; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein;

KW musculoskeletal system; ds.

XX Homo sapiens.

XX WO200155367-A1.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001MO-US01338.

XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225267.
XX 14-AUG-2000; 2000US-0225268.
XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226868.
XX 22-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227009.
XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 01-SEP-2000; 2000US-0229345.
XX 05-SEP-2000; 2000US-0229509.
XX 05-SEP-2000; 2000US-0229513.
XX 06-SEP-2000; 2000US-0230437.
XX 06-SEP-2000; 2000US-0230438.
XX 08-SEP-2000; 2000US-0231242.
XX 08-SEP-2000; 2000US-0231243.
XX 08-SEP-2000; 2000US-0231244.
XX 08-SEP-2000; 2000US-0231413.
XX 08-SEP-2000; 2000US-0231414.
XX 08-SEP-2000; 2000US-0232080.
XX 08-SEP-2000; 2000US-0232081.
XX 12-SEP-2000; 2000US-0231968.
XX 14-SEP-2000; 2000US-0232397.
XX 14-SEP-2000; 2000US-0232398.
XX 14-SEP-2000; 2000US-0232399.
XX 14-SEP-2000; 2000US-0232400.
XX 14-SEP-2000; 2000US-0232401.
XX 14-SEP-2000; 2000US-0233063.
XX 14-SEP-2000; 2000US-0233064.
XX 14-SEP-2000; 2000US-0233065.
XX 21-SEP-2000; 2000US-0234222.
XX 21-SEP-2000; 2000US-0234274.
XX 25-SEP-2000; 2000US-0234997.

PR 06-APR-2000; 2000DE-1019058.
PR 07-APR-2000; 2000DE-1019173.
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI: 2001-602752/68.
XX
XX
PT Fragments of chemically modified genes associated with tumour suppressor
PT genes and oncogenes, useful in designing primers and probes for
PT analysing diseases associated with cytosine methylation state e.g.
PT cancer
XX
PS Claim 1; SEQ ID NO 78; 27pp; English.
XX
XX The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and
CC oncogenes having a sequence taken from 536 (actually 533 since
CC numbers 408, 458 and 500 are missing from the sequence listing) sequences
CC (Ss) and sequences complementary to (Ss). The nucleic acid may be a
CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
CC form part of a set of probes for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms and also to be used in an
CC array for analysing diseases associated with CpG dinucleotides e.g.
CC cancers and tumours. The probes can also be used in a method for
CC ascertaining genetic and/or epigenetic parameters for the diagnosis
CC and/or therapy of existing diseases or the predisposition to specific
CC diseases, by analysing cytosine methylations. The parameters may be
CC compared to another set of genetic and/or epigenetic parameters, the
CC differences serving as basis for diagnosis and/or prognosis events which
CC are disadvantageous to patients. The present sequence is one of the
CC 533 genomic sequences derived from tumour suppressor genes and
CC oncogenes. Sequences with even numbered Seq ID numbers are the
CC complementary sequence of the corresponding odd numbered sequence (e.g.
CC ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
CC is missing).
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 14537 BP; 3628 A; 495 C; 3778 G; 6636 T; 0 other;
XX
Query Match 29.3%; Score 35.2; DB 22; Length 14537;
Best Local Similarity 60.4%; Pred. No. 0.2;
Matches 58; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
OY 20 atagaagagcagacctggagcagaagaatatacttaactcgtcgtcatt 79
DB 1336 ATTCATAAACTCTAACCTTATCTAATCACTAATTAATTAATCACTAACCCGCTACT 1277
OY 80 tattaactaacatcttgcacatglttccttaagct 115
DB 1276 TATTAAACAATATAACCTTAATAATTAATTAATCT 1241
RESULT 11
AAK65581
ID AAK65581 standard; DNA; 56632 BP.
XX
AC AAK65581;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:20393.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX

XX Homo sapiens.
OS
XX
PN MO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216680.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0224513.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0233397.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233400.
PR 14-SEP-2000; 2000US-0233401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
XX

PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
XX WPI; 2001-244356/25.
XX
XX
XX Treating a lower than normal high density lipoprotein-cholesterol
PR (HDL-C) level, a higher than normal triglyceride level, or a
PR cardiovascular disease, by administering a compound that modulates LXR-
PR or RXR-mediated transcriptional activity -
XX
XX Claim 8; Fig 1; 317p; English.
XX
XX The present invention relates to a method for treating a patient
CC diagnosed as having a lower than normal high density
CC lipoprotein-cholesterol (HDL-C) level, a higher than normal
CC triglyceride level, or a cardiovascular disease, involving
CC administering a compound that modulates LXR- or RXR-mediated
CC transcriptional activity or ABC1 expression or activity.
CC The LXR gene product may be used in an assay to identify
CC compounds useful for the treatment of a disease or condition selected a
CC lower than normal HDL cholesterol level, a higher than normal
CC triglyceride level, and a cardiovascular disease.
XX
XX Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
S0
Query Match 29.3%; Score 35.2; DB 22; Length 183999;
Best Local Similarity 62.5%; Pred. No. 0.43;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 32 ggaacttgaggagcaagaatctaaagtttaattcctgactcgtatttacttaacc 91
Db 145152 gggaggttgagcacaagagcagtggaatccgactctgactattgctatat 145211
QY 92 atcttgccaatgttgcttaagctttt 119
Db 145212 gaccttgaggcaagctgctagtctctc 145239
RESULT 13
AAL13265
ID AAL13265 standard; cDNA; 267 BP.
XX
XX AAL13265;
XX
XX 07-DEC-2001 (first entry)
XX
XX Human breast cancer expressed polynucleotide 5722.
DE Human breast cancer; cell marker; cytostatic; ss.
XX
XX Human; breast cancer; cell marker; cytostatic; ss.
KM
XX Homo sapiens.
OS
XX WO200151628-A2.
PN
XX 19-JUL-2001.
XX
XX 10-JAN-2001; 2001WO-US00798.
PF
XX
XX 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Lillie J, Xu Y, Wang Y, Steinmann K;
PI WPI; 2001-451856/48.
XX
XX New peptide useful as a marker for the diagnosis of breast cancer -

XX
XX Claim 1; Page 1029; 3695pp; English.
PS
XX
XX The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
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XX Sequence 267 BP; 77 A; 46 C; 51 G; 90 T; 3 other;
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Db 31 gggaaaaaaatcgtggaatttgagagacaacaacatccagntaattcctcacttgc 90
QY 77 atttaactaacatct 95
Db 91 acttaacttaataattct 109
RESULT 14
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ID AAL22135 standard; cDNA; 305 BP.
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XX 07-DEC-2001 (first entry)
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XX Human breast cancer expressed polynucleotide 14592.
DE Human breast cancer; cell marker; cytostatic; ss.
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XX Human; breast cancer; cell marker; cytostatic; ss.
KM
XX Homo sapiens.
OS
XX WO200151628-A2.
PN
XX 19-JUL-2001.
XX
XX 10-JAN-2001; 2001WO-US00798.
PF
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XX 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Lillie J, Xu Y, Wang Y, Steinmann K;
PI WPI; 2001-451856/48.
XX
XX New peptide useful as a marker for the diagnosis of breast cancer -
PS Claim 1; Page 2627; 3695pp; English.
XX
XX The invention relates to human breast cancer expressed polynucleotides
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CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing treating and

PR	14-AUG-2000;	2000US-0225447
PR	14-AUG-2000;	2000US-0225757

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PR	14-SEP-2000	2000US-0232400
PR	14-SEP-2000	2000US-0233401
PR	14-SEP-2000	2000US-0233403
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PR	08-NOV-2000	2000US-0246532
PR	08-NOV-2000	2000US-0246539
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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3	120	100.0	321.2	6	AX026089	AX026089	Sequence	C
4	120	100.0	187.313	6	AL157394	AL157394	Human DNA	C
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9	45.8	38.2	166076	2	AC090587	AC090587	Homo sapi	C
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18	43.2	36.0	160071	2	AC016926	AC016926	Homo sapi	C
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24	42.4	35.3	176698	2	AL355996	AL355996	Homo sapi	C
25	42.4	35.3	179614	2	AC012471	AC012471	Homo sapi	C
26	42.2	35.2	63722	2	AC103740	AC103740	Homo sapi	C
27	42.2	35.2	149042	2	AC016410	AC016410	Homo sapi	C
28	42.2	35.2	187005	2	AC024309	AC024309	Homo sapi	C
29	41.6	34.7	143899	2	AC013606	AC013606	Homo sapi	C
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31	41.6	34.7	187566	2	AC015685	AC015685	Homo sapi	C
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33	41.6	34.7	200841	2	AL162423	AL162423	Human DNA	C
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37	41.2	34.5	179966	2	AC023247	AC023247	Homo sapi	C
38	40.6	33.8	71794	2	AC023647	AC023647	Homo sapi	C
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40	40.6	33.8	131329	9	AC004873	AC004873	Homo sapi	C
41	40.6	33.8	153254	2	AC015920	AC015920	Homo sapi	C
42	40.6	33.8	160254	2	AC007763	AC007763	Homo sapi	C
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44	40.6	33.8	170867	9	AC068295	AC068295	Homo sapi	C
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ALIGNMENTS

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LOCUS	2344 bp DNA linear PRI 05-FEB-1997
DEFINITION	H.sapiens CD95 gene 5' flanking region.
ACCESSION	X87625
VERSION	X87625.1 GI:902311
KEYWORDS	Beta interferon; CD95 gene; silencer. human.
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 (bases 1 to 2344)
AUTHORS	Rudert,F., Visser,E., Forbes,L., Lindridge,E., Wang,Y. and Watson,J.
TITLE	Identification of a silencer, enhancer, and basal promoter region in the human CD95 (Fas/Apo-1) gene
JOURNAL	DNA Cell Biol. 14 (11), 931-937 (1995)
MEDLINE	96069539
REFERENCE	2 (bases 1 to 2344)
AUTHORS	Rudert,F.H.
TITLE	Direct Submission
JOURNAL	Submitted (26-MAY-1995) F.H. Rudert, Genesis Research & Development, Corporation Ltd., PO Box 50, Auckland, NEW ZEALAND

COMMENT Overlaps with X81335, & X82279-X82286.
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717..801
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Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 514 AATTCCTGACTGCTGATTATTACTAACCACTTTGGCAATGTTGCTTAAGCTTTT 573

QY 61 aattcctgactctgtatttataactaacacatttgcacattgttcttaagcttttt 120
DB 514 AATTCCTGACTGCTGATTATTACTAACCACTTTGGCAATGTTGCTTAAGCTTTT 573

RESULT 2
AX026092 2827 bp DNA linear PAT 16-SEP-2000
LOCUS
DEFINITION Sequence 4 from Patent DE19847779.
ACCESSION AX026092
VERSION AX026092.1 GI:10187523
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2827)
Muller-Schilling, M., Kramer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 4 03-FEB-2000;
JOURNAL DEUTSCHES KREBSFORSCH (DE)
FEATURES
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Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 aattcctgactctgtatttataactaacacatttgcacattgttcttaagcttttt 120
DB 397 AATTCCTGACTGCTGATTATTACTAACCACTTTGGCAATGTTGCTTAAGCTTTT 456

RESULT 3
AX026089 3212 bp DNA linear PAT 16-SEP-2000
LOCUS
DEFINITION Sequence 1 from Patent DE19847779.
ACCESSION AX026089
VERSION AX026089.1 GI:10187520
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 3212)
Muller-Schilling, M., Kramer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 1 03-FEB-2000;
JOURNAL DEUTSCHES KREBSFORSCH (DE)
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DB 397 AATTCCTGACTGCTGATTATTACTAACCACTTTGGCAATGTTGCTTAAGCTTTT 456

RESULT 4
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LOCUS
DEFINITION Human DNA sequence from clone RP11-395019 on chromosome 10,
complete sequence.
ACCESSION AL157394
VERSION AL157394.15 GI:15384622
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 187313)
Blakey, S.
Direct Submission
Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
On Aug 31, 2001 this sequence version replaced gi:14161146.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP

database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/BCP/Chr10>
 RPI1-399019 is from the library RPI1-11.2 constructed by the group of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>

VECTOR: pBAC3.6
 This sequence is the entire insert of clone RPI1-399019. The true left end of clone RPI1-496H23 is at 166408 in this sequence. The true right end of clone RPI1-30415 is at 18704 in this sequence.

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Db 142365 AATTCCGACTGCTGCTATTATTACTACCATCTTGCACATGCTTAAAGCTTTT 142424

RESULT 5

AB053451 131286 bp DNA linear MAM 05-JAN-2002

LOCUS AB053451 131286 bp DNA linear MAM 05-JAN-2002
 DEFINITION Sus scrofa DNA, constant regions and joining segments of T cell receptor alpha/delta chain.

ACCESSION AB053451
 VERSION AB053451.1 GI:18147392

KEYWORDS

SOURCE

Sus scrofa DNA.

ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

REFERENCE 1 (sites)
 Thome, A., Saalmueller, A. and Pfaff, E.
 Molecular cloning of porcine T cell receptor alpha, beta, gamma and delta chains using polymerase chain reaction fragments of the constant regions

JOURNAL Eur. J. Immunol. 23 (5), 1005-1010 (1993)

REFERENCE

MEDLINE 93238851

AUTHORS

TITLE Yang, Y.G., Ohta, S., Yamada, S., Shimizu, M. and Takagaki, Y.
 Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old pig

JOURNAL J. Immunol. 155 (4), 1981-1993 (1995)

REFERENCE

MEDLINE 95363165
 TITLE Uenishi, H.
 Complete sequence of segments of joining and constant region of

JOURNAL porcine TCR gene alpha/delta locus
 unpublished
 4 (bases 1 to 131286)

REFERENCE Uenishi, H.

AUTHORS Direct Submission

TITLE Submitted (10-JAN-2001) Hirohide Uenishi, National Institute of Animal Industry, MAFF, Department of Animal Breeding and Genetics; P.O. Box 5, Tsukuba 305-0901, Japan (E-mail: huenishi@affrc.go.jp, Tel: 81-298-38-8627, Fax: 81-298-38-8793)

FEATURES

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 /db_xref="GI:18147396"
 /translation="SWDTROMYFGAGTKLVEVP"
 11131..11137
 /note="putative recombination recognition sequence"
 join(14002..14280,14849..14914,15573..15685)
 /standard_name="TCR delta chain constant region"

exon	Query Match	Best Local Similarity	Matches	70; Conservative	41.3%; Score 49.6; DB 4; Length 131286; 67.3%; Pred. No. 0.00016; Mismatches 34; Indels 0; Gaps 0
misc_signal	/note="putative"	complement(20767..>20875)	/note="putative	reverse transcriptional orientation"	/number=2
misc_signal	/product="TCR delta-5 chain variable region"	27793..27801	/note="putative	recombination recognition sequence"	27814..27820
J_segment	/note="putative	recombination recognition sequence"	27821..27880	/standard_name="possible TCR α 61 gene segment"	<27821..>27880
CDS	/standard_name="possible TCR α 61 gene segment"	/standard_name="possible TCR α 61 gene segment"	/note="putative"	/codon_start=3	/protein_id="BAB83182.1"
misc_signal	/db_xref="GI:18147399"	/translation="KVVNKKLTFGATKRLIKL"	28789..28797	/note="putative	recombination recognition sequence"
misc_signal	28810..28816	/note="putative	recombination recognition sequence"	<28817..>28873	/standard_name="possible TCR α 60 gene segment"
CDS	/note="putative"	/codon_start=3	/protein_id="BAB83183.1"		
Query Match	41.3%; Score 49.6; DB 4; Length 131286; 67.3%; Pred. No. 0.00016; Mismatches 34; Indels 0; Gaps 0				
Db 16	tgagctagaagaagcagcgaccccttgggaagcaagaatctcaagttcaattccctcgtcgc 75				
Db 16474	TTGCTATTAATAAAGAGCACTCCCTAGGAATTCAGAAAGAGCTTAAGTTTCTCCTGACTTTG 16533				
Db 76	tatttataactaacaccatctttgccaatgttgccttaagctttt 119				
Db 16534	CACCTAACCTCACCTGTGTACTTACCTTAGCCAGGTTGCTTACTCTCT 16577				
RESULT 6	AC073148/c	166847 bp	DNA	linear	PRI 03-JAN-2000
LOCUS	AC073148				
DEFINITION	Homo sapiens chromosome 7 clone RP11-801B4, complete sequence.				
ACCESSION	AC073148				
VERSION	AC073148.7	GI:11415226			
KEYWORDS	Htg.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (bases 1 to 166847)				
TITLE	Waterston,R.H.				
JOURNAL	The sequence of Homo sapiens clone				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 166847)				
TITLE	Waterston,R.H.				
JOURNAL	Direct Submission				
REFERENCE	Submitted (08-JUN-2000) Genome Sequencing Center, Washington				
AUTHORS	MO 63108, USA				
TITLE	3 (bases 1 to 166847)				
JOURNAL	Waterston,R.H.				
REFERENCE	Direct Submission				
AUTHORS	Submitted (29-NOV-2000) Genome Sequencing Center, Washington				
TITLE	University School of Medicine, 4444 Forest Park Parkway, St. Louis,				
JOURNAL	MO 63108, USA				
REFERENCE	4 (bases 1 to 166847)				
AUTHORS	Waterston,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-MAY-2001) Department of Genetics, Washington				

REFERENCE	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
AUTHORS	5 (bases 1 to 166847)
TITLE	Waterston, R. H.
JOURNAL	Direct Submission
COMMENT	Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On Nov 29, 2000 this sequence replaced g1:11128450.

FEATURES	SOURCE
Center: Washington University Genome Sequencing Center	genome Center
Center code: WUGSC	
Web site: http://genome.wustl.edu/gsc/index.shtml	
Contact: submissions@watson.wustl.edu	
Project Information	
Center project name: H_NH0801B04	
Location/Qualifiers	
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/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/chromosome="7"	
/clone="RP11-801B4"	
48276 a 31805 c 33820 g 53946 t	
ORIGIN	

Query Match	39.7%	Score 47.6;	DB 9;	length 166847;
Best Local Similarity	69.1%	Pred. No. 0.0006;		
Matches 65;	Conservative 0;	Mismatches 29;	Indels 0;	Gaps 0;

Oy 25 aagacgagaccttggcgcaagaatactaaagttaattcctgactcgtatlatla 84
||||| | ||||| ||||| ||||| ||||| |||||
Db 10828 AAGACATGATTACAGAGCCAGATACTCATGTTCATCCTGCCTTCACTACTATTAA 10

Qy	85	actaacacatcttgcgaatgttgcctaagctt	118
Db	10768	gctactacttctgggcagttctttaacctct	10735

AL355852/c	LOCUS	DEFINITION
AL355852	128765 bp	DNA
Human DNA sequence from clone RP11-403E24	linear	PRI 09-MAR-2001
sequence.	on chromosome X, complete	

VERSION	AL355852.23	GI:13274693
KEYWORDS	HTG.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE	1 (bases 1 to 128765)
AUTHORS	Heath, P.
TITLE	Direct Submission
JOURNAL	Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,

COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/ChrX> Rpl11-403E24 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone Rpl11-403E24. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. This sequence. The true left end of clone Rpl11-403E24 is at 1 in this sequence. The true left end of clone Rpl11-284B18 is at 128666 in this sequence. The true right end of clone Rpl11-33N11 is at 69175 in this sequence.

FEATURES	Location/Qualifiers
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	/chromosome="X"
	/clone="RP11-403E24"
	/clone.lib="RPCT-11.2"
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repeat_region	6313..6419
repeat_region	/note="MER91C repeat: matches 15..139 of consensus"
repeat_region	6875..7385
repeat_region	/note="L1MC4 repeat: matches 7269..7643 of consensus"
repeat_region	7784..7892
repeat_region	/note="MIR repeat: matches 20..130 of consensus"
repeat_region	9981..10022
repeat_region	/note="21 copies 2 mer aa 81% conserved"
repeat_region	11037..11084
repeat_region	/note="MIR repeat: matches 100..145 of consensus"
repeat_region	11410..11615
repeat_region	/note="MIR repeat: matches 12..219 of consensus"
repeat_region	11683..11714
repeat_region	/note="16 copies 2 mer ct 100% conserved"
repeat_region	11715..11918
repeat_region	/note="L2 repeat: matches 2513..2708 of consensus"
repeat_region	12338..12441
repeat_region	/note="MIR repeat: matches 45..147 of consensus"
repeat_region	/complement(12973..13643)
repeat_region	/note="match: STS: Em:HSC63F11"
repeat_region	13218..13465
repeat_region	/note="MIR repeat: matches 13..262 of consensus"
repeat_region	13474..13595
repeat_region	/note="L2 repeat: matches 2591..2719 of consensus"
repeat_region	13854..14060
repeat_region	/note="L2 repeat: matches 2060..2281 of consensus"
repeat_region	14358..14451
repeat_region	/note="L2 repeat: matches 2418..2511 of consensus"
repeat_region	14559..14592
repeat_region	/note="17 copies 2 mer ct 94% conserved"
repeat_region	14817..15016
repeat_region	/note="MIR repeat: matches 8..216 of consensus"
repeat_region	16127..16404
repeat_region	/note="MIR repeat: matches 5..262 of consensus"
repeat_region	16822..16881
repeat_region	/note="L2 repeat: matches 2644..2705 of consensus"
repeat_region	16971..17060
repeat_region	/note="L2 repeat: matches 2589..2748 of consensus"
repeat_region	1752..17815
repeat_region	/note="match: STS: Em:G05256"
repeat_region	17870..18109
repeat_region	/note="L2 repeat: matches 2252..2519 of consensus"
repeat_region	18562..18822
repeat_region	/note="L2 repeat: matches 1630..1882 of consensus"
repeat_region	19119..19214

repeat_region	/note="MER5A repeat: matches 11. .106 of consensus"
repeat_region	20487. .20579
repeat_region	/note="L12 repeat: matches 2042. .2135 of consensus"
repeat_region	20593. 21070
repeat_region	/note="L1M1 repeat: matches 5558. .6033 of consensus"
repeat_region	21074. .21182
repeat_region	/note="L1P11 repeat: matches 6068. .6164 of consensus"
repeat_region	21201. .22910
repeat_region	/note="L1M1 repeat: matches 3839. .5546 of consensus"
repeat_region	22919. .28163
repeat_region	/note="L1P3 repeat: matches 902. .6146 of consensus"
repeat_region	28160. .28375
repeat_region	/note="L1P3 repeat: matches 569. .777 of consensus"
repeat_region	28374. .29301
repeat_region	/note="L1S repeat: matches 5219. .6146 of consensus"
repeat_region	29302. .29635
repeat_region	/note="L1S repeat: matches 4877. .5210 of consensus"
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repeat_region	/note="L1P repeat: matches 2. .595 of consensus"
repeat_region	30310. .30395
repeat_region	/note="L1M4 repeat: matches 6095. .6180 of consensus"
repeat_region	30399. .31074
repeat_region	/note="L1P13 repeat: matches 5476. .6156 of consensus"
repeat_region	31086. .35151
repeat_region	/note="L1P11 repeat: matches 2107. .6164 of consensus"
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repeat_region	35265. .35365
repeat_region	/note="L1M3 repeat: matches 6203. .6304 of consensus"
repeat_region	35361. .37144
repeat_region	/note="L1M1 repeat: matches 4262. .6079 of consensus"
repeat_region	37144. .40022
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repeat_region	40103. .41274
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repeat_region	41274. .41312
repeat_region	/note="L1ME repeat: matches 2253. .2291 of consensus"
repeat_region	41313. .41618
repeat_region	/note="L1USX repeat: matches 2. .305 of consensus"
repeat_region	41619. .42194
repeat_region	/note="L1MEC repeat: matches 2012. .2254 of consensus"
repeat_region	42212. .42343
repeat_region	/note="L1 repeat: matches 3217. .3348 of consensus"
repeat_region	42345. .42525
repeat_region	/note="L1M4 repeat: matches 2508. .2689 of consensus"
repeat_region	42537. .42636
repeat_region	/note="L1 repeat: matches 3467. .3570 of consensus"
repeat_region	42648. .44277
repeat_region	/note="L1M4 repeat: matches 4023. .5667 of consensus"
repeat_region	44280. .44493
repeat_region	/note="L1ub repeat: matches 2. .207 of consensus"
repeat_region	44561. .45101
repeat_region	/note="L1M4 repeat: matches 5654. .6163 of consensus"
repeat_region	45484. .45849
repeat_region	/note="MER4A repeat: matches 1. .366 of consensus"
repeat_region	45983. .46045
repeat_region	/note="L2 repeat: matches 2572. .2634 of consensus"
repeat_region	46069. .51314
repeat_region	/note="L1P3 repeat: matches 900. .6146 of consensus"
repeat_region	51310. .52068
repeat_region	/note="L1P4 repeat: matches 2. .776 of consensus"
repeat_region	52097. .52180
repeat_region	/note="L2 repeat: matches 2668. .2750 of consensus"
repeat_region	52330. .52415
repeat_region	/note="L2 repeat: matches 2623. .2706 of consensus"
repeat_region	52646. .52878
repeat_region	/note="MIR repeat: matches 7. .261 of consensus"
repeat_region	53213. .53900
repeat_region	/note="L2 repeat: matches 1999. .2707 of consensus"
repeat_region	54715. .55084
repeat_region	/note="L2 repeat: matches 2364. .2750 of consensus"
repeat_region	55251. .55292
repeat_region	/note="S repeat: matches 1. .42 of consensus"

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repeat_region 55293. .55623 /note="L1M4 repeat: matches 3719. .4071 of consensus"
repeat_region 55831. .58846 /note="L1PA5 repeat: matches 3139. .6143 of consensus"
repeat_region 61230. .61450 /note="BURL repeat: matches 11069. .11275 of consensus"
repeat_region 61467. .61997 /note="L1PA13 repeat: matches 5629. .6155 of consensus"
repeat_region 62098. .62298 /note="MER5A repeat: matches 2. .189 of consensus"
repeat_region 62913. .63274 /note="THEIC repeat: matches 3. .371 of consensus"
repeat_region 63277. .64587 /note="THEIC-internal repeat: matches 314. .1646 of consensus"
repeat_region 64586. .64689 /note="THE1-INTERNAL repeat: matches 694. .791 of consensus"
repeat_region 64696. .65003 /note="THEIC-internal repeat: matches 4. .309 of consensus"
repeat_region 65007. .65373 /note="THEIC repeat: matches 1. .371 of consensus"
repeat_region 65376. .65571
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Matches 67; Conservative 0; Indels 0; Gaps 0;	67.0%;	47.2;	9;	128765;
Pred. No. 0.0008;				
DB 89210	TCGTAGAGACACACACTTTTACGCTAGAGATGCTTAGGTCACATCCGTGACTTGGCTACCT	89211		
QY 21	tagaagaacacagaccttggagacaagaatatactaaagttaatttcctgactctgattt	80		
DB 89210	TCGTAGAGACACACACTTTTACGCTAGAGATGCTTAGGTCACATCCGTGACTTGGCTACCT	89211		
QY 81	attaactaacacatccttgcgaatgtctgcttaagcttttt	120		
DB 89210	AATTACTATGTGCACATTGACACAGATTGCTTGAAGTTTCTT	89171		

RESULT	8			
AC018803/c				
LOCUS	AC018803	162043 bp	DNA	linear
DEFINITION	Human sapiens chromosome 11 clone RPL1-348A20, WORKING			DRAFT
SEQUENCE	SEQUENCE, 23 unordered pieces.			
ACCESSION	AC018803			
VERSION	AC018803.2	GI:7231004		
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.			
SOURCE	human.			

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 162043)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 162043)
Waterston,R.H.
Direct Submission
Submitted (20-DEC-1999) Genome Sequencing Center, Washington

COMMENT

```

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Center project name: H.NH0348A20
                        Project Information
                        Summary Statistics
Sequencing vector: M13: 71%
Sequencing vector: plasmid: 29%
Chemistry: Dye-Primer ET; 71% of reads
Chemistry: Dye-terminator Big Dye; 29% of reads
Assembly program: Phrap; version 0.990319

```

	* NOTE: This is a 'working draft' sequence. It currently
	* consists of 23 contigs. The true order of the pieces
	* is not known and their order in this sequence record is
	* arbitrary. Gaps between the contigs are represented as
	* runs of N, but the exact sizes of the gaps are unknown.
	* This record will be updated with the finished sequence
	* as soon as it is available and the accession number will
	* be preserved.
	1 1403: contig of 1403 bp in length
*	1404 1503: gap of unknown length
*	1504 3139: contig of 1636 bp in length
*	3140 3239: gap of unknown length
*	3240 4924: contig of 1685 bp in length
*	4925 5024: gap of unknown length
*	5025 7122: contig of 2098 bp in length
*	7123 7222: gap of unknown length
*	7223 9988: contig of 2766 bp in length
*	9989 10088: gap of unknown length
*	10089 12884: contig of 2796 bp in length
*	12885 12984: gap of unknown length
*	12985 15878: contig of 2894 bp in length
*	15879 15978: gap of unknown length
*	15979 21740: contig of 5762 bp in length
*	21741 21840: gap of unknown length
*	21841 26572: contig of 4732 bp in length
*	26573 26672: gap of unknown length
*	26673 30641: contig of 3969 bp in length
*	30642 30741: gap of unknown length
*	30742 35422: contig of 4681 bp in length
*	35423 35522: gap of unknown length
*	35523 40850: contig of 5328 bp in length
*	40851 40950: gap of unknown length
*	40951 45830: contig of 4880 bp in length
*	45831 45930: gap of unknown length
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*	45940 50549: gap of unknown length
*	50549 50550 56392: contig of 5843 bp in length
*	50550 56392: gap of unknown length
*	56393 56492: gap of unknown length
*	56493 63159: contig of 6667 bp in length
*	63160 63259: gap of unknown length
*	63260 65949: contig of 6390 bp in length
*	65950 69749: gap of unknown length
*	69749 77072: contig of 7323 bp in length
*	77073 77172: gap of unknown length
*	77173 89806: contig of 12634 bp in length
*	89807 89906: gap of unknown length
*	89907 103817: contig of 13911 bp in length
*	103818 103917: gap of unknown length
*	103918 117239: contig of 13322 bp in length
*	117240 117339: gap of unknown length
*	117340 139330: contig of 21991 bp in length
*	139331 139430: gap of unknown length
*	139431 162043: contig of 22613 bp in length.
FEATURES	Location/Qualifiers
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	/db_xref="taxon:9606"
	/chromosome="11"
	/clone="RP11-348A20"
misc_feature	1..1403
	/note="assembly_name:Contig10"
misc_feature	1504..3139
	/note="assembly_name:Contig11"
misc_feature	3240..4924
	/note="assembly_name:Contig12"

Query Match	Best Local Similarity	Score	DB 2	Length
Matches 68; Conservative 0; Mismatches 37; Indels 0; Gaps 0;	64.8%; Pred. No. 0.002;	38.2%;	45380 a 35428 c 35430 g 43508 t 2297 others	162043;
QY 15 atgcgatagaagacgagacctgtggagcaagaatactaagttaattctctgactctg 74	ATGTCGTAGAAAGCACAATAAAGCTGTGGCGCCAGACAAATAAGGTCAATTCGTATTTCG 145827			
QY 75 ctattatlaactaacacatctgttcgaatgtgtcctaagctttt 119	CTATTTCCTAGCTGTGTAAACCTGTGAAAAATATGCTTAACCTCTGT 145782			
RESULT 9				
AC090587	166076 bp	DNA	linear	HTG 21-JUL-2001
LOCUS				
DEFINITION	Homo sapiens chromosome 11 clone RP11-348A20 map 11, WORKING DRAFT			
FEATURES	SEQUENCE, 18 unordered pieces.			
ACCESSION	AC090587			
VERSION	AC090587.3 GI:14971229			
KEYWORDS	HTG, HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
	1 (bases 1 to 166076)			
	Britten, B., Linton, L., Nusbaum, C. and Lander, E.			

TITLE
JOURNAL
REFERENCE
AUTHORS

Homo sapiens chromosome 11, clone RP11-348A20

Unpublished
2 (bases 1 to 166076)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barina, N., Bastien, V., Boguslavsky, L., Bouckhagalter, B., Brown, A., Camarata, J., Campolano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Garday, S., Glnde, S., Goyette, M., Graham, L., Grand-Pierre, N., Haas, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., Laroque, K., Lamazares, R., Landers, T., Lenoczky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J., Meneus, L., Minova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Ribback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnupack, R., Seaman, S., Severy, P., Sougniez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Testfay, S., Theodore, J., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

TITLE
JOURNAL
COMMENT

Submitted (03-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 20, 2001 this sequence version replaced gi:14210549.
All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: 348_A-20

Center clone name: 111802

Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 160051 bases at least Q40

Consensus quality: 162378 bases at least Q30

Consensus quality: 163489 bases at least Q20

Insert size: 164000; agarose-ff

Quality coverage: 8.2 in Q20 bases; sum-of-coverage

Quality coverage: 8.2 in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 5708: contig of 5708 bp in length
* 5709 5808: gap of 100 bp
* 5809 6864: contig of 1056 bp in length
* 6865 6964: gap of 100 bp
* 6965 8333: contig of 1369 bp in length
* 8334 8433: gap of 100 bp
* 8434 10150: contig of 1717 bp in length
* 10151 10250: gap of 100 bp
* 10251 11856: contig of 1606 bp in length
* 11857 11956: gap of 100 bp
* 11957 13685: contig of 1729 bp in length
* 13686 13785: gap of 100 bp
* 13786 16872: contig of 3087 bp in length
* 16873 16972: gap of 100 bp

FEATURES
source

* 16973 20146: contig of 3174 bp in length
* 20147 20246: gap of 100 bp
* 20247 53285: contig of 33039 bp in length
* 53286 53385: gap of 100 bp
* 53386 56431: contig of 3046 bp in length
* 56432 56531: gap of 100 bp
* 56532 64713: contig of 8182 bp in length
* 64714 64813: gap of 100 bp
* 64814 72676: contig of 7863 bp in length
* 72677 72776: gap of 100 bp
* 72777 87626: contig of 14850 bp in length
* 87627 87727: gap of 100 bp
* 87728 102250: contig of 14524 bp in length
* 102251 102350: gap of 100 bp
* 102351 114827: contig of 12477 bp in length
* 114828 114927: gap of 100 bp
* 114928 129464: contig of 14537 bp in length
* 129465 129564: gap of 100 bp
* 129565 163190: contig of 33626 bp in length
* 163191 163290: gap of 100 bp
* 163291 165076: contig of 2786 bp in length.
* 165077 Location/Qualifiers
1. 166076
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-348A20"
/clone_11b="RPC1-11 Human Male BAC"
1. 5708
/note="assembly-fragment
clone_end:SP6
vector_side:left"

misc_feature

/note="assembly-fragment
clone_end:SP6
vector_side:left"

misc_feature

/note="assembly-fragment"

misc_feature

/note="assembly-fragment"

misc_feature

/note="assembly-fragment"

misc_feature

/note="assembly-fragment"

misc_feature

/note="assembly-fragment"

misc_feature

/note="assembly-fragment"

misc_feature

/note="assembly-fragment"

misc_feature

/note="assembly-fragment"

misc_feature

/note="assembly-fragment"

BASE COUNT 47135 a 36452 c 36434 g 44341 t 1714 others
ORIGIN

9q34.11-34.2. Contains an MTND3 (mitochondrial NADH dehydrogenase 3) pseudogene, STSs and GSSs, complete sequence.
AL133413
AL133413.5 GI:6967346
HTG: MTND3.
human
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 157790)
Lloyd,D.
Direct Submission
Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Feb 11, 2000 this sequence version replaced gi:6966862.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unSURE' feature key.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
EM: EMBL; SW: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/c-elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9
RP11-54K22 is from the library RPCR-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: pBACE3.6
This sequence is the entire insert of clone RP11-54K22.

FEATURES
source
Location/Qualifiers
1..157790
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/map="q34.11-34.2"
/clone="RP11-54K22"
/clone_lib="RPC1-11.1"
1..576
/note="match: GSS: Em:AQ079263"
12..400
/note="match: GSS: Em:AQ083232
match: STS: Em:G53956"
17..242
/note="match: GSS: Em:B8674"
51..593
/note="match: GSS: Em:B89369"
51..397
/note="match: GSS: Em:B85038"
380..507
/note="MIR repeat: matches 56..192 of consensus"
586..630
/note="MIR repeat: matches 209..253 of consensus"
2127..2232
/note="MIR repeat: matches 2..120 of consensus"
2368..2510
/note="MIR repeat: matches 14..162 of consensus"
2856..2919
/note="MIR repeat: matches 45..112 of consensus"
2957..3102
/note="LIM8 repeat: matches 6140..6288 of consensus"

repeat_region
3096..3492
/note="LIM3 repeat: matches 5112..5529 of consensus"
3800..3904
/note="L2 repeat: matches 2393..2490 of consensus"
4484..4687
/note="TRIGER2 repeat: matches 2334..2690 of consensus"
4908..5087
/note="AluSg/x repeat: matches 134..312 of consensus"
5108..5152
/note="TRIGER2 repeat: matches 1..45 of consensus"
6647..6994
/note="LIMB7 repeat: matches 5821..6167 of consensus"
8067..8217
/note="MER1 repeat: matches 268..421 of consensus"
8488..10072
/note="LIMD repeat: matches -1..1597 of consensus"
10112..10338
/note="MER2 repeat: matches 89..335 of consensus"
10339..10650
/note="AluYb8 repeat: matches 1..312 of consensus"
10651..10720
/note="MER2 repeat: matches 24..89 of consensus"
13021..13179
/note="MER45 repeat: matches 1..178 of consensus"
13830..13915
/note="LRR38 repeat: matches 1..87 of consensus"
13953..14420
/note="LRR38 repeat: matches 86..556 of consensus"
14730..14896
/note="LRR16 repeat: matches 208..371 of consensus"
16330..16929
/note="LIP3 repeat: matches 5547..6146 of consensus"
complement(17541..18049)
/note="match: GSS: Em:AQ677358"
complement(17569..17992)
/note="match: GSS: Em:AQ580536"
18024..18471
/note="LIMD2 repeat: matches 5842..6239 of consensus"
18472..18807
/note="MER1 repeat: matches 1..336 of consensus"
18808..18903
/note="LIMD2 repeat: matches 6239..6341 of consensus"
18901..19479
/note="LIM3A repeat: matches 5285..5895 of consensus"
19408..19879
/note="match: GSS: Em:AQ476746"
complement(19557..19992)
/note="match: GSS: Em:AQ177739"
21042..21464
/note="match: GSS: Em:AQ679820"
21067..21431
/note="match: GSS: Em:AQ409649"
21081..21546
/note="match: GSS: Em:AQ314497"
21180..21640
/note="match: GSS: Em:AQ228996"
21370..21677
/note="AluSg repeat: matches 1..304 of consensus"
21806..21845
/note="L2 repeat: matches 5252..6163 of consensus"
24419..24952
/note="MER1 repeat: matches 4..527 of consensus"
24953..25312
/note="LIM1 repeat: matches 4904..5252 of consensus"
25525..25670
/note="L2 repeat: matches 1781..1927 of consensus"
25755..25941
repeat_region


```

repeat_region /note="MLT1A2 repeat: matches 13. .114 of consensus"
11392. .11770 /note="MLT1A2 repeat: matches 9. .374 of consensus"
repeat_region 11771. .11884 /note="MLT1A2-internal repeat: matches 1. .113 of
consensus"
repeat_region 11895. .12082 /note="LIME1 repeat: matches 5964. .6164 of consensus"
12140. .12436 /note="ALUy8 repeat: matches 1. .289 of consensus"
repeat_region 12831. .13985 /note="TRIGER1 repeat: matches 771. .1964 of consensus"
13993. .14056 /note="LIP1A6 repeat: matches 6093. .6157 of consensus"
repeat_region 14057. .14363 /note="LIP1A6 repeat: matches 1. .309 of consensus"
14364. .14376 /note="LIP1A6 repeat: matches 6081. .6093 of consensus"
repeat_region 14377. .14687 /note="ALUSX repeat: matches 1. .301 of consensus"
14688. .15421 /note="LIP1A6 repeat: matches 5329. .6081 of consensus"
repeat_region 15422. .15678 /note="ALUSX repeat: matches 8. .289 of consensus"
15679. .16039 /note="LIP1A6 repeat: matches 4960. .5329 of consensus"
repeat_region 16040. .16351 /note="ALUSX repeat: matches 1. .312 of consensus"
16352. .17086 /note="LIP1A6 repeat: matches 4252. .4960 of consensus"
repeat_region 17079. .17509 /note="match: GSS: Em:A0079766"
17089. .17465 /note="TRIGER1 repeat: matches 1950. .2359 of consensus"
repeat_region 17922. .18108 /note="ALUSP repeat: matches 1. .185 of consensus"
18784. .19104 /note="ALUSG repeat: matches 1. .293 of consensus"
repeat_region 19121. .20765 /note="LIP1A2 repeat: matches 4493. .6146 of consensus"
21580. .21989 /note="match: GSS: Em:B03931"
23411. .23714 /note="ALUSX repeat: matches 1. .302 of consensus"
24111. .24395 /note="MER1A repeat: matches 1. .292 of consensus"
24400. .24489 /note="45 copies 2 mer ta 66% conserved"
repeat_region 25259. .25559 /note="ALUSP repeat: matches 1. .299 of consensus"
complement(25341. .25695) /note="match: GSS: Em:B40764"
26535. .26614 /note="MIR repeat: matches 32. .112 of consensus"
30408. .30779 /note="LIM1A9 repeat: matches 5959. .6303 of consensus"
30869. .31357 /note="MER1A repeat: matches 1. .527 of consensus"
31376. .31910 /note="MIR2D repeat: matches 42. .553 of consensus"
31947. .33134 /note="L2 repeat: matches 1366. .2713 of consensus"
complement(32984. .33714) /note="match: GSS: Em:A0377120"
33454. .33536 /note="LIM1A10 repeat: matches 6240. .6319 of consensus"
33537. .34804 /note="HSMAR2 repeat: matches 1. .1300 of consensus"
34805. .34877 /note="LIM1A10 repeat: matches 6167. .6240 of consensus"
35046. .41168 /note="LIP1A2 repeat: matches 2. .6144 of consensus"
41169. .41589

```

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repeat_region /note="LIMEC repeat: matches 1580. .2001 of consensus"
41590. .41864 /note="ALUy repeat: matches 30. .304 of consensus"
repeat_region 41865. .43166 /note="LIMEC repeat: matches 283. .1580 of consensus"
43772. .43857 /note="43 copies 2 mer aa 62% conserved"
repeat_region 44560. .44695 /note="FLAM C repeat: matches 1. .133 of consensus"
44654. .44851 /note="match: GSS: Em:A0451420"
44655. .45072 /note="match: GSS: Em:A0789501"
45717. .45996 /note="LIM4 repeat: matches 3517. .3671 of consensus"
46098. .46235 /note="LIM4 repeat: matches 3572. .3761 of consensus"
46280. .46464 /note="L1 repeat: matches 3983. .4145 of consensus"
46547. .46703 /note="LIME1 repeat: matches 4320. .4648 of consensus"
47012. .47330 /note="LIME1 repeat: matches 4648. .5569 of consensus"
47331. .47707 /note="MSTR repeat: matches 1. .426 of consensus"
47708. .48529 /note="LIME1 repeat: matches 3. .311 of consensus"
48530. .48838 /note="ALUSX repeat: matches 3. .311 of consensus"
48839. .49096 /note="LIME1 repeat: matches 5569. .5834 of consensus"
49147. .49207 /note="MER2 repeat: matches 25. .84 of consensus"
49259. .49538 /note="LIME1 repeat: matches 5833. .6099 of consensus"
49359. .49823 /note="ALUyb repeat: matches 6. .287 of consensus"
49824. .49884 /note="LIME1 repeat: matches 6099. .6155 of consensus"
50712. .51086 /note="match: STS: Em:G60437"
50862. .50911 /note="25 copies 2 mer ca 74% conserved"
51044. .51354 /note="ALUyab repeat: matches 1. .309 of consensus"
51364. .51491 /note="L2 repeat: matches 2042. .2191 of consensus"
51492. .51812 /note="ALUyab repeat: matches 1. .309 of consensus"

```

```

Query Match 36.5%; Score 43.8; DB 9; Length 57449;
Best Local Similarity 66.3%; Pred. No. 0.0084;
Matches 63; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
OY 25 aagaagcagccttggagcaagaataatgaatttaattctgactctgcatlata 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3061 AAGAGGATGAGCTACAGCAAGACTTCCAAACCAAGTCTGCTGCTACTTAAT 3002
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 85 actaacatcttgcgaatgttgcttaagctttt 119
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3001 ACCTTGGACCTTGACACAGTTAATTAACCTTGT 2967

```

```

RESULT 13
AL136384 172516 bp DNA linear HTG 26-Jul-2000
AL136384/c LOCUS
DEFINITION Homo sapiens chromosome 11 clone RP1-68P15 map p13-14.2. ***
ACCESSION AL136384
VERSION AL136384.8 GI:9542701
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens

```

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
TITLE 1 (bases 1 to 172516)
JOURNAL Direct Submission
Submitted (25-Jul-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jul 27, 2000 this sequence version replaced gi:9501161.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: d168P15
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Consensus quality: 155880 bases at least Q40
Consensus quality: 155942 bases at least Q30
Insert size: 172416; sum-of-contigs
Insert size: 150759; 12.6% error; agarose-fp
Quality coverage: 0.00x in Q20 bases; sum-of-contigs Quality
coverage: 0.00x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 16300: contig of 16300 bp in length
* 16301 16400: gap of 100 bp
* 16401 172516: contig of 156116 bp in length.
*
Location/Qualifiers
1..172516
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="p13-14.2"
/clone_11b="RP1-68P15"
/clone_11b="RP1-1"
1..16300
/note="assembly_fragment:02897.0"
16401..172516
/note="assembly_fragment:02915.0"
BASE COUNT 56528 a 30286 c 30207 g 55395 t 100 others
ORIGIN
Query Match 36.5%; Score 43.8; DB 2; Length 172516;
Best Local Similarity 66.3%; Pred. No. 0.0078;
Matches 63; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
OY 25 aagagcggagcctggagcagaataatcgaattatcctgcctgcctcattatata 84
|||||
DB 97986 AAGGAGTGACTCTCAGCAAGACTTTCACAAACGTCGCTGCTACTTAATT 97927
|||||
OY 85 actacacatttgcacatgttgccttaagctttt 119
|||||
DB 97926 ACTTTGGACCTTGACACAAGTTAATTAACTTTGT 97892
|||||
RESULT 14
HS37J18/C 131427 bp DNA linear PRI 23-NOV-1999
LOCUS
DEFINITION Human DNA sequence from clone 37J18 on chromosome 1p36.2-36.3.

ACCESSION Z98747
VERSION Z98747.1 GI:3947813
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1 (bases 1 to 131427)
AUTHORS Grafham,D.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Dec 2, 1998 this sequence version replaced gi:3925562.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence is the entire insert of clone 37J18. This sequence
has been finished according to sequence map criteria as follows. An
attempt is made to resolve all sequencing problems, such as
compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
This sequence was generated from part of bacterial clone contigs of
human chromosome 1, constructed by the Sanger Centre Chromosome 1
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
37J18 is from the library RP11 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/VECTOR: PCYPAC2.

Location/Qualifiers
1..131427
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="p36.2-36.3"
/clone_11b="RP1-37J18"
/clone_11b="RP1-1"
179..403
/note="L1M4A repeat: matches 6071..6295 of consensus"
423..518
/note="4 copies 24 mer 81% conserved"
521..1156
/note="212 copies 3 mer cac 80% conserved"
521..1168
/note="27 copies 24 mer 79% conserved"
563..1156
/note="9 copies 66 mer 82% conserved"
1544..1613
/note="MIR repeat: matches 141..210 of consensus"
2191..2709
/note="MIR repeat: matches 25..508 of consensus"
2834..3125
/note="AluX repeat: matches 1..294 of consensus"
3603..3882
/note="14 copies 20 mer 58% conserved"
3618..3699
/note="141 copies 2 mer cc 57% conserved"
3674..3784
/note="3 copies 37 mer 79% conserved"
3816..3926
/note="3 copies 37 mer 86% conserved"
3976..4031
/note="28 copies 2 mer tt 79% conserved"
4051..4141
/note="MIR repeat: matches 53..144 of consensus"
5386..5765
/note="MLT1B repeat: matches 1..381 of consensus"

```
repeat_region 5862..6059
/note="LIMB7 repeat: matches 5654..5862 of consensus"
repeat_region 6060..6116
/note="Charliel repeat: matches 2407..2463 of consensus"
repeat_region 6180..6476
/note="LIMB7 repeat: matches 5847..6143 of consensus"
repeat_region 6535..6856
/note="Charliel repeat: matches 2146..2458 of consensus"
repeat_region 7077..7103
/note="9 copies 3 mer tga 93% conserved"
repeat_region 7430..7481
/note="13 copies 4 mer catt 77% conserved"
repeat_region 7536..7712
/note="LIM4 repeat: matches 5086..5272 of consensus"
repeat_region 7784..7911
/note="LIP4 repeat: matches 5288..5414 of consensus"
repeat_region 8170..8475
/note="Alusg repeat: matches 1..308 of consensus"
repeat_region 8477..8512
/note="12 copies 3 mer taa 83% conserved"
repeat_region 8517..8646
/note="Alusx repeat: matches 6..132 of consensus"
repeat_region 8647..8960
/note="Alusg repeat: matches 1..313 of consensus"
repeat_region 8961..9108
/note="Alusx repeat: matches 132..289 of consensus"
repeat_region 10990..11231
/note="MIR repeat: matches 2..249 of consensus"
repeat_region 11467..11756
/note="L2 repeat: matches 2359..2625 of consensus"
repeat_region 12285..12575
/note="Alusx repeat: matches 8..309 of consensus"
repeat_region 12358..12800
/note="match: GSS AQ203924"
repeat_region 14049..14489
/note="MER31B repeat: matches 1..543 of consensus"
repeat_region 14734..15230
/note="71 copies 7 mer gctgtgt 90% conserved"
repeat_region 14747..15236
/note="7 copies 70 mer 91% conserved"
repeat_region 14748..15237
/note="14 copies 35 mer 90% conserved"
repeat_region 14755..15209
/note="5 copies 91 mer 93% conserved"
repeat_region 15124..15428
/note="Tandem repeat: poor quality data over region"
repeat_region 15210..15320
/note="3 copies 37 mer 78% conserved"
repeat_region 15230..15684
/note="5 copies 91 mer 92% conserved"
repeat_region 15231
/note="Forced join in tandem repeat; gap sized by puc
clones and PAC PCR to be 1-200bp"
repeat_region 15312..15661
/note="5 copies 70 mer 93% conserved"
repeat_region 15459..15668
/note="6 copies 35 mer 91% conserved"
repeat_region 15681..15827
/note="L2 repeat: matches 2538..2685 of consensus"
repeat_region 15866..16348
/note="MIR1D repeat: matches 1..504 of consensus"
repeat_region 16463..16529
/note="L2 repeat: matches 2413..2474 of consensus"
repeat_region 16974..17269
/note="MER77 repeat: matches 5..331 of consensus"
repeat_region 18532..18555
/note="6 copies 4 mer atg 100% conserved"
repeat_region 18712..19007
/note="MIR repeat: matches 249..562 of consensus"
repeat_region 19100..19140
/note="MIR repeat: matches 72..112 of consensus"
repeat_region 19854..19922
/note="MIR repeat: matches 87..163 of consensus"

repeat_region 19928..19988
/note="MER53 repeat: matches 128..187 of consensus"
repeat_region 20239..20321
/note="MER53 repeat: matches 94..182 of consensus"
repeat_region 20236..20337
/note="MER53 repeat: matches 1..89 of consensus"
repeat_region 21622..21785
/note="MER63A repeat: matches 42..208 of consensus"
repeat_region 22083..22359
/note="L2 repeat: matches 2416..2710 of consensus"
repeat_region 22441..22574
/note="L2 repeat: matches 2638..2747 of consensus"
repeat_region 23173..23288
/note="MIR repeat: matches 13..126 of consensus"
repeat_region 23472..23858
/note="MER70A repeat: matches 127..545 of consensus"
repeat_region 23472..23858
/note="match: GSS AQ192529"
repeat_region 26500..26778
/note="Alusx repeat: matches 21..297 of consensus"
repeat_region 26856..27160
/note="Alusg repeat: matches 1..301 of consensus"
repeat_region 27460..27770
/note="Alusg repeat: matches 1..311 of consensus"
repeat_region 27999..28292
/note="Alub repeat: matches 1..305 of consensus"
repeat_region 29036..29175
/note="2 copies 70 mer 84% conserved"
repeat_region 29037..29168
/note="2 copies 66 mer 83% conserved"
repeat_region 29040..29119
/note="5 copies 16 mer 73% conserved"
repeat_region 29048..29167
/note="5 copies 24 mer 70% conserved"
repeat_region 29057..29147
/note="7 copies 13 mer 69% conserved"
repeat_region 29072..29151
/note="20 copies 4 mer aaat 66% conserved"
repeat_region 29200..29504
/note="Alusg repeat: matches 1..304 of consensus"
repeat_region 29581..29692
/note="7 copies 16 mer 69% conserved"
repeat_region 29690..29725
/note="18 copies 2 mer ta 81% conserved"
repeat_region 29766..29865
/note="LIPAS repeat: matches 5943..6042 of consensus"
repeat_region 29872..29911
/note="20 copies 2 mer aa 80% conserved"
repeat_region 30042..30253
/note="LIME3 repeat: matches 5937..6164 of consensus"
repeat_region 30493..30540
/note="3 copies 16 mer 88% conserved"

Query Match 36.3%: Score 43.6; DB 9; Length 131427;
Best Local Similarity 65.3%; Pred. No. 0.0091;
Matches 64; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 22 agaaagagcagagacctgggagcaagaatatacgaatgaatttaattctgtctgcatlta 81
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81097 AGGAGGAGCATGATTTGGGGCCAGAAAGCCAGGTTCAATCTGACCTGCACCTTA 81038

QY 82 ttaactaacatcttggccaatgttgccttaagctttt 119
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81037 CTAGCTATGTGGCTTTGGGCAAAATTACTACACCTCTCT 81000

RESULT 15
AC064798 AC064798 157185 bp DNA linear HTG 17-MAY-2000
LOCUS Homo sapiens chromosome 1 clone RP11-182C20 map 1, WORKING DRAFT
DEFINITION SEQUENCE: 26 unordered pieces.
ACCESSION AC064798
VERSION AC064798.2 GI:7885063
```


[illegible]

Query Match	36.3%	Score 43.6	DB 2	Length 157185
Best Local Similarity	65.3%	Pred. No. 0.009		
Matches 64	Conservative 0	Mismatches 34	Indels 0	Gaps 0
0Y	22	agaagagcagaccttggagcaagatattcaatttaattccttgactctgcatlta	81	
Db 154492	AGGTAGGGCAGTGGATTGTTGGAGCCAGAAAGCCAGATTCATAATCCTGACTCGCACCTTA	154551		
0Y	82	ttaactaacatcttggccaatgttgcttaagctttt	119	
Db 154552	CTAGCTATGTGGCTTTGGGCAATTATCAACACTCTCT	154589		

Search completed: September 7, 2002, 18:23:45
Job time: 28924 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 14:51:24 : Search time 8462.63 Seconds
(without alignments)
31.898 Million cell updates/sec

Title: US-09-834-291-1_COPY_1266_1285
Perfect score: 20
Sequence: 1 aaactacctaagatcatct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estbda:*
2: em_estbhm:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pin:*
16: em_gss_vrt:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.4	92.0	256	9 A1629829	A1629829 486039F12
2	18.4	92.0	527	10 BG267668	BG267668 1000135F1
3	17.4	87.0	632	9 AW943206	AW943206 LD33880.3
4	17.4	87.0	714	12 AZ966012	AZ966012 2M0236018
5	17.4	87.0	1028	12 CNS010LK	AL099122 Drosophila
6	17.4	87.0	1101	12 CNS0024V	AL062157 Drosophila
7	16.8	84.0	320	9 BB066589	BB066589 BB066589
8	16.8	84.0	331	9 BB559660	BB559660 BB559660
9	16.8	84.0	374	12 A2110509	A2110509 RPCI-23-4
10	16.8	84.0	409	12 A0475625	A0475625 CIRBI-E1
11	16.8	84.0	424	12 BH400996	BH400996 AG-ND-124
12	16.8	84.0	442	9 AL509860	AL509860 AL509860
13	16.8	84.0	540	12 BB8004	BB8004 RPCI-16C2
14	16.8	84.0	576	12 A2483186	A2483186 IM0308N08
15	16.8	84.0	673	9 AV834315	AV834315 AV834315
16	16.8	84.0	785	12 BH116550	BH116550 RPCI-24-2
17	16.8	84.0	831	10 BE704507	BE704507 SC01_05H0

C 18	16.4	82.0	269	9 AV016820	AV016820 AV016820
C 19	16.4	82.0	407	12 A0814525	A0814525 HS_5265_A
C 20	16.4	82.0	812	12 BH268838	BH268838 CH230-162
C 21	16	80.0	849	10 BG445507	BG445507 GA_Ea002
C 22	15.8	79.0	208	12 A2509241	A2509241 IM0352P04
C 23	15.8	79.0	287	10 Z28847	Z28847 HSBAS5E061 S
C 24	15.8	79.0	328	9 AU097685	AU097685 AU097685
C 25	15.8	79.0	330	10 BF331881	BF331881 OVI-BT063
C 26	15.8	79.0	341	9 AV645999	AV645999 A645999
C 27	15.8	79.0	343	12 BH041588	BH041588 RPCI-24-3
C 28	15.8	79.0	368	10 T87445	T87445 yd69h05.r1
C 29	15.8	79.0	378	12 B27343	B27343 TSD14TR TAM
C 30	15.8	79.0	385	9 AM802137	AM802137 ILS-UM007
C 31	15.8	79.0	403	12 A0147024	A0147024 HS_2269-A
C 32	15.8	79.0	416	9 BE120640	BE120640 UT-R-CA0-
C 33	15.8	79.0	418	12 A2445420	A2445420 IM0241M12
C 34	15.8	79.0	433	12 A0716681	A0716681 HS_5463-A
C 35	15.8	79.0	442	10 N41676	N41676 yw90e07.r1
C 36	15.8	79.0	446	12 A0436731	A0436731 HS_5068.B
C 37	15.8	79.0	459	10 BF413605	BF413605 UT-R-CA0-
C 38	15.8	79.0	459	10 BF413606	BF413606 UT-R-CA0-
C 39	15.8	79.0	469	12 B65834	B65834 CIT-HSP-202
C 40	15.8	79.0	486	12 A2695007	A2695007 UP_312-24
C 41	15.8	79.0	493	12 A0205575	A0205575 HS_3225.A
C 42	15.8	79.0	493	12 A0304517	A0304517 HS_3138.B
C 43	15.8	79.0	495	10 N29128	N29128 yx47e08.r1
C 44	15.8	79.0	497	12 A0880539	A0880539 HS_5045-B
C 45	15.8	79.0	499	9 AA401233	AA401233 zv63e02.r

ALIGNMENTS

RESULT 1
A1629829
LOCUS 486039F12.x3 486 - leaf primordia cDNA library from Hake lab Zea
DEFINITION mays cDNA, mRNA sequence.
ACCESSION A1629829
VERSION A1629829.1 GI:4681159
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 256)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 486039 row: F column: 12.
FEATURES
source location/Qualifiers
1..256
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_lib="486 - leaf primordia cDNA library from Hake lab"
/tissue_type="leaf primordia"
/dev_stage="P7-p11 leaf"
/lab_host="E.coli XL1-Blue MFR"
/note="Organ: shoot; Vector: Lambda zap; Hake lab cDNA library."
BASE COUNT 69 a 70 c 51 g 66 t

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SUC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0236 row: 0 column: 18
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 714.
Location/Qualifiers

FEATURES

source

1. 714
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0236018"
/clone.lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

258 a 151 c 163 g 142 t

ORIGIN

Query Match 87.0%; Score 17.4; DB 12; Length 714;
Best Local Similarity 94.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 aactacctaagactatct 20
|||||
Db 76 AACCACTAAGACTATCT 94

RESULT

5

CNS010LK 1028 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence sp6 end of BAC
DEFINITION BACN04103 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION AL099122.1 GI:5610733
VERSION AL099122
KEYWORDS GSS.

SOURCE

ORGANISM

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1028)

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -

http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES

source

Location/Qualifiers
1. 1028
/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
/clone.lib="DrosBAC"
/clone="BACN04103"
/note="end : sp6"

BASE COUNT

231 a 244 c 250 g 285 t 18 others

ORIGIN

Query Match 87.0%; Score 17.4; DB 12; Length 1028;
Best Local Similarity 94.7%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 aactacctaagactatct 19
|||||
Db 461 AACCACTAAGACTATCT 443

RESULT

6

CNS0024V 1101 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION BACR05E09 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION

AL062157

VERSION

AL062157.1 GI:4940317

KEYWORDS

GSS.

SOURCE

ORGANISM

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)

Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammose in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

Location/Qualifiers
1. 1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone.lib="RPCI-98"
/clone="BACR05E09"
/note="end : T7"

BASE COUNT

297 a 255 c 248 g 250 t 51 others

ORIGIN

Query Match		87.0%	Score 17.4:	DB 12:	Length 1101,
Best Local Similarity		94.7%;	Pred. No. 3.6e+02;		
Matches	18;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;

QY	1	aactactagaagctatc	19		
Dd	628	AAACTACCAAGAGCTATC	646		

RESULT	7				
LOCUS	BB066589				
DEFINITION	BB066589 RIKEN full-length enriched, 15 days embryo male testis Mus musculus cDNA clone 8030453F10 3 similar to U9385 Mus musculus CTP synthetase homolog (CTPsh) mRNA, mRNA sequence.				
VERSION	BB066589.1	GI:8524003			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 320)				
AUTHORS	Kono,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukuinishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Horii,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sugabe,Y., Suganara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,E., Tomlinaga,N., Toya,T., Tsunoda,Y., Watabiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiaki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.				
TITLE	RIKEN Mouse ESTs (Kono,H., et al.)				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagooka,S., Sasaki,M., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermotabilization and thermoinactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itohi,M., Kitsuina,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.				

FEATURES	
source	Location/Qualifiers
	1..320
	/organism="Mus musculus"
	/strain="C57BL/6J"
	/db_xref="taxon:10090"
	/clone_id="RIKEN full-length enriched, 15 days embryo male testis"
	/sex="male"
	/tissue_type="testis"
	/dev_stage="15 days embryo"
	/lab_host="DH10B"

/note="Site.1: Sali; site.2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 185.0 Second strand cDNA was prepared with the primer adapter of sequence [5' GAGGAGAGATTCGAGTTAAATTAAATATATCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified plasmidscript KS(+) after bulk excision from LambdaFLC I. Cloning sites, 5' end: Sali; 3' end: BamHI"


```

/db_xref="taxon:9606"
/clone="2589J3"
/clone_lib="CITBI-E1"
/sex="male"
/cell_type="sperm"
/notes="Vector: pBeloBAC11, Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT      122 a      54 c      64 g      168 t      1 others
ORIGIN

Query Match      84.0%; Score 16.8; DB 12; Length 409;
Best Local Similarity 90.0%; Pred. No. 5.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 aaactactaagaagctatct 20
        |||||
Db      215 AAACCTACCTAAGATCATCT 196

RESULT 11
LOCUS      BH400996      424 bp      DNA      linear      GSS 11-DEC-2001
DEFINITION AG-ND-12404.TF ND-TAM Anopheles gambiae genomic clone AG-ND-12404,
            DNA sequence.
ACCESSION      BH400996
VERSION      BH400996.1 GI:17347212
KEYWORDS      GSS.
SOURCE      African malaria mosquito.
ORGANISM      Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae
            ; Anophelinae.
REFERENCE      1 (bases 1 to 424)
AUTHORS      Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.
TITLE      Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL      Unpublished (2001)
COMMENT      Other GSSs: AG-ND-12404.TF
            Contact: Brendan J Loftus
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0208
            Fax: 301 838 3543
            Email: bjoftus@tigr.org
            This clone is from an A. gambiae BAC library (ND-TAM) provided by
            F.H. Collins and sequenced by The Institute for Genomic Research
            (TIGR). The BAC library was generated from A. gambiae PEST strain
            DNA. All DNA was extracted from newly hatched first instar larvae
            to minimize the inclusion of DNA from microorganisms that inhabit
            the gut. The DNA is derived from mixed sexes of larvae. The BAC
            library was constructed at Texas A&M University BAC Center
            University, College Station, Texas 77843-2123, USA using a HindIII
            partial digest.
            Seg primer: M13 For
            Class: BAC ends
            Location/Qualifiers
                location=1..424
                /organism="Anopheles gambiae"
                /strain="PEST"
                /db_xref="taxon:7165"
                /clone="AG-ND-12404"
                /clone_lib="ND-TAM"
                /note="Vector: pBeloBAC1; Site_1: HindIII"
BASE COUNT      159 a      93 c      65 g      107 t
ORIGIN

Query Match      84.0%; Score 16.8; DB 12; Length 424;
Best Local Similarity 90.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 aaactactaagaagctatct 20

```

```

||| ||| ||||| ||||| |||
Db      140 AAAATACATAGAGCTATCT 159

RESULT 12
LOCUS      AL509860      442 bp      mRNA      linear      EST 04-JAN-2001
DEFINITION AL509860 Hordeum vulgare Barke developing caryopsis (3'-15.DAP)
            Hordeum vulgare cDNA clone HY03B17u 3', mRNA sequence.
ACCESSION      AL509860
VERSION      AL509860.1 GI:12036363
KEYWORDS      EST.
SOURCE      barley.
            Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
            ; Triticeae; Hordeum.
REFERENCE      1 (bases 1 to 442)
AUTHORS      Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
TITLE      EST sequencing and analysis in barley
JOURNAL      Unpublished (2000)
COMMENT      Contact: Michalek W
            Institute for Plant Genetics and Crop Plant Research
            Corrensstr.3, D-06466 Gatersleben, Germany
            Email: michalek@ipk-gatersleben.de, http://pgic.ipk-gatersleben.de
            Seq primer: M13uni primer for 3' end.
            Location/Qualifiers
                location=1..442
                /organism="Hordeum vulgare"
                /cultivar="Barke"
                /db_xref="taxon:4513"
                /clone="HY03B17u"
                /clone_lib="Hordeum vulgare Barke developing caryopsis
                (3'-15.DAP)"
                /tissue_type="developing caryopsis (3.-15.DAP)"
                /lab_host="XLDLR"
                /note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2:
                XhoI; mRNA was made from developing caryopsis (3.-15.DAP)
                of spring barley variety 'Barke', a high quality malting
                variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI
                (3'-end of cDNA). NOTE: Due to a cloning artefact caused
                by the kit, in most cases the EcoRI site is NOT present,
                as well as the EcoRI adapter. Average insert size is 1 kb
                Sequence trimming: Vector sequences and sequence ends were
                trimmed from the 5'- and 3'-end until a 50 bp window
                contains less than two ambiguities. The maximum length was
                set to 700 bp"
BASE COUNT      115 a      117 c      84 g      124 t      2 others
ORIGIN

Query Match      84.0%; Score 16.8; DB 9; Length 442;
Best Local Similarity 90.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 aaactactaagaagctatct 20
        |||||
Db      333 AGACTACCTCAGAGCTATCT 352

RESULT 13
LOCUS      B88004      540 bp      DNA      linear      GSS 09-APR-1999
DEFINITION RPI11-16C24.TFB RPI1-11 Homo sapiens genomic clone RPI1-11-16C24,
            DNA sequence.
ACCESSION      B88004
VERSION      B88004.1 GI:2929136
KEYWORDS      GSS.
SOURCE      human.
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 540)

```

AUTHORS Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P., and Venter, J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other GSSs: RPC11-16C24.TP RPC11-16C24.TVB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdamads@tigr.org
Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieter@jeng.med.bufileo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.bufileo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..540
/organism="Homo sapiens"
/db_xref="GDB:7505831"
/db_xref="taxon:9606"
/clone="RPC1-11-16C24"
/clone_lib="RPC1-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC11 Human Male BAC Library"

BASE COUNT 187 a 104 c 106 g 143 t
ORIGIN

Query Match 84.0%; Score 16.8; DB 12; Length 540;
Best Local Similarity 90.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 aaactacctaaagctatct 20
Db 186 AACCTACCTAAGACTTATAT 167

RESULT 14
AZ483186 576 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0308N08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0308N08 R. DNA sequence.
ACCESSION AZ483186
VERSION AZ483186.1 GI:10646948
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 576)
Islam, H., Longacre, S., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0308 row: N column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 576.
FEATURES
source Location/Qualifiers
1..576
/organism="Mus musculus"
/strain="C57Bl/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0308N08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-gold, T1-resistant, F-"
/note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57Bl/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (911473211419b/AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-GOLD (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 166 a 91 c 113 g 206 t
ORIGIN

Query Match 84.0%; Score 16.8; DB 12; Length 576;
Best Local Similarity 90.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 aaactacctaaagctatct 20
Db 489 AAGATACCTAAGACTTATCT 470

RESULT 15
AV834315 673 bp mRNA linear EST 22-JUN-2001
LOCUS AV834315 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
DEFINITION vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA
clone rBAGs14a02, mRNA sequence.
ACCESSION AV834315
VERSION AV834315.1 GI:14526404
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Triticeae; Hordeum.
1 (bases 1 to 673)
Sato, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2001)
Contact: Kazuhito Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL: <http://www.rib.okayama-u.ac.jp/barley/>
Sato, K., Saitoh, D., Takeda, K., Shini, T., and Kohara, Y. Direct submission:
database: <http://www.shigen.nig.ac.jp/barley/barley.html>.

FEATURES

source

Location/Qualifiers
1 673

1. .673

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/organism="Hordeum vulgare subsp. vulgare"  
/cultivar="Haruna Nijo"
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/db_xref="taxon:112509"
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/clone="rbags14a02"
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/clone_lib="k. Sato unpublished cDNA library: Hordeum  
vulgare subsp. vulgare shoots germination"
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vulgare subsp. vulgare shoots germination"

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/tissue_type="shoots"

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/dev_stage="germination"
173  133  16

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a	172	c	133	g	165	t
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BASE COUNT
ORIGIN

ORIGIN

Query Match
Best Local

84.08;	Score 16.8;	DB 9;	Length 673;
90.08;	Pred NO. 6	2e+02;	

Best Local Similarity 90.0%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 3

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 aaactacctaagatct 20

— — — — —

Db 500 AGACTACCTCAGAGCTATCT 519

Search completed: September 7, 2002, 14:51:28
Job time: 16187 sec

Job time: 161.87 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 8, 2002, 01:09:44 ; Search time 1826.34 Seconds
(without alignments)
33.350 Million cell updates/sec

Title: US-09-834-291-1_COPY_1266_1285
Perfect score: 20
Sequence: 1 aaactacctaagagctatct 20

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2036664 seqs, 1522705736 residues
Total number of hits satisfying chosen parameters: 4073328

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New:
1: /cgn2_6/prodata/2/pna/PCNT_NEW_COMB.seq:*
2: /cgn2_6/prodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/prodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/prodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/prodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/prodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	45121	6	US-10-035-832-1262
2	17.4	87.0	96599	6	US-10-035-832-1349
3	16.8	84.0	461	6	US-10-035-832-1349
4	16.8	84.0	1022	7	US-10-027-632-258416
5	16.8	84.0	1022	7	US-10-027-632-258417
6	16.8	84.0	1223	6	US-10-098-754-11812
7	16.8	84.0	2500	7	US-10-027-632-111702
8	16.8	84.0	2500	7	US-10-027-632-111703
9	15.8	79.0	337	5	US-09-721-844-17137
10	15.8	79.0	498	7	US-10-027-632-50682
11	15.8	79.0	498	7	US-10-027-632-50683
12	15.8	79.0	498	7	US-10-027-632-50684
13	15.8	79.0	498	7	US-10-027-632-50685
14	15.8	79.0	1022	1	PCT-US02-12378-67
15	15.8	79.0	1022	7	US-10-124-805-67
16	15.8	79.0	1592	5	US-09-705-256A-1146
17	15.8	79.0	2774	7	US-10-104-047-248
18	15.8	79.0	5775	6	US-10-198-846-9873
19	15.4	77.0	129710	7	US-10-027-632-118902
20	15.2	76.0	118	5	US-09-698-495-511
21	15.2	76.0	401	5	US-09-918-002-11325
22	15.2	76.0	455	5	US-10-027-632-185243
23	15.2	76.0	498	6	US-10-182-995-2106
24	15.2	76.0	498	6	US-10-182-995-2106
25	15.2	76.0	498	6	US-10-182-993-2148

c 26	15.2	76.0	498	6	US-10-182-997-2121	Sequence 2121, Ap
c 27	15.2	76.0	498	6	US-10-182-998-2092	Sequence 2092, Ap
c 28	15.2	76.0	498	6	US-10-203-135-2064	Sequence 2064, Ap
c 29	15.2	76.0	498	6	US-10-203-137-2220	Sequence 2220, Ap
c 30	15.2	76.0	498	6	US-10-203-139-2197	Sequence 2197, Ap
c 31	15.2	76.0	571	7	US-10-027-632-201021	Sequence 201021, Ap
c 32	15.2	76.0	582	7	US-10-027-632-274673	Sequence 274673, Ap
c 33	15.2	76.0	637	7	US-10-027-632-226676	Sequence 226676, Ap
c 34	15.2	76.0	915	7	US-10-156-995-16	Sequence 16, Appl
c 35	15.2	76.0	915	7	US-10-156-995-71	Sequence 71, Appl
c 36	15.2	76.0	946	7	US-10-027-632-120073	Sequence 120073, Ap
c 37	15.2	76.0	1045	7	US-10-027-632-119014	Sequence 119014, Ap
c 38	15.2	76.0	1143	7	US-10-027-632-201020	Sequence 201020, Ap
c 39	15.2	76.0	1143	8	US-60-360-039-46954	Sequence 46954, A
c 40	15.2	76.0	12304	6	US-10-205-428-677	Sequence 677, App
c 41	15	75.0	30042	6	US-10-080-170-650	Sequence 650, App
c 42	15	75.0	30042	7	US-10-080-170B-650	Sequence 650, App
c 43	14.8	74.0	235	5	US-09-539-331D-2086	Sequence 2086, Ap
c 44	14.8	74.0	378	5	US-09-918-995-37657	Sequence 37657, A
c 45	14.8	74.0	523	7	US-10-027-632-93635	Sequence 93635, A

ALIGNMENTS

RESULT 1
US-10-035-832-1262
; Sequence 1262, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Engelhard, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1262
; LENGTH: 45121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-832-1262

Query Match 100.0%; Score 20; DB 6; Length 45121;
Best Local Similarity 100.0%; Pred. No. 0.89; 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0;
QY 1 aaactacctaagagctatct 20
Db 9260 aaactacctaagagctatct 9279
RESULT 2
US-10-035-832-1349
; Sequence 1349, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1

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SEQ ID NO 1349
LENGTH: 96599
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (3729)..(3748)
OTHER INFORMATION: "n" at positions 3729 thru 3748 can be any base
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4902)..(4921)
OTHER INFORMATION: "n" at positions 4902 thru 4921 can be any base
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7901)..(8020)
OTHER INFORMATION: "n" at positions 7901 thru 8020 can be any base
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12187)..(12206)
OTHER INFORMATION: "n" at positions 12187 thru 12206 can be any base
FEATURE:
NAME/KEY: misc_feature
LOCATION: (36676)..(36765)
OTHER INFORMATION: "n" at positions 36676 thru 36765 can be any base
FEATURE:
NAME/KEY: misc_feature
LOCATION: (51928)..(51947)
OTHER INFORMATION: "n" at positions 51928 thru 51947 can be any base
FEATURE:
NAME/KEY: misc_feature
LOCATION: (56214)..(56713)
OTHER INFORMATION: "n" at positions 56214 thru 56713 can be any base
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NAME/KEY: misc_feature
LOCATION: (58367)..(58386)
OTHER INFORMATION: "n" at positions 58367 thru 58386 can be any base
FEATURE:
NAME/KEY: misc_feature
LOCATION: (63327)..(63350)
OTHER INFORMATION: "n" at positions 63327 thru 63350 can be any base
FEATURE:
NAME/KEY: misc_feature
LOCATION: (66416)..(66549)
OTHER INFORMATION: "n" at positions 66416 thru 66549 can be any base
FEATURE:
NAME/KEY: misc_feature
LOCATION: (67304)..(67872)
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (84883)..(84902)
OTHER INFORMATION: "n" at positions 84883 thru 84902 can be any base
FEATURE:
NAME/KEY: misc_feature
LOCATION: (91740)..(91802)
OTHER INFORMATION: "n" at positions 91740 thru 91802 can be any base
FEATURE:
NAME/KEY: misc_feature
LOCATION: (95348)..(95367)
OTHER INFORMATION: "n" at positions 95348 thru 95367 can be any base
US-10-035-832-1349

Query Match      87.0%; Score 17.4; DB 6; Length 96599;
Best Local Similarity 94.7%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 aaactactaagagctatc 19
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Db 22555 aaactactaagagctatc 22573
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RESULT 3

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US-10-098-754-5310
Sequence 5310, Application US/10098754
GENERAL INFORMATION:
APPLICANT: Harrington, John J.
APPLICANT: Jackson, P. David
APPLICANT: Sherf, Bruce A.
APPLICANT: Cain, Scott
APPLICANT: Rundlett, Stephen E.
APPLICANT: Ramchandran, Rakesh
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND PROTEIN HOMOLOGS AND USES THEREOF
FILE REFERENCE: AIX-001CN
CURRENT APPLICATION NUMBER: US/10/098,754
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 09/791539
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 21107
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5310
LENGTH: 461
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-754-5310

Query Match      84.0%; Score 16.8; DB 6; Length 461;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 aaactactaagagctatc 20
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Db 283 aaactactaagagctatc 302
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```
RESULT 4
US-10-027-632-258416
Sequence 258416, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 258416
LENGTH: 1022
TYPE: DNA
ORGANISM: Human
US-10-027-632-258416
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Query Match      84.0%; Score 16.8; DB 7; Length 1022;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 902 aaactactaagagctatc 921
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RESULT 5
US-10-027-632-258417
; Sequence 258417, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 258417
; LENGTH: 1022
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-258417

Query Match      84.0%; Score 16.8; DB 7; Length 1022;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
||||| ||||| ||||| |||||
Db 902 aaactacctaagatcatct 921

RESULT 6
US-10-098-754-11812
; Sequence 11812, Application US/10098754
; GENERAL INFORMATION:
; APPLICANT: Harrington, John J.
; APPLICANT: Jackson, P. David
; APPLICANT: Sherf, Bruce A.
; APPLICANT: Cain, Scott
; APPLICANT: Rundlett, Stephen E.
; APPLICANT: Ramachandran, Rakesh
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND PROTEIN HOMOLOGS AND USES THEREOF
; FILE REFERENCE: AIX-001CN
; CURRENT APPLICATION NUMBER: US/10/098,754
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 09/791539
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 21107
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 11812
; LENGTH: 1223
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1223)
; OTHER INFORMATION: n = A,T,C or G
US-10-098-754-11812
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Query Match      84.0%; Score 16.8; DB 6; Length 1223;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 347 aaactgctaagagccatct 366

RESULT 7
US-10-027-632-111702
; Sequence 111702, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 111702
; LENGTH: 2500
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-111702

Query Match      84.0%; Score 16.8; DB 7; Length 2500;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
||||| ||||| ||||| |||||
Db 1358 aaactgctaagagccatct 1377

RESULT 8
US-10-027-632-111703
; Sequence 111703, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
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;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 111703
;; LENGTH: 2500
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-111703
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Query Match      84.0%; Score 16.8; DB 7; Length 2500;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1358 aactcctaagactct 1377
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RESULT 9
US-09-721-544-17137/C
; Sequence 17137, Application US/09721544
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickinson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Hunter, Kelly
; APPLICANT: Jessen, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Kila, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Phuong
; APPLICANT: Palencia, Servando
; APPLICANT: Raisi, Fariba
; APPLICANT: Smith, Benjamin
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Yang, Fel
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; TITLE OF INVENTION: From a cDNA Library of Fetal Liver-Spleen
; FILE REFERENCE: 728CIP
; CURRENT APPLICATION NUMBER: US/09/721,544
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 09/515,128
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/034,341
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 2489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17137
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-721-544-17137
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Query Match      79.0%; Score 15.8; DB 5; Length 337;
Best Local Similarity 89.5%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Oy 2 aactacctaagactct 20
    | ||||| ||||| |||||
Db 133 ACCTACCTAAGACTCT 115
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RESULT 10
US-10-027-632-50682
; Sequence 50682, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50682
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50682
```

```
Query Match      79.0%; Score 15.8; DB 7; Length 498;
Best Local Similarity 89.5%; Pred. No. 94;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Oy 2 aactacctaagactct 20
    | ||||| ||||| |||||
Db 473 agtactacctaagactct 491
```

```
RESULT 11
US-10-027-632-50683
; Sequence 50683, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 50683
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50683

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Query Match	79.08;	Score 15.8;	DB 7;	Length 498;
Best Local Similarity	89.58;	Pred. No. 94;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

```

QY      2 aactacctaagagctatct 20
        | ||||| ||||| |||
Db     473 agctacctaagagcttct 491

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RESULT 12
US-10-027-632-50684
; Sequence 50684, Application US/10027632
; GENERAL INFORMATION:

Query Match	79.0%	Score 15.8:	DB 7:	Length 458:
Best local Similarity	89.5%	Pred. No. 94:		
Matches 17: Conservative	0:	Mismatches	2:	Indels 0: Gaps 0

```
Qy      2 aaactacctaagagctatct 20
          | | | | | | | | | | | |
Db      473 agctacctaagagcttct 491
```

```

RESULT 13
US-10-027-632-50685
Sequence 50685, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotides
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827, 129
CURRENT APPLICATION NUMBER: US/10/027, 632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218, 006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198, 676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193, 483

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? PRIOR FILING DATE: 2000-03-29
? PRIOR APPLICATION NUMBER: US 60/185,218
? PRIOR FILING DATE: 2000-02-24
? PRIOR APPLICATION NUMBER: US 60/167,363
? PRIOR FILING DATE: 1999-11-23
? PRIOR APPLICATION NUMBER: US 60/156,358
? PRIOR FILING DATE: 1999-09-28
? PRIOR APPLICATION NUMBER: US 60/146,002
? PRIOR FILING DATE: 1999-08-09
? NUMBER OF SEQ ID NOS: 325720
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 50685
? LENGTH: 498
? TYPE: DNA
? ORGANISM: Human
? US-10-027-632-50685

Query Match      79.0%; Score 15.8; DB 7; Length 498;
Best Local Similarity 89.5%; Pred. No. 94;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0

```

```
QY      2 aactacctagaagctatct 20
         | |||||
Db      473 agctacctagaagctttct 491
```

```

RESULT 14
PCT-US02-12378-67
Sequence 67, Application PC/TUS0212378
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Persing, David H.
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, Davlin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: McNeill, Patricia D.
APPLICANT: Durham, Margaritha
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.47003PC
CURRENT APPLICATION NUMBER: PCT/US02/12378
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 67
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 67
LENGTH: 1022
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-12378-67

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Query Match	79.0%;	Score 15.8;	DB 1;	Length 1022;
Best Local Similarity	89.5%;	Pred. No. 1e+02;		
Matches 17; Conservative	0;	Mismatches	0;	Gaps 0

```
Qy      2 aactacctagagctatct 20
          | | | | | | | | | | | |
Db     539 acctacctaatagctatct 557
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RESULT 15
US-10-124-805-67
; Sequence 67, Application US/10124805
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.

```

; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C12
; CURRENT APPLICATION NUMBER: US/10/124,805
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 67
; LENGTH: 1022
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-124-805-67

```

```

Query Match      79.0%; Score 15.8; DB 7; Length 1022;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 aactacctagaagctactct 20
        | | | | | | | | | | | | | |
Db      539 aactacctatagctactct 557

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Search completed: September 8, 2002, 01:09:47
 Job time: 37065 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Comphen Ltd.

OK nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:31:46 : Search time 13836.9 Seconds
(without alignments)
31.271 Million cell updates/sec

Title: US-09-834-291-1_COPY_1266_1285
Perfect score: 20
Sequence: 1 aaactacctaagactatct 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Result	No.	Score	Query	Length	ID	Description
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45:	2	20	100.0	40	32	US-09-834-291-22
46:	3	20	100.0	40	32	US-09-834-291-30
47:	4	20	100.0	1608	7	US-08-377-522-1
48:	5	20	100.0	1608	7	US-08-377-522-1
49:	6	20	100.0	1608	7	US-08-377-522-1
50:	7	20	100.0	1608	7	US-08-377-522-1
51:	8	20	100.0	2165	26	US-09-665-615B-94
52:	9	20	100.0	2165	31	US-09-802-669-94
53:	10	20	100.0	2280	32	US-09-834-291-3
54:	11	20	100.0	2827	32	US-09-834-291-4
55:	12	20	100.0	3212	32	US-09-834-291-1
56:	13	20	100.0	45121	36	US-09-997-728-10
57:	14	20	100.0	238	17	US-09-298-328A-1327
58:	15	20	100.0	238	47	US-09-085-147-1327
59:	16	20	100.0	285	17	US-09-303-031A-8707
60:	17	20	100.0	285	33	US-09-894-949-8707
61:	18	20	100.0	285	33	US-09-894-949A-8707
62:	19	20	100.0	285	33	US-09-894-949A-8707
63:	20	20	100.0	290	33	US-09-303-031A-7338
64:	21	20	100.0	290	33	US-09-894-949A-7338
65:	22	20	100.0	290	33	US-09-894-949A-7338
66:	23	20	100.0	290	33	US-09-894-949A-7338
67:	24	20	100.0	290	33	US-09-894-949A-7338
68:	25	20	100.0	290	33	US-09-894-949A-7338
69:	26	20	100.0	290	33	US-09-894-949A-7338
70:	27	20	100.0	290	33	US-09-894-949A-7338
71:	28	20	100.0	290	33	US-09-894-949A-7338
72:	29	20	100.0	290	33	US-09-894-949A-7338
73:	30	20	100.0	290	33	US-09-894-949A-7338
74:	31	20	100.0	290	33	US-09-894-949A-7338
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C 32 18.4 92.0 894 25 US-09-654-617-269389
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C 34 18.4 92.0 1239 28 US-09-708-427-74487
C 35 18.4 92.0 1239 28 US-09-708-427-84689
C 36 18.4 92.0 1529 28 US-09-708-427-84689
C 37 18.4 92.0 1961 70 US-60-312-544-2159
C 38 17.4 87.0 1961 70 US-60-312-544-2159
C 39 17.4 87.0 1737 23 US-09-614-150-13760
C 40 17.4 87.0 1737 23 US-09-614-150-13760
C 41 17.4 87.0 1740 58 US-60-191-637-13801
C 42 17.4 87.0 2815 23 US-09-614-150-11371
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Sequence 955, App
Sequence 13760, A
Sequence 13801, A
Sequence 13830, A
Sequence 11371, A
Sequence 11403, A
Sequence 11396, A
Sequence 13759, A

ALIGNMENTS

RESULT 1
US-09-834-291-16
Sequence 16, Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
TITLE OF INVENTION: Oren, Moshé
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834, 291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 20
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-834-291-16

Query Match 100.0%; Score 20; DB 32; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 aaactacctaagagctatct 20
Db 1 aaactacctaagagctatct 20

RESULT 2
US-09-834-291-22
Sequence 22, Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
TITLE OF INVENTION: Oren, Moshé
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834, 291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 40
TYPE: DNA
ORGANISM: Homo Sapiens

US-09-834-291-22

Query Match 100.0%; Score 20; DB 32; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
Db 11 aaactacctaagagctatct 30

RESULT 3
US-09-834-291-30
Sequence 30, Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
TITLE OF INVENTION: Oren, Moshé
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834, 291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 40
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-834-291-30

Query Match 100.0%; Score 20; DB 32; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
Db 11 aaactacctaagagctatct 30

RESULT 4
US-08-377-522-1
Sequence 1, Application US/08377522
GENERAL INFORMATION:
APPLICANT: Mountz, John D.
APPLICANT: Liu, Changdan
APPLICANT: Cheng, Jianhua
APPLICANT: Koopman, William J.
APPLICANT: Zhou, Tong
TITLE OF INVENTION: Human Fas Gene Promoter Region
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,522
FILING DATE: 20-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Sertlich, Gary J.
REGISTRATION NUMBER: 34,430
REFERENCE/DOCKET NUMBER: UOAB:034/SER
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1467..1496
US-08-377-522-1

Query Match 100.0%; Score 20; DB 7; Length 1608;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 aaactacctaagatctatct 20
|||||
Db 507 AACCTACCTAAGAGCTATCT 526

RESULT 5
US-08-377-522C-1
Sequence 1, Application US/08377522C
GENERAL INFORMATION:
APPLICANT: Mountz et al.
TITLE OF INVENTION: Human Fas Gene Promoter Region
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
STREET: 8011 Candle Lane
CITY: Houston
STATE: TX
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,522C
FILING DATE: January 20, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5919
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 bp
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:

ORGANISM: human
TISSUE TYPE: placental
IMMEDIATE SOURCE:
LIBRARY: (FIX1; EMBL-SP6/T7
CLONE: FIX1, FIX2, FIX3; EMBL1, EMBL2, EMBL3
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
US-08-377-522C-1

Query Match 100.0%; Score 20; DB 7; Length 1608;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 aaactacctaagatctatct 20
|||||
Db 507 AACCTACCTAAGAGCTATCT 526

RESULT 6
US-08-377-522D-1
Sequence 1, Application US/08377522D
GENERAL INFORMATION:
APPLICANT: Mountz et al.
TITLE OF INVENTION: Human Fas Gene Promoter Region
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
STREET: 8011 Candle Lane
CITY: Houston
STATE: TX
ZIP: 77071
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,522D
FILING DATE: January 20, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5919
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 bp
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placental
IMMEDIATE SOURCE:
LIBRARY: (FIX1; EMBL-SP6/T7
CLONE: FIX1, FIX2, FIX3; EMBL1, EMBL2, EMBL3
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:

US-08-377-522D-1

Query Match 100.0%; Score 20; DB 7; Length 1608;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aaactacctaagagctatct 20
|||||
Db 507 AAACCTAGAGCTATCT 526

RESULT 7

US-09-665-615B-94
; Sequence 94, Application US/09665615B
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0502
; CURRENT APPLICATION NUMBER: US/09/665,615B
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 94
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1782)...(1813)
US-09-665-615B-94

Query Match 100.0%; Score 20; DB 26; Length 2165;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aaactacctaagagctatct 20
|||||
Db 821 aaactacctaagagctatct 840

RESULT 8

US-09-802-669-94
; Sequence 94, Application US/09802669
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 94
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1782)...(1813)
US-09-802-669-94

Query Match 100.0%; Score 20; DB 31; Length 2165;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aaactacctaagagctatct 20
|||||
Db 821 aaactacctaagagctatct 840

RESULT 9

US-09-834-291-3
; Sequence 3, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Kramer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-3

Query Match 100.0%; Score 20; DB 32; Length 2380;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aaactacctaagagctatct 20
|||||
Db 820 aaactacctaagagctatct 839

RESULT 10

US-09-834-291-4
; Sequence 4, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Kramer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2827
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-4

Query Match 100.0%; Score 20; DB 32; Length 2827;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aaactacctaagagctatct 20
|||||

Db 1267 aaactactaagagctatct 1286

RESULT 11

US-09-834-291-1
Sequence 1, Application US/09834291

GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 3212
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-834-291-1

Query Match 100.0%; Score 20; DB 32; Length 3212;

Best Local Similarity 100.0%; Pred. No. 8.8; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

OY 1 aaactactaagagctatct 20

Db 1266 aaactactaagagctatct 1285

RESULT 12

US-09-997-722-10
Sequence 10, Application US/09997722

GENERAL INFORMATION:
APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71171/RMS/DCE
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: Patent In version 3.1
SEQ ID NO 10
LENGTH: 45121
TYPE: DNA
ORGANISM: Homo sapiens
US-09-997-722-10

Query Match 100.0%; Score 20; DB 36; Length 45121;

Best Local Similarity 100.0%; Pred. No. 13; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

OY 1 aaactactaagagctatct 20

Db 9260 aaactactaagagctatct 9279

RESULT 13

US-09-298-328A-1327/C
Sequence 1327, Application US/09298328A
GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath, V.

APPLICANT: Ito, Laura, Y
APPLICANT: Sherman, Bradley, K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN LEAF
FILE REFERENCE: PL-0013 US
CURRENT APPLICATION NUMBER: US/09/298,328A
CURRENT FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,146
PRIOR FILING DATE: May 12, 1998
NUMBER OF SEQ ID NOS: 6550
SOFTWARE: PERL Program
SEQ ID NO 1327
LENGTH: 238
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 700164576H1
NAME/KEY: unsure
LOCATION: 159
OTHER INFORMATION: a, t, c, g, or other
US-09-298-328A-1327

Query Match 92.0%; Score 18.4; DB 16; Length 238;

Best Local Similarity 95.0%; Pred. No. 42; Indels 1; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

OY 1 aaactactaagagctatct 20

Db 209 AAACCTACCTGACGACGTATCT 190

RESULT 14

US-60-085-147-1327/C
Sequence 1327, Application US/60085147

GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath
APPLICANT: Ito, Laura Y.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
NUMBER OF SEQUENCES: 6550
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/085,147
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PL-0013 P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1327:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 700164576H1
US-60-085-147-1327

Query Match 92.0%; Score 18.4; DB 47; Length 238;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
|||||
Db 209 AAACCTACCTGAGAGCTATCT 190

RESULT 15

US-09-303-031A-8707/C
Sequence 8707, Application US/09303031A
GENERAL INFORMATION:
APPLICANT: Raghunath, Laligudi
APPLICANT: Larosa, Thomas J.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN CALLUS
FILE REFERENCE: PL-0011 US
CURRENT APPLICATION NUMBER: US/09/303,031A
CURRENT FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 60/084,493
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 9627
SOFTWARE: PERL Program
SEQ ID NO 8707
LENGTH: 285
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID NO: 700476268H1
NAME/KEY: unsure
LOCATION: 36, 158
OTHER INFORMATION: a, t, c, g, or other
US-09-303-031A-8707

Query Match 92.0%; Score 18.4; DB 17; Length 285;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
|||||
Db 189 AAACCTACCTGAGAGCTATCT 170

Search completed: September 7, 2002, 22:31:48
Job time: 43802 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:21:16 : Search time 212.3 seconds
(without alignments)
23.140 Million cell updates/sec

Title: US-09-834-291-1_COPY_1266_1285
Perfect score: 20
Sequence: 1 aaactactaagatcatct 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/prodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCBUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.8	84.0	6831	2 US-08-609-049A-27	Sequence 27, Appl
2	16.8	84.0	6831	4 US-09-170-996-27	Sequence 27, Appl
3	14.2	71.0	126	1 US-07-744-282C-21	Sequence 21, Appl
4	14.2	71.0	126	1 US-07-744-282C-22	Sequence 22, Appl
5	14.2	71.0	126	1 US-07-744-282C-24	Sequence 24, Appl
6	14.2	71.0	1276	4 US-08-981-957D-12	Sequence 12, Appl
7	14.2	71.0	2809	1 US-08-484-105-3	Sequence 3, Appl
8	14.2	71.0	2809	1 US-08-484-106-3	Sequence 3, Appl
9	14.2	71.0	3119	3 US-09-299-843A-31	Sequence 31, Appl
10	14.2	71.0	3119	4 US-09-088-337B-31	Sequence 31, Appl
11	14.2	71.0	90050	4 US-09-245-041-5	Sequence 31, Appl
12	14.2	70.0	25	2 US-08-713-557B-30	Sequence 30, Appl
13	13.8	69.0	362	1 US-08-322-742-9	Sequence 9, Appl
14	13.8	69.0	631	4 US-08-998-416-670	Sequence 670, App
15	13.8	69.0	749	4 US-09-073-587-1	Sequence 1, Appl
16	13.8	69.0	2340	3 US-08-492-459-5	Sequence 5, Appl
17	13.8	69.0	2340	3 US-08-492-459-7	Sequence 5, Appl
18	13.8	69.0	2340	3 US-08-423-752-5	Sequence 7, Appl
19	13.8	69.0	2340	3 US-08-423-752-7	Sequence 5, Appl
20	13.8	69.0	2340	4 US-08-716-873-19	Sequence 19, Appl
21	13.8	69.0	2340	4 US-08-716-873-21	Sequence 21, Appl
22	13.8	69.0	2340	4 US-09-368-431-19	Sequence 19, Appl
23	13.8	69.0	2340	4 US-09-368-431-21	Sequence 21, Appl
24	13.8	69.0	2340	4 US-09-414-006-5	Sequence 5, Appl
25	13.8	69.0	2340	4 US-09-414-006-7	Sequence 7, Appl
26	13.8	69.0	3515	1 US-08-596-985-1	Sequence 1, Appl
27	13.8	69.0	4307	3 US-08-944-594-1	Sequence 1, Appl

28	13.8	69.0	4371	1 US-08-803-973-1	Sequence 1, Appl
29	13.8	69.0	4371	1 US-08-803-973-1	Sequence 1, Appl
30	13.8	69.0	176373	3 US-09-128-155-17	Sequence 17, Appl
31	13.6	68.0	48	1 US-08-374-770-2	Sequence 2, Appl
32	13.6	68.0	48	1 US-08-461-593B-2	Sequence 2, Appl
33	13.6	68.0	48	1 US-08-651-323A-2	Sequence 2, Appl
34	13.6	68.0	99	5 PCT-US92-06821A-23	Sequence 23, Appl
35	13.6	68.0	126	1 US-07-744-282C-23	Sequence 23, Appl
36	13.6	68.0	337	4 US-08-594-031-79	Sequence 79, Appl
37	13.6	68.0	683	4 US-09-328-111-168	Sequence 168, App
38	13.6	68.0	1161	1 US-08-086-439C-1	Sequence 1, Appl
39	13.6	68.0	1161	1 US-08-434-877-1	Sequence 1, Appl
40	13.6	68.0	1328	4 US-08-930-285-13	Sequence 13, Appl
41	13.6	68.0	1464	2 US-08-938-858-1	Sequence 1, Appl
42	13.6	68.0	1475	3 US-08-641-291A-92	Sequence 92, Appl
43	13.6	68.0	1531	1 US-08-449-986-1	Sequence 1, Appl
44	13.6	68.0	1531	2 US-08-756-855-1	Sequence 1, Appl
45	13.6	68.0	2447	2 US-09-014-969-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-609-049A-27
; Sequence 27, Application US/08609049A
; Patent No. 5948664
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Molz, Lisa
; APPLICANT: Chen, Yen-Wen
; TITLE OF INVENTION: No. 5948664el PI 3-Kinase Polypeptides
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609, 049A
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-063700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 148..5775
; US-08-609-049A-27

Query Match 84.0%; Score 16.8; DB 2; Length 6831;
Best local Similarity 90.0%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaactacctaagaagctatct 20
|||||
Db 6690 AAACCTACCTAAGACGTATCT 6709

RESULT 2

US-09-170-996-27
Sequence 27, Application US/09170996
Patent No. 6291220
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Chen, Yen-Wen
TITLE OF INVENTION: No. 6291220e1 PI 3-Kinase Polypeptides
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/170,996
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/609,049
FILING DATE: 29-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-063700US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2420
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 6831 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 148..5775
US-09-170-996-27

Query Match 84.0%; Score 16.8; DB 4; Length 6831;

Best Local Similarity 90.0%; Pred. No. 3.4;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaactacctaagaagctatct 20
|||||

Db 6690 AAACCTACCTAAGACGTATCT 6709

RESULT 3

US-07-744-282C-21/C
Sequence 21, Application US/07744282C
Patent No. 5521300
GENERAL INFORMATION:
APPLICANT: Shah, Jyotsna S.
APPLICANT: Nietupski, Raymond M.
FILING DATE: August 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kevin M. Farrell
REGISTRATION NUMBER: 35,505

NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,282C
FILING DATE: August 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kevin M. Farrell
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: GTR90-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-07-744-282C-21

Query Match 71.0%; Score 14.2; DB 1; Length 126;

Best Local Similarity 80.0%; Pred. No. 52;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 aaactacctaagaagctatct 20
|||||

Db 26 AAACNACCTAAGACGTCTT 7

RESULT 4

US-07-744-282C-22/C
Sequence 22, Application US/07744282C
Patent No. 5521300
GENERAL INFORMATION:
APPLICANT: Shah, Jyotsna S.
APPLICANT: Nietupski, Raymond M.
FILING DATE: August 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kevin M. Farrell
REGISTRATION NUMBER: 35,505

```

? REFERENCE/DOCKET NUMBER: GTR90-05
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (207) 363-0558
? TELEFAX: (207) 363-0528
? INFORMATION FOR SEQ ID NO: 22:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 126 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: RNA (genomic)
? US-07-744-282C-22

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Query Match	71.0%	Score 14.2	DB 1	length 126
Best Local Similarity	80.0%	Precl. No. 52		
Matches 16	Conservative	0	Mismatches 4	Indels 0
Gaps				0
QY	1	aaactacctaaagactatct	20	-
				-
bb	26	AAACNACCTAGAGCTCTTT	7	-

RESULT 5
US-07-744-282C-24/c
Sequence 24, Application US/07744282C
Patent No. 5521300
GENERAL INFORMATION:
APPLICANT: Shah, Jyotsna S.
APPLICANT: Nietupski, Raymond M.
APPLICANT: Liu, Jing
TITLE OF INVENTION: Oligonucleotides Complementary to
TITLE OF INVENTION: Mycobacterial Nucleic Acids
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/077444.282C
FILING DATE: August 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kevin M. Farrell
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: GTR90-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ. ID NO.: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-07-744-282C-24

	Query Match	71.0%;	Score 14.2;	DB 1;	Length 126;
	Best Local Similarity	80.0%;	Pred. No. 52;		
	Matches 16;	Conservative	0;	Mismatches 4;	Indels
Qy	1 aaactactactaagactatct 20				

Db 26 AACNACCTACGAGCTCTTT 7

RESULT 6
US-08-981-957D-12
Sequence 12, Application US/08981957D
Patent No. 6312935
GENERAL INFORMATION:
APPLICANT: KIT, THOMAS
APPLICANT: SCHULTZ, JOACHIM
TITLE OF INVENTION: CATEPSIN-L, ITS PREPRO FORM AND THE CORRESPONDING
FILE REFERENCE: 514426-3595
CURRENT APPLICATION NUMBER: US/08/981,957D
CURRENT FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: PCT/EP97/02388
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 19619366.4
PRIOR FILING DATE: 1996-01-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 1276
TYPE: DNA
ORGANISM: Parametium tetraurelia
US-08-981-957D-12

Query Match	71.0%;	Score 14.2;	DB 4;	Length 1276;
Best Local Similarity	84.2%;	Pred. No. 69;		
Matches 16; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	2	aactactagaagctatct	20	
05	103	aaatacatttcccttttc	201	

RESULT 7
US-06-484-105-3/C
Sequence 3, Application US/08484105
Patent No. 5589341
GENERAL INFORMATION:
APPLICANT: STILLMAN, Bruce
APPLICANT: BELL, Stephen P
APPLICANT: KOBAYASHI, Ryuji
APPLICANT: RINE, Jasper
APPLICANT: FOSS, Margit
APPLICANT: MCNALLY, Francis J
APPLICANT: LAURENSEN, Patricia
APPLICANT: HERSKOWITZ, Ira
APPLICANT: LI, Joachim J
TITLE OR INVENTION: GAVIN, Kimberly
ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSER: FLIER, HOBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
City: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,105
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36 627


```

? REFERENCE/DOCKET NUMBER: A-59032/DJB/RAC
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 494-8700
? TELEFAX: (415) 494-8771
? TELEX: 910 277299
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2809 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 807..2666
? US-08-484-105-3

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Query Match	71.0%;	Score 14.2;	DB 1;	Length 2809;
Best Local Similarity	84.2%;	Pred. No. 75;		
Matches 16;	Conservative	0;	Mismatches 3;	Indels 0

Qy	2	aactacctaagactatct	20
Db	2539	ATCGACCTAGAGCTATCT	2521

RESULT 8
US-08-484-106-3/c
; Sequence 3, Application US/08484106
; Patent No. 5614618
; GENERAL INFORMATION:

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ADDRESSEE: FEHRL, HOBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.33
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,106
FILING DATE:

```

CLASSIFICATION: 433
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2809 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

```

;          TOPOLOGY: linear
;          MOLECULE TYPE: CDNA
;          FEATURE:
;          NAME/KEY: CDS
;          LOCATION: 807..26
US-08-484-106-3

```

Query Match	71.0%;	Score 14.2;	DB 1;	Length 2809;
Best Local Similarity	84.2%;	Pred. No. 75;		
Matches 16; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

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QY      2 aactacctaagagctatct 20
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Db      2539 ATGCACCTTAGAGCTATCT 2521
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RESULT 9
US-09-299-843A-31/c
; Sequence 31, Application US/09299843A
; Patent No. 6107475

APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66

ADDRESS: Marshall, O'Toole, Gerstein, Murray
ADDRESS: Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/088,337
;; FILING DATE: 01-JUN-1998
;; PRIOR APPLICATION DATA:
;; ADDITIONAL NUMBERS: US 08/453,645

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/977,452
;; FILING DATE: 17-NOV-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: JILL E. TH1

REGISTRATION NUMBER: 43,413
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:

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INFORMATION FOR SEQ. ID NO.: 31
SEQUENCE CHARACTERISTICS:
LENGTH: 3119 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: exon
LOCATION: 7..80
FEATURE:
NAME/KEY: CDS

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-713-557B-30

Query Match 70.0%; Score 14; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaactacctaagag 14
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Db 12 AAACCTACTAAGAG 25

RESULT 13
US-08-322-742-9
Sequence 9, Application US/08322742
Patent No. 5688641
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,742
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938, 823
FILING DATE: September 1, 1992
APPLICATION NUMBER: 07/844,296
FILING DATE: February 28, 1992
APPLICATION NUMBER: 07/552,216
FILING DATE: February 28, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34, 819
REFERENCE/DOCKET NUMBER: 00530/048003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 362
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-322-742-9

Query Match 69.0%; Score 13.8; DB 1; Length 362;
Best Local Similarity 88.2%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 aaactacctaagagcta 17
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Db 63 AAGCAACCTAAGAGCTA 79

RESULT 14
US-08-998-416-670
Sequence 670, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Turgun
APPLICANT: Knechtle, Philipp
APPLICANT: Redischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 670:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1446UP
US-08-998-416-670

Query Match 69.0%; Score 13.8; DB 4; Length 631;
Best Local Similarity 86.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 aaactacctaagagcta 17
|||
Db 168 AAAATACCAAGAGCTA 184

RESULT 15
US-09-073-587-1
Sequence 1, Application US/09073587
Patent No. 6268552
GENERAL INFORMATION:
APPLICANT: Li, Yi

TITLE OF INVENTION: Transgenic Seedless Plants
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,587
FILING DATE: 06-MAY-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,725
FILING DATE: 06-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Feiber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 4-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 749 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-073-587-1

Query Match 69.0%; Score 13.8; DB 4; length 749;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 ctactaagactatct 20
||||| |||||||
Db 693 CTACCTATTGCTATCT 709

Search completed: September 7, 2002, 18:21:19
Job time: 28773 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:40:27 ; Search time 1139.19 Seconds
(without alignments)
30.143 Million cell updates/sec

Title: US-09-834-291-1-COPY_1266_1285

Sequence: 1 aaactactaagactatct 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N.Geneseq_032802:*

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5:	/SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1984.DAT:*
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19:	/SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT:*
20:	/SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:*
21:	/SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:*
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23:	/SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:*
24:	/SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	21	AA288725	Human CD95 recepto
2	20	100.0	1608	17	AA734162	Fas promoter regio
3	17.4	87.0	1737	23	ABL11013	Drosophila melanog
4	17.4	87.0	2815	23	ABLI09420	Drosophila melanog
5	17.4	87.0	3916	23	ABLI1012	Drosophila melanog
6	16.8	84.0	1608	24	ABLI34419	Human immune syste
7	16.8	84.0	2279	23	ABLI18046	Drosophila melanog
8	16.8	84.0	6831	18	AA780200	Phosphatidylinositol
9	16.8	84.0	6871	23	ABLI03307	Drosophila melanog

10	16.8	84.0	7191	23	ABLI20119	Drosophila melanog
11	16.8	84.0	17344	23	ABLI20118	Drosophila melanog
12	16.8	84.0	17358	23	ABLI10306	Drosophila melanog
13	15.8	79.0	1022	22	AA547012	Human breast cancer
14	15.8	79.0	1022	22	AA547012	Human breast cancer
15	15.8	79.0	1642	19	AAV21213	Human type II GARR
16	15.8	79.0	2755	21	AA09173	Human znp1 (ribon
17	15.8	79.0	2864	22	AAK94811	Human full-length
18	15.8	79.0	3293	23	AA586514	DNA encoding novel
19	15.8	79.0	4663	22	AAK80489	Human immune/haema
20	15.8	79.0	6788	22	AAK26789	Human breast cancer
21	15.8	79.0	89047	22	AA78547	Genomic fragment #
22	15.4	77.0	2526	20	AA06819	Chlamydia pneumonia
23	15.2	76.0	276	23	ABLI27109	Drosophila melanog
24	15.2	76.0	447	23	ABLI19509	Drosophila melanog
25	15.2	76.0	498	22	ABAI5892	Human foetal liver
26	15.2	76.0	498	22	ABA23640	Probe #2106 for ge
27	15.2	76.0	498	22	AAK02157	Human brain expres
28	15.2	76.0	498	22	AAI12188	Probe #2121 for ge
29	15.2	76.0	498	22	AAI13534	Probe #2220 used t
30	15.2	76.0	498	22	AAI02101	Zea mays DNA fragm
31	15.2	76.0	1061	21	AAAC4644	Drosophila melanog
32	15.2	76.0	1865	23	ABLI06426	Drosophila melanog
33	15.2	76.0	2276	23	ABLI27108	Drosophila melanog
34	15.2	76.0	2328	22	ABAI4997	Human nervous syst
35	15.2	76.0	2447	23	ABLI19508	Drosophila melanog
36	15.2	76.0	2918	23	ABLI25058	Drosophila melanog
37	15.2	76.0	2922	22	AAK94738	Human full-length
38	15.2	76.0	3262	21	AAA98383	Human regulation f
39	15.2	76.0	5945	24	ABLI32085	Human immune syste
40	15.2	76.0	6012	24	ABLI34564	Human metastasis a
41	15.2	76.0	6204	22	AA545482	Chemically pretrea
42	15.2	76.0	6204	24	ABLI34003	Human immune syste
43	15.2	76.0	6204	24	ABLI34003	Human immune syste
44	15.2	76.0	12304	22	ABA07882	Human ovarian and
45	15.2	76.0	12304	22	AAI03699	Human reproductive

ALIGNMENTS

RESULT 1	AA288725	standard: DNA; 20 BP.
ID	AA288725	
XX	AA288725;	
AC		
DT	11-MAY-2000 (first entry)	
XX		
DE	Human CD95 receptor promoter DNA p53 binding fragment #3.	
XX		
KW	p53; CD95 receptor; human; screening; apoptosis-modulation;	
KM	Cancer chemotherapy; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	DE19847779-Cl.	
XX		
PD	03-FEB-2000.	
XX		
PF	16-OCT-1998; 98DE-1047779.	
XX		
PR	16-OCT-1998; 98DE-1047779.	
XX		
PA	(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.	
XX		
PI	Krammer P, Mueller-Schilling M, Oren M;	
XX		
DR	WPI, 2000-162245/15.	
XX		
PT	Novel receptor DNA useful for identifying apoptosis-modulating	
XX	substances potentially useful for cancer chemotherapy	

P5 Claim 2; Fig 5; 12pp; German.

CC This invention describes a novel p53-binding region of a human CD95
 CC receptor DNA molecule. The p53-binding region, or a vector containing
 CC it, can be used to screen for apoptosis-modulating substances
 CC potentially useful for cancer chemotherapy. This sequence represents a
 CC fragment of the human CD95 receptor promoter which is capable of
 CC binding p53.

XX Sequence 20 BP; 8 A; 5 C; 2 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.35;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aactacctagaagctatct 20
 |||
 Db 1 aactacctagaagctatct 20

RESULT 2

AAT34162 ID AAT34162 standard; DNA; 1608 BP.

XX AAT34162;

XX 22-0CT-1996 (first entry)

XX Fas promoter region.

XX Fas gene promoter; apoptosis; aging; autoimmune disease;
 KW T-cell senescence; ss.

XX Homo sapiens.

XX Key location/Qualifiers

FT 1..1074

FT /tag= a

FT /note= "Fas gene promoter region"

FT protein_bind

FT /tag= b

FT /function= GFI transcription factor binding site

FT protein_bind

FT /tag= c

FT /function= EBP20 transcription factor binding site

FT protein_bind

FT /tag= d

FT /function= Myb transcription factor binding site

FT protein_bind

FT /tag= e

FT /function= NF-Y transcription factor binding site

FT protein_bind

FT /tag= f

FT /function= GF-1 transcription factor binding site

FT protein_bind

FT /tag= g

FT /function= NF-Y transcription factor binding site

FT protein_bind

FT /tag= h

FT /function= AP-1 transcription factor binding site

FT protein_bind

FT /tag= i

FT /function= CP2 transcription factor binding site

FT exon

FT /tag= j

FT /codon_start=1479..1469
 FT /product= Fas protein leader
 FT intron 1497..1608

FT /tag= j

FT /note= "5' end of intron 1 (full length approx.
 14 kb"

PN MO9622370-A1.

XX 25-JUL-1996.

XX 19-JAN-1996; 96WO-US00606.

XX 20-JAN-1995; 95US-0377522.

XX (UABR-) UAB RES FOUND.

XX Cheng J, Koopman WJ, Liu C, Mountz JD, Zhou T;

XX WPI; 1996-354527/35.

XX P-PsDB; AAR99471.

PT Human Fas gene promoter region - used for heterologous protein
 PT expression and for developing products for treating Fas-mediated
 PT apoptosis disorders

PS Claim 11; Fig 2; 123pp; English.

CC A novel DNA segment (AAT34162) has an isolated sequence region
 CC defined as the Fas gene promoter region. This includes a number
 CC of transcription factor binding sites. A coding sequence for
 CC the N-terminal portion (AAR99471) of the Fas protein leader peptide
 CC is also included. The DNA segment was isolated from a human
 CC placental DNA library using a 32P-labeled segment of human Fas cDNA
 CC corresponding to nt 23-346. It can be combined with a structural
 CC gene so that the gene is under the transcriptional control of the
 CC transcription factor binding sites. The promoter region can be used
 CC to regulate Fas gene expression, e.g. in tumour or immune cells, as
 CC a means of treating Fas-mediated apoptosis disorders such as
 CC malignancies and autoimmune diseases.

XX Sequence 1608 BP; 398 A; 421 C; 423 G; 366 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 1608;

Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Gaps 0;

Matches 20; Conservative 0; Indels 0; Gaps 0;

QY 1 aactacctagaagctatct 20
 |||

Db 507 aactacctagaagctatct 526

RESULT 3

ABLI1013 ID ABLI1013 standard; cDNA; 1737 BP.

XX ABLI1013;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide seq ID NO 27521.

XX Drosophila: developmental biology; cell signalling; insecticide;

XX pharmaceutical; gene; ss.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PMD, Myers EW;
XX
DR MPI; 2001-656860/75.
DR P-PSDB; ABB66910.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
PS Claim 1; SEQ ID NO 27521; 21bp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB101840-AB16175), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1737 BP; 446 A; 460 C; 475 G; 356 T; 0 other;
XX
Query Match 87.0%; Score 17.4; DB 23; Length 1737;
Best Local Similarity 94.7%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 aaactacctaagactatc 19
|||||
Db 1576 aaactacctaagactatc 1594
XX
RESULT 4
AB109420/c
ID ABL09420 standard; cDNA; 2815 BP.
XX
AC ABL09420;
XX
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22742.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PMD, Myers EW;
XX
XX MPI; 2001-656860/75.
XX
XX P-PSDB; ABB65317.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT

PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 22742; 21bp + Sequence Listing; English.
XX
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB101840-AB16175), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2815 BP; 653 A; 671 C; 708 G; 783 T; 0 other;
XX
Query Match 87.0%; Score 17.4; DB 23; Length 2815;
Best Local Similarity 94.7%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 aaactacctaagactatc 19
|||||
Db 2076 AAACATCCCAAGAGCTATC 2058
XX
RESULT 5
AB11012/c
ID ABL11012 standard; cDNA; 3916 BP.
XX
XX ABL11012;
XX
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 27518.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PMD, Myers EW;
XX
XX MPI; 2001-656860/75.
XX
XX P-PSDB; ABB66909.
XX
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 27518; 21bp + Sequence Listing; English.
XX
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB101840-AB16175), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC

CC (AB57737-AB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 3916 BP; 1026 A; 965 C; 927 G; 998 T; 0 other;

Query Match 87.0%; Score 17.4; DB 23; Length 3916;
Best Local Similarity 94.7%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 aaactactaagagctatc 19
|||||
DB 1162 AAACACCAAGAGCTATC 1144

RESULT 6
ABL34419/C
ID ABL34419 standard; DNA: 1608 BP.
XX
AC ABL34419;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 2392.
XX
XX Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antiasthmatic; cytosine methylation; antiasthmatic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
XX Homo sapiens.
XX
OS WO200200928-A2.
XX
PN 03-JAN-2002.
XX
PD 02-JUL-2001; 2001WO-EP07537.
XX
PF 30-JUN-2000; 2000DE-1032529.
XX
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIC-) EPICENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2002-130909/17.

XX
XX Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
PS Claim 1; SEQ ID NO 2392; 32pp + Sequence Listing; German.
XX
XX The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 1608 BP; 366 A; 51 C; 421 G; 770 T; 0 other;

Query Match 84.0%; Score 16.8; DB 24; Length 1608;
Best Local Similarity 90.0%; Pred. No. 27;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 aaactactaagagctatc 20
|||||
DB 1102 AAACACCAAGAGCTATC 1083

RESULT 7
ABL18046
ID ABL18046 standard; DNA: 2279 BP.
XX
AC ABL18046;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 5611.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
WPI; 2001-656860/75.

XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 5611; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (AB57737-AB72072).
CC (AB57737-AB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 2279 BP; 751 A; 417 C; 442 G; 669 T; 0 other;

Query Match 84.0%; Score 16.8; DB 23; Length 2279;
Best Local Similarity 90.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 aaactactaagagctatc 20
|||||
DB 622 aaactactaagagctatc 641

RESULT 8
AAT80200
ID AAT80200 standard; CDNA: 6831 BP.
XX
AC AAT80200;
XX

DT 22-JUN-1998 (first entry)
 DE Phosphatidylinositol 3-kinase cdk cDNA.
 XX
 XX Phosphatidylinositol 3-kinase; signal transduction; cell cycle;
 KW antagonist; inflammatory joint disease; cell proliferation; cancer;
 KW psoriasis; restenosis; atherosclerosis; therapy; diagnosis; cpk; ss.
 XX
 OS Drosophila melanogaster.
 XX
 FH Key Location/Qualifiers
 FT CDS 148..5778
 FT /tag= a
 XX
 PN WO9731650-A1.
 XX
 XX 04-SEP-1997.
 PD
 XX 12-FEB-1997; 97WO-US02193.
 PF
 XX 29-FEB-1996; 96US-0609049.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 PI Chen Y, Molz L, Williams LT;
 XX WPI: 1997-448442/41.
 DR P-PSDB; AAW38757.
 XX
 XX New isolated phosphatidylinositol-3 kinase polypeptide - used to
 PT develop products for diagnosis and therapy, particularly for
 PT proliferative disorders, e.g. inflammatory joint diseases, or cancer
 XX
 XX Example 1; Fig 9; 77pp; English.
 XX
 CC This cDNA sequence codes for cpk (see AAW38757), a Drosophila
 CC polypeptide that belongs to a novel class of phosphatidylinositol
 CC 3-kinases that contain a C2 domain, are capable of phosphorylating
 CC a D3 hydroxyl of an inositol ring in phosphatidylinositol and
 CC phosphatidylinositol 4-phosphate, but not in phosphatidylinositol
 CC 4,5-bisphosphate, and which are involved in cell signalling cascades
 CC that control e.g. cell cycle progression and intracellular protein
 CC sorting. Short fragments of cpk cDNA were obtained from a
 CC Drosophila cDNA library by PCR (see AAW80195-96). These short
 CC fragments were used to screen the cDNA library to obtain larger
 CC fragments, and missing 5' ends were obtained by RACE. A
 CC recombinant host cell, transfected with a vector comprising a cpk
 CC nucleic acid is claimed. Novel phosphatidylinositol 3-kinases
 CC can be used to screen for agonists/antagonists of activity and
 CC in a claimed method of treating a disorder caused by dysregulation
 CC of a growth factor activation signalling cascade. Antagonists
 CC may reduce Ras activation allowing treatment of proliferative
 CC disorders such as atherosclerosis, inflammatory joint disease,
 CC psoriasis, restenosis following angioplasty, and cancer.
 XX
 SQ Sequence 6831 BP; 1829 A; 1685 C; 1669 G; 1648 T; 0 other;
 XX
 XX Query Match 84.0%; Score 16.8; DB 18; Length 6831;
 XX Best Local Similarity 90.0%; Pred. No. 31;
 XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 1 aaactacctaagactatct 20
 XX |||||||||||||
 DB 6690 aaactacctaagactatct 6709
 XX
 XX RESULT 9
 XX ABL10307
 XX ID ABL10307 standard; cDNA; 6871 BP.
 XX AC ABL10307;
 XX

DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25403.
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 KW
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI: 2001-656860/75.
 DR P-PSDB; ABB66204.
 DR
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 XX Claim 1; SEQ ID NO 25403; 21pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (AB157737-AB172072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 6871 BP; 1830 A; 1690 C; 1669 G; 1682 T; 0 other;
 XX
 XX Query Match 84.0%; Score 16.8; DB 23; Length 6871;
 XX Best Local Similarity 90.0%; Pred. No. 31;
 XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 1 aaactacctaagactatct 20
 XX |||||||||||||
 DB 6731 aaactacctaagactatct 6750
 XX
 XX RESULT 10
 XX ABL20119
 XX ID ABL20119 standard; DNA; 7191 BP.
 XX AC ABL20119;
 XX 26-MAR-2002 (first entry)
 DT
 XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 11830.
 DE
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ds.
 KW
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 XX 27-SEP-2001.
 PD

XX 23-MAR-2001; 2001WO-US09231.
PF 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PS
PS Claim 1; SEQ ID NO 11830; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 7191 BP; 1931 A; 1730 C; 1740 G; 1790 T; 0 other;

Query Match 84.0%; Score 16.8; DB 23; Length 7191;
Best Local Similarity 90.0%; Pred. No. 31;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 aaactactaagaagctatct 20
D 7051 aaactactaagaagctatct 7070

RESULT 11

ABL20118
ID ABL20118 standard; DNA; 17344 BP.
XX
AC ABL20118;

26-MAR-2002 (first entry)

Drosophila melanogaster genomic polynucleotide SEQ ID NO 11827.

Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

23-MAR-2001; 2001WO-US09231.

23-MAR-2000; 2000US-191637P.

11-JUL-2000; 2000US-0614150.

(PEKE) PE CORP NY.

Venter JC, Adams M, Li PWD, Myers EW;
WPI; 2001-656860/75.

New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PS
PS Claim 1; SEQ ID NO 11827; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 17344 BP; 4659 A; 3886 C; 3857 G; 4942 T; 0 other;

Query Match 84.0%; Score 16.8; DB 23; Length 17344;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 aaactactaagaagctatct 20
D 16204 aaactactaagaagctatct 16223

RESULT 12

ABL10306
ID ABL10306 standard; cDNA; 17358 BP.
XX
AC ABL10306;

26-MAR-2002 (first entry)

Drosophila melanogaster expressed polynucleotide SEQ ID NO 25400.

Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

23-MAR-2001; 2001WO-US09231.

23-MAR-2000; 2000US-191637P.

11-JUL-2000; 2000US-0614150.

(PEKE) PE CORP NY.

Venter JC, Adams M, Li PWD, Myers EW;
WPI; 2001-656860/75.

P-PSDB; ABB66203.

New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -

Claim 1; SEQ ID NO 25400; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins

CC (AB57737-AB872072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
S0 Sequence 17358 BP; 4664 A; 3890 C; 3861 G; 4943 T; 0 other:

Query Match 84.0%; Score 16.8; DB 23; Length 17358;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aactacctaaagctatct 20
Db 16218 aactacctaaagctatct 16237

RESULT 13
AAS47012
ID AAS47012 standard; cDNA; 1022 BP.
XX
AC AAS47012;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human breast cancer CDNA clone B725P.
XX
KW Human; ss; breast cancer protein; tumour; cancer; cytostatic;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200179286-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US12164.
XX
PR 17-APR-2000; 2000US-0551621.
XX
PR 08-JUN-2000; 2000US-0590751.
XX
PR 22-JUN-2000; 2000US-0604287.
XX
PR 20-JUL-2000; 2000US-0620405.
XX
PA (CORI-) CORIXA CORP.
XX
PI Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
XX
DR WPI; 2001-611721/70.
XX
PT Breast Tumour Proteins and nucleic acids useful for the prevention,
PT diagnosis and treatment of breast cancer -
XX
PS Claim 1; Page 165; 297pp; English.
XX
XX
XX The invention relates to isolated breast tumour proteins and
XX nucleic acids that encode them, including immunogenic fragments of the
XX proteins. Also included are expression vectors expressing the
XX proteins, transformed cells and antibodies raised against the proteins or
XX an antigen presenting cell expressing the protein. The proteins and
XX nucleic acids may be used in the prevention, diagnosis and treatment of
XX diseases associated with inappropriate breast tumour protein expression,
XX i.e. breast tumours and breast cancer e.g. by gene therapy. The nucleic
XX acids and their complements may also be used as DNA probes in diagnostic
XX assays to detect and quantitate the presence of similar nucleic acids in
XX samples, and therefore which patients may be in need of restorative
XX therapy. The proteins, nucleic acids and antibodies may be used in assays
XX to identify modulators (e.g. antagonists) of breast tumour protein
XX expression and activity. The antibodies and antagonists may also be used
XX to down regulate expression and activity. The antibodies may also be used
XX as diagnostic agents for detecting the presence of the proteins in
XX samples (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other
XX immuno-purification diagnostic techniques. The present sequence is
XX a CDNA from a breast tumour CDNA library isolated by subtractive

CC hybridisation against a normal breast cDNA library.
XX
XX
S0 Sequence 1022 BP; 254 A; 262 C; 210 G; 296 T; 0 other:

Query Match 79.0%; Score 15.8; DB 22; Length 1022;
Best Local Similarity 89.5%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 aactacctaaagctatct 20
Db 539 aactacctaaagctatct 557

RESULT 14
AAF17582
ID AAF17582 standard; cDNA; 1022 BP.
XX
AC AAF17582;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human breast cancer associated B725P coding sequence.
XX
KW Human; breast cancer associated gene; vaccine; diagnosis; therapy; ss.
KW Homo sapiens.
XX
PN WO200060076-A2.
XX
PD 12-OCT-2000.
XX
PF 15-FEB-2000; 2000WO-US05308.
XX
PR 02-APR-1999; 99US-0285480.
XX
PR 23-JUN-1999; 99US-0339338.
XX
PR 02-SEP-1999; 99US-0389681.
XX
PR 03-NOV-1999; 99US-0433826.
XX
PA (CORI-) CORIXA CORP.
XX
PI Yuqiu J, Dillon DC, Mitcham JL, Xu J, Harlocker SL;
XX
DR WPI; 2001-122627/13.
XX
PT An isolated polypeptide useful for the treatment and diagnosis of
PT tumors e.g. breast cancer comprises at least an immunogenic portion of
PT a breast tumor protein -
XX
PS Claim 6; Page 105-106; 238pp; English.
XX
XX
XX The present invention provides the coding sequences and some protein
XX sequences of proteins associated with breast cancer in humans. These
XX sequences can be used in the diagnosis and treatment of cancers,
XX particularly breast tumours.
XX
S0 Sequence 1022 BP; 254 A; 262 C; 210 G; 296 T; 0 other:

Query Match 79.0%; Score 15.8; DB 22; Length 1022;
Best Local Similarity 89.5%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 aactacctaaagctatct 20
Db 539 aactacctaaagctatct 557

RESULT 15
AAV21213
ID AAV21213 standard; DNA; 1642 BP.
XX
AC AAV21213;

```

XX 23-JUL-1998 (first entry)
DT
XX
XX
DE Human type II GnRH-R C-terminal genomic DNA fragment.
XX
XX Type II Gonadotropin releasing hormone receptor; GnRH-H II; impotence;
KM identification; diagnosis; detection; modulator; treatment; libido;
KW hormone-dependent tumour; neuromodulation; sexual behaviour; ds.
XX
OS Homo sapiens.
XX
XX W09747743-A1.
XX
XX 18-DEC-1997.
XX
XX 11-JUN-1997; 97MO-US10144.
XX
XX 13-JUN-1996; 96US-0019733.
XX
XX (UYCA-) UNIV CAPE TOWN.
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Conklin DC, Hapgood J, Illing N, Millar R, Rumbak E;
XX Troskie B;
XX
XX WPI: 1998-168750/15.
XX
XX New isolated type II gonadotropin-releasing hormone receptor - used
XX to develop products for use in the treatment of hormone-dependent
XX tumours or for neuromodulation of sexual behaviour
XX
XX Claim 11; Page 37-38; 54pp; English.
XX
XX This sequence encodes a novel human type II gonadotropin-releasing
XX hormone receptor (GnRH II) polypeptide. This protein and its products
XX can be used for identifying compounds which modulate GnRH II-mediated
XX metabolism in cells. Compounds identified as agonists or antagonists
XX can be used for treating hormone-dependent tumours. Agonists and
XX antagonists may also prove useful in the study of GnRH II-directed
XX neuromodulation of sexual behaviour, e.g. agonists may be used in the
XX treatment of diminished libido and impotence. The products can also be
XX used for detection and diagnosis.
XX
XX Sequence 1642 BP; 449 A; 399 C; 324 G; 470 T; 0 other;
SQ

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```

Query Match 79.0%; Score 15.8; DB 19; Length 1642;
Best Local Similarity 89.5%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2 aactactaagaactatct 20
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Db 788 aactactaataagctatct 806

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Search completed: September 7, 2002, 18:40:29
 Job time: 29923 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:23:45 ; Search time 12179.2 Seconds
(without alignments)
34.364 Million cell updates/sec

Title: US-09-834-291-1_COPY_1266_1285
Perfect score: 20
Sequence: 1 aaactacctaagagctatct 20

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_cm:*
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6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_or:*
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22: em_ov:*
23: em_ov:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	20	100.0	20	5	AX026104	AX026104 Sequence
2	20	100.0	40	5	AX026110	AX026110 Sequence
3	20	100.0	40	5	AX026118	AX026118 Sequence
4	20	100.0	1608	9	HSEFASX1	X82279 H.sapiens F
5	20	100.0	1877	9	HSAPT1	X81335 H.sapiens A
6	20	100.0	2165	9	HUMFAS	D31968 Human DNA f
7	20	100.0	2344	9	HSCD955FR	X87625 H.sapiens C
8	20	100.0	2380	6	AX026091	AX026091 Sequence
9	20	100.0	2827	6	AX026092	AX026092 Sequence
10	20	100.0	3212	6	AX026089	AX026089 Sequence
11	20	100.0	187313	2	AL157394	AL157394 Human DNA
12	19	95.0	172269	2	AC106508	AC106508 Rattus no
13	19	95.0	245997	2	AC093360	AC093360 Mus muscu
14	17.4	87.0	1814	3	AY051836	AY051836 Drosophi1
15	17.4	87.0	154771	3	AC009214	AC009214 Drosophi1
16	17.4	87.0	165283	3	AC005711	AC005711 Drosophi1
17	17.4	87.0	165412	2	AC010811	AC010811 Homo sapi
18	17.4	87.0	170195	9	AC025452	AC025452 Homo sapi
19	17.4	87.0	184506	2	AC009448	AC009448 Homo sapi
20	17.4	87.0	185070	2	AC087279	AC087279 Homo sapi
21	17.4	87.0	207821	2	AC092258	AC092258 Mus muscu
22	17.4	87.0	245803	3	AE003636	AE003636 Drosophi1
23	17.4	87.0	250968	2	AC014140	AC014140 Drosophi1
24	16.8	84.0	20	6	AX026105	AX026105 Sequence
25	16.8	84.0	526	11	G61139	G61139 SHGC-84832
26	16.8	84.0	1608	6	AX347321	AX347321 Sequence
27	16.8	84.0	5737	1	AF143911	AF143911 Mycoplasma
28	16.8	84.0	6831	3	DM052192	U52192 Drosophila
29	16.8	84.0	6831	6	AR072895	AR072895 Sequence
30	16.8	84.0	6831	6	AR170087	AR170087 Sequence
31	16.8	84.0	7060	1	AF143912	AF143912 Mycoplasma
32	16.8	84.0	7215	3	DMP13K68D	X92892 D.melanogas
33	16.8	84.0	12083	1	MP059896	U59896 Mycoplasma
34	16.8	84.0	16249	1	AE000051	AE000051 Mycoplasma
35	16.8	84.0	22183	2	AC014957	AC014957 Drosophi1
36	16.8	84.0	36787	2	AC023619	AC023619 Mus muscu
37	16.8	84.0	57257	2	AC109308	AC109308 Mus muscu
38	16.8	84.0	59411	9	AC004040	AC004040 Homo sapi
39	16.8	84.0	73900	9	AC092484	AC092484 Homo sapi
40	16.8	84.0	74874	2	AC097666	AC097666 Rattus no
41	16.8	84.0	81672	8	AB020755	AB020755 Arabidops
42	16.8	84.0	84904	9	AP001051	AP001051 Homo sapi
43	16.8	84.0	92948	8	AF000657	AF000657 Arabidops
44	16.8	84.0	110000	2	AC003656_6	Continuation (7 of
45	16.8	84.0	137670	2	AC025616	AC025616 Homo sapi

ALIGNMENTS

RESULT	1	AX026104	20 bp	DNA	linear	PAT 16-SEP-2000
LOCUS	AX026104	Sequence 16 from Patent DE19847779.				
DEFINITION	AX026104					
ACCESSION	AX026104.1	GI:10187535				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 20)
Mueller-Schilling, M., Krammer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 16 03-FEB-2000;
JOURNAL
DEUTSCHES KREBSFORSCH (DE)
FEATURES
source
1. 20
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT
8 a 5 c 2 g 5 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
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    1 AACTACTCTAGAGCTATCT 20

RESULT 2
LOCUS AX026110 40 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 22 from Patent DE19847779.
ACCESSION AX026110
VERSION AX026110.1 GI:10187541
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Mueller-Schilling,M., Krammer,P. and Oren,M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
        substances potentially useful for cancer chemotherapy
        Patent: DE 19847779-C 22 03-FEB-2000;
        DEUTSCHES KREBSFORSCH (DE)
FEATURES
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BASE COUNT 14 a 11 c 4 g 11 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
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    11 AACTACTCTAGAGCTATCT 30

RESULT 3
LOCUS AX026118 40 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 30 from Patent DE19847779.
ACCESSION AX026118
VERSION AX026118.1 GI:10187549
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Mueller-Schilling,M., Krammer,P. and Oren,M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
        substances potentially useful for cancer chemotherapy
        Patent: DE 19847779-C 30 03-FEB-2000;
        DEUTSCHES KREBSFORSCH (DE)
FEATURES
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BASE COUNT 14 a 11 c 4 g 11 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
    |||||||
    11 AACTACTCTAGAGCTATCT 30

RESULT 3
LOCUS AX026118 40 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 30 from Patent DE19847779.
ACCESSION AX026118
VERSION AX026118.1 GI:10187549
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Mueller-Schilling,M., Krammer,P. and Oren,M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
        substances potentially useful for cancer chemotherapy
        Patent: DE 19847779-C 30 03-FEB-2000;
        DEUTSCHES KREBSFORSCH (DE)
FEATURES
    source 1..40
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
BASE COUNT 14 a 11 c 4 g 11 t
ORIGIN

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QY 1 aaactacctaagagctatct 20
    |||||||
    11 AACTACTCTAGAGCTATCT 30

RESULT 4
LOCUS HSFASX1 1608 bp DNA linear PRI 17-FEB-1995
DEFINITION H.sapiens Fas, Apo-1 gene (promoter and exon 1).
ACCESSION X82279
VERSION X82279.1 GI:673405
KEYWORDS APO-1 gene; Fas gene.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1608)
AUTHORS Cheng,J., Liu,C., Koopman,W.J. and Mountz,J.D.
TITLE Characterization of human Fas gene. Exon/Intron organization and
        promoter region
        J. Immunol. 154 (3), 1239-1245 (1995)
JOURNAL 95123075
MEDLINE 2 (bases 1 to 1608)
REFERENCE Cheng,J.
AUTHORS Direct Submission
TITLE Submitted (20-OCT-1994) J. Cheng, Univ. of Alabama at Birmingham,
        Univ. of Alabama, 701 South 19th street, UAB Station, LHRB 473,
        Birmingham, AL 35294-0007, USA
        Related sequences: M67454 and X63717.
FEATURES
    source 1..1608
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /tissue_type="placenta"
            /clone_lib="placental genomic DNA"
            /map="10q23 or 10q24.1"
            /gene="Fas, Apo-1"
            /gene="Fas, Apo-1"
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BASE COUNT 398 a 421 c 423 g 366 t
ORIGIN

Query Match      100.0%; Score 20; DB 9; Length 1608;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
    |||||||
    507 AACTACTCTAGAGCTATCT 526

RESULT 5
LOCUS HSAFPI 1877 bp DNA linear PRI 08-JUN-1995
DEFINITION H.sapiens APT gene, exon 1.
ACCESSION X81335
VERSION X81335.1 GI:537410
KEYWORDS APO-1 gene; apt gene.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1877)
AUTHORS Behnmann,I., Walczak,H. and Krammer,P.H.
TITLE Structure of the human APO-1 gene
        Eur. J. Immunol. 24 (12), 3057-3062 (1994)
JOURNAL 95104292
MEDLINE 2 (bases 1 to 1877)
REFERENCE Krammer,P.H.
AUTHORS Direct Submission
TITLE

```

JOURNAL Submitted (03-SEP-1994) P.H. Kramer, German Cancer Research Center, Tumorimmunology Programm, Im Neuenheimer Feld 280, 69120 Heidelberg, FRG

FEATURES

source Location/Qualifiers
1. 1877
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone_lib="cosmid, pcso2EMBL"
/clone="CAPO-1"
/map="10q23"
151..261
misc_feature /note="Pyrimidine rich region"
151..261
join(1653..1810,X81336.1:155..320,X81337.1:146..283,
X81338.1:145..253,X81339.1:552..613,X81339.1:766..828,
X81340.1:79..161,X81341.1:255..279,X81342.1:103..1757)
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/product="APO-1"
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X81341.1:255..279,X81342.1:103..1757)
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/number=1
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/number=1
/usedin=X81335:HsmRNA2
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X81340.1:79..161,X81341.1:255..279,X81342.1:103..1757)
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join(1689..1810,X81336.1:155..320,X81337.1:146..283,
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X81340.1:79..161,X81341.1:255..279,X81342.1:103..1757)
/gene="AP7"
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/number=1
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X81340.1:79..161,X81341.1:255..279,X81342.1:103..1757)
/gene="AP7"
/label="HsmRNA4"
/product="APO-1"
1704..1810
/gene="AP7"
/label="ex1d"
/number=1
/usedin=X81335:HsmRNA4
1707..1810
/gene="AP7"
/label="ex1e"
/number=1
/usedin=X81335:HsmRNA5
join(1707..1810,X81336.1:155..320,X81337.1:146..283,
X81338.1:145..253,X81339.1:552..613,X81339.1:766..828,
X81340.1:79..161,X81341.1:255..279,X81342.1:103..1757)
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1708..1810
exon

MRNA

/gene="AP7"
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/usedin=X81335:HsmRNA6
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X81340.1:79..161,X81341.1:255..279,X81342.1:103..1757)
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/product="APO-1"
BASE COUNT 469 a 477 c 432 g 499 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 aaactaccctaagagctatct 20
|||||
Db 820 AAACCTACCTAAGAGCTATCT 839

RESULT 6

HUMFAS 2165 bp DNA linear PRI 14-APR-2000
LOCUS Human DNA for Fas antigen, promoter region.
DEFINITION D31968
ACCESSION D31968.1 GI:961455
VERSION D31968.1 GI:961455
KEYWORDS Fas antigen.
SOURCE Homo sapiens blood DNA, clone pF7.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2165)
Wada,N., Matsuura,M., Ohba,Y., Kobayashi,N., Takizawa,T. and
Nakanishi,Y.

Transcription stimulation of the Fas-encoding gene by nuclear
factor for interleukin-6 expression upon influenza virus infection
J. Biol. Chem. 270 (30), 18007-18012 (1995)

REFERENCE

2 (bases 1 to 2165)
Nakanishi,Y.
Direct Submission
Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University,
Faculty of Pharmaceutical Sciences, 13-1 Takara-machi, Kanazawa,
Ishikawa 920-0934, Japan (E-mail:nakanaka@cds.p.kanazawa-u.ac.jp,
Tel:076-234-4424, Fax:076-234-4480)

FEATURES

source Location/Qualifiers
1..2165
/organism="Homo sapiens"
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481..489
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772..780
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934..940
/bound_moiety="NF-IL6"
948..955
/bound_moiety="AP-1"
1298..1306
/bound_moiety="Ets"
1436..1781
/bound_moiety="NF-IL6"
1436..1813
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CDS

/product="Fas antigen"
/protein_id="BAA20850.1"
/db_xref="GI:4433150"
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BASE COUNT 508 a 555 c 555 g 547 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 2165;
Best Local Similarity 100.0%; Pred. No. 7;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
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Db 821 AACTACTTAAGAGCTATCT 840

RESULT 7
HSCD955FR 2344 bp DNA linear PRI 05-FEB-1997
LOCUS H.sapiens CD95 gene 5' flanking region.
DEFINITION X87625
ACCESSION X87625.1 GI:902311
VERSION beta interferon; CD95 gene; silencer.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2344)
AUTHORS Rudert,F., Visser,E., Forbes,L., Lindridge,E., Wang,Y. and
Watson,J.
TITLE Identification of a silencer, enhancer, and basal promoter region
in the human CD95 (Fas/APO-1) gene
JOURNAL DNA Cell Biol. 14 (11), 931-937 (1995)
MEDLINE 96069539
REFERENCE 2 (bases 1 to 2344)
AUTHORS Rudert,F.H.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-1995) F.H. Rudert, Genesis Research &
Development, Corporation Ltd., PO Box 50, Auckland, NEW ZEALAND
COMMENT Overlaps with X81335, & X82279-X82286.
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/db_xref="taxon:9606"
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/tissue_type="placenta"
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564..1337
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717..801
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misc_signal complement(1237..1244)
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1338..1919
enhancer 1920..2344
promoter /note="basal promoter"
BASE COUNT 637 a 546 c 511 g 650 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
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Db 1384 AACTACTTAAGAGCTATCT 1403

RESULT 8
AX026091 2380 bp DNA linear PAT 16-SEP-2000
LOCUS Sequence
DEFINITION AX026091
ACCESSION AX026091
VERSION AX026091.1 GI:10187522
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2380)
AUTHORS Mueller-Schilling,M., Krammer,P. and Oren,M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
JOURNAL Patent: DE 19847779-C 3 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
FEATURES
source Location/Qualifiers
1..2380
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 579 a 595 c 568 g 638 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
|||||
Db 820 AACTACTTAAGAGCTATCT 839

RESULT 9
AX026092 2827 bp DNA linear PAT 16-SEP-2000
LOCUS Sequence 4 from Patent DE19847779.
DEFINITION AX026092
ACCESSION AX026092
VERSION AX026092.1 GI:10187523
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2827)
AUTHORS Mueller-Schilling,M., Krammer,P. and Oren,M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
JOURNAL Patent: DE 19847779-C 4 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 728 a 676 c 657 g 766 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
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Db 1267 AACTACTTAAGAGCTATCT 1286

RESULT 10
AX026089 3212 bp DNA linear PAT 16-SEP-2000
LOCUS Sequence 1 from Patent DE19847779.
DEFINITION AX026089
ACCESSION AX026089

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VERSION      AX026089.1  GI:10187520
KEYWORDS
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE    1 (bases 1 to 3212)
AUTHORS      Mueller-Schilling, M., Kramer, P. and Oren, M.
TITLE        Novel receptor data useful for identifying apoptosis-modulating
             substances potentially useful for cancer chemotherapy
JOURNAL      Patent: DE 1984779-C 1 03-FEB-2000;
             DEUTSCHES KREBSFORSCH (DE)
FEATURES
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               /db_xref="taxon:9606"
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 aaactactaagaagctatct 20
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Db 1266 AAACCTACCTAAGAGCTATCT 1285

RESULT 11
LOCUS      AL157394      187313 bp      DNA      linear      PRI 22-AUG-2001
DEFINITION Human DNA sequence from clone RP11-399019 on chromosome 10,
LOCUS      AL157394
ACCESSION  AL157394.15  GI:15384622
VERSION    HTG.
KEYWORDS   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 187313)
AUTHORS    Blakey, S.
TITLE      Direct Submission
JOURNAL    Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
             CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
             requests: clonerequest@sanger.ac.uk
             On Aug 31, 2001 this sequence version replaced gi:14161146.
             During sequence assembly data is compared from overlapping clones.
             Where differences are found these are annotated as variations
             together with a note of the overlapping clone name. Note that the
             variation annotation may not be found in the sequence submission
             corresponding to the overlapping clone, as we submit sequences with
             only a small overlap as described above.
             This sequence was finished as follows unless otherwise noted: all
             regions were either double-stranded or sequenced with an alternate
             chemistry or covered by high quality data (i.e., phred quality >=
             30); an attempt was made to resolve all sequencing problems, such
             as compressions and repeats; all regions were covered by at least
             one plasmid subclone or more than one M13 subclone; and the
             assembly was confirmed by restriction digest. The following
             abbreviations are used to associate primary accession numbers given
             in the feature table with their source databases: Em, EMBL; SW,
             SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP
             database can be found at
             http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
             was generated from part of bacterial clone contigs of human
             chromosome 10, constructed by the Sanger Centre Chromosome 10
             Mapping Group. Further information can be found at
             http://www.sanger.ac.uk/HGP/Chr10
             RP11-399019 is from the library RPCT-11.2 constructed by the group
             of Pieter de Jong. For further details see
             http://www.chori.org/Bacpac/home.htm
COMMENT

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VECTOR: PBAC3.6
This sequence is the entire insert of clone RP11-399019 The true
left end of clone RP11-496H23 is at 166408 in this sequence. The
true right end of clone RP11-30415 is at 18704 in this sequence.
FEATURES
SOURCE       Location/Qualifiers
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             100157..100198
               /note="Sequence confirmed by AC015461 sequenced by WIBR."
             105808..105972
               /note="Sequence confirmed by AC015461 sequenced by WIBR."
             105973..105989
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BASE COUNT   55669 a 36398 c 36888 g 58358 t
ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 187313;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 aaactactaagaagctatct 20
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Db 143235 AAACCTACCTAAGAGCTATCT 143254

RESULT 12
LOCUS      AC106508      172269 bp      DNA      linear      HTG 12-JAN-2002
DEFINITION Rattus norvegicus clone CH230-205114, *** SEQUENCING IN PROGRESS
LOCUS      AC106508
ACCESSION  AC106508.1  GI:18139030
VERSION    HTG; HTGS_PHASE1.
KEYWORDS   Norway rat.
ORGANISM   Rattus norvegicus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
             Rattus.
REFERENCE  1 (bases 1 to 172269)
AUTHORS    Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
             Alsprouck, S.L., Amaral, H.C., Are, J.R., Banks, T., Barbarta, J.,
             Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J.,
             Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
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             Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
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             Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
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Oguth, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
 Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.,
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 Sisson, I., Sodergren, E., Sonake, T., Sparks, A., Stanley, H.,
 Stone, H., Sutton, A., Svatek, A., Tabot, P., Tamerisa, A., Tamerisa, R.,
 Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, L.,
 Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R.,
 Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
 Wallington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S.,
 Morley, K., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G., and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 172269)
 Morley, K. C.
 Direct Submission
 Submitted (12-JUN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc.help@bcm.tmc.edu

 Project Information
 Center project name: GLAZ
 Center clone name: CH230-205114

 Summary Statistics
 Assembly program: Phrap; version 0.990329first call to
 findphraplist
 Consensus quality: 145908 bases at least Q40
 Consensus quality: 152564 bases at least Q30
 Consensus quality: 158487 bases at least Q20
 Estimated insert size: 150457; sum-of-coverage estimation
 Quality coverage: 0x in Q20 bases; agarose-gel estimation
 Quality coverage: 2.7x in Q20 bases; sum-of-coverage estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 54 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 1 7929: contig of 7929 bp in length
 * 7930 8029: gap of unknown length
 * 8030 15875: contig of 7846 bp in length
 * 15876 15975: gap of unknown length
 * 15976 22987: contig of 7012 bp in length
 * 22988 23088: gap of unknown length
 * 23088 29199: contig of 6112 bp in length
 * 29200 29239: gap of unknown length
 * 29239 34852: contig of 5553 bp in length
 * 34853 34952: gap of unknown length
 * 34953 41848: contig of 6896 bp in length
 * 41849 41948: gap of unknown length
 * 41949 47070: contig of 5122 bp in length
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 * 47171 52475: contig of 5305 bp in length
 * 52476 52575: gap of unknown length
 * 52576 55243: contig of 2668 bp in length
 * 55244 55343: gap of unknown length
 * 55344 59535: contig of 4192 bp in length
 * 59536 59635: gap of unknown length
 * 59636 63660: contig of 4025 bp in length
 * 63661 63760: gap of unknown length
 * 63761 67569: contig of 3809 bp in length
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 * 72788: contig of 5119 bp in length

 * 72789 72888: gap of unknown length
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 * 88742 91375: contig of 2634 bp in length
 * 91376 91476: gap of unknown length
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 * 99063 99162: gap of unknown length
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 * 109903 110002: gap of unknown length
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 * 121002 123643: contig of 2642 bp in length
 * 123644 123744: gap of unknown length
 * 123744 125267: contig of 1524 bp in length
 * 125268 125367: gap of unknown length
 * 125368 128094: contig of 2727 bp in length
 * 128095 128194: gap of unknown length
 * 128195 132125: contig of 3931 bp in length
 * 132126 132225: gap of unknown length
 * 132226 135571: contig of 3346 bp in length
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 * 143066 143165: gap of unknown length
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 * 145248 145347: gap of unknown length
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 * 161697 163409: contig of 1713 bp in length
 * 163410 163509: gap of unknown length
 * 163510 164698: contig of 1189 bp in length
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 * 166168 166267: gap of unknown length

FEATURES
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Location/Qualifiers
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/clone="CH230-205114"

BASE COUNT
48455 a 35040 c 34181 g 49053 t 5540 others

Query Match
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 aactacctaagactatct 20
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Db 121229 AACTACTTAAGACTATCT 121211

RESULT 13
AC093360
LOCUS
DEFINITION
AC093360
AC093360
AC093360.1 GI:15213905
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP;
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 245997)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
2 (bases 1 to 245997)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhalter,B.,
Brown,A., Camarata,J., Campoliano,A., Chang,J., Chazaro,B.,
Chopel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Coyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heatford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., Lacroque,K.,
Lamezas,R., Landers,T., Lehoczy,J., Levine,N., Matthews,C.,
Maclean,C., Macdonald,P., Major,J., Marguis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheters,R., Meldrum,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Piere,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Roselli,M., Roy,A., Santos,R., Schauer,S., Schnupack,R.,
Seaman,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Teffaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL
COMMENT
Submitted (20-AUG-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR

Web site: http://www-seg.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L14296
Center clone name: 57_F_18
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 242847 bases at least Q40
Consensus quality: 244315 bases at least Q30
Consensus quality: 244906 bases at least Q20
Insert size: 25000; agarose-fp
Insert size: 245397; sum-of-ctgigs
Quality coverage: 9.9 in Q20 bases; agarose-fp
Quality coverage: 10.1 in Q20 bases; sum-of-ctgigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 9445 13083: contig of 3639 bp in length
* 13084 13183: gap of 100 bp
* 13184 15745: contig of 2562 bp in length
* 15746 15845: gap of 100 bp
* 15846 20539: contig of 4694 bp in length
* 20540 20639: gap of 100 bp
* 20640 62896: contig of 42257 bp in length
* 62897 62996: gap of 100 bp
* 62997 193684: contig of 130688 bp in length
* 193685 193784: gap of 100 bp
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13184..15745
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20640..62896
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62997..193684
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BASE COUNT 73285 a 49514 c 49348 g 73250 t 600 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 aactacctaagactatct 20
|||||

Db 232480 AACTACTTAAGACTATCT 232498

RESULT 14
AY051836 1814 bp mRNA linear INV 27-AUG-2001
LOCUS Drosophila melanogaster LD33880 full length cDNA.
ACCESSION AY051836
VERSION AY051836.1 GI:15291982
KEYWORDS FLI,CDNA.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1814)
Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Carlson,J.,
Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R.,
Gonzalez,M., Guarin,H., Li,P., Liao,G., Miranda,A., Mungall,C.J.,
Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanavong,S., Wan,K.,
Yu,C., Lewis,S.E., Rubin,G.M. and Celniker,S.
JOURNAL Direct Submission
Submitted (10-AUG-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
COMMENT Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(http://fruitfly.berkeley.edu) or send email to
cdna@fruitfly.berkeley.edu.
FEATURES
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10..1746
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MTLWLTGPOPERPAVDLDPGCCPRFLDGMOCVADGLLVTATDMVLANAPRE
ACYKYGSVPLRMKCKHEKALILHICISHANRKYIIEPLISADFTIRITRYV
VGAQCKLSMSKQSWIYQCTGCEFTLQGLGTRPNTAQNPOOLKFGIPGPAVNSQ
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BASE COUNT 481 a 476 c 481 g 376 t

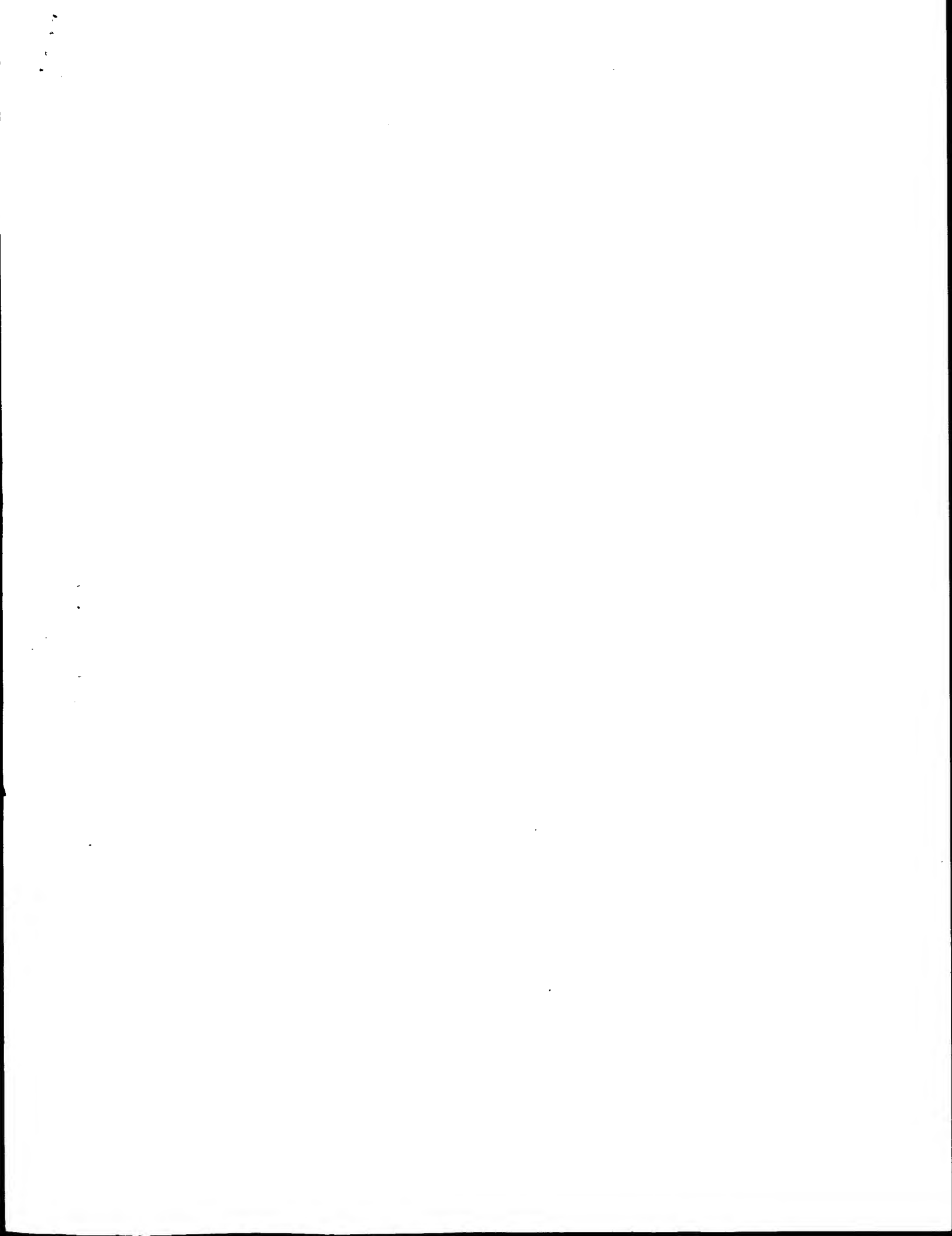
ORIGIN
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Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1585 AACTACCACAGAGCTATC 1603
RESULT 15
AC009214 154771 bp DNA linear INV 06-SEP-2001
LOCUS Drosophila melanogaster, chromosome 2L, region 33E-33F, BAC clone
DEFINITION BACRO5E09, complete sequence.
ACCESSION AC009214
VERSION AC009214.7 GI:15451504
KEYWORDS HTG.
SOURCE Drosophila melanogaster
fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 154771)
Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
Rogers,Y., An,H., Baldwin,D., Bazzon,J., Beeson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,
Fierreira,S., Frise,E., Galle,R.F., Gary,N.S., George,R.A.,
Gonzalez,M., Hovick,J., Hoskins,R.A., Hoslin,D., Howland,T.J.,
Idegian,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
Phouanavong,S., Piltman,G.S., Puri,V., Richards,S., Scheepler,F.,
Stapleton,M., Strong,R., Svitskas,R., Tector,C., Williams,S.M.,
Zaveri,D.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
JOURNAL Sequencing of Drosophila chromosome 2L, region 33E-33F
Unpublished
TITLE 2 (bases 1 to 154771)
JOURNAL Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazek,R.G.,
Butenhoft,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Houston,K.A., Humastli,S.R., Karra,K., Kearney,L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Svitskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
Rubin,G.M.
TITLE Direct Submission
JOURNAL Submitted (06-AUG-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
COMMENT On Sep 6, 2001 this sequence version replaced g1:13324753.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome
shotgun and from subclones of this BAC and its neighboring clones.
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruitfly.org/sequence/) or send email
to bdg@fruitfly.berkeley.edu.
location/qualifiers
1. 154771
/organism="Drosophila melanogaster"
/strain="y: cn bw sp"
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/chromosome="2L"
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/clone.lib="RPCT-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial ECORI in
pBACE3.6)"
BASE COUNT 47347 a 29741 c 30511 g 47172 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 3; Length 154771;
Best Local Similarity 94.7%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 aaactactaagaagctatc 19
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Db 663 AAACCTACCCCAAGAGCTATC 681

Search completed: September 7, 2002, 18:23:58
Job time: 28937 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 10:21:46 ; Search time 212.3 Seconds
(without alignments)
3716.320 Million cell updates/sec

Title: US-09-834-291-1
Perfect score: 3212
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/prodata/2/ina/5B.COMB.seq:*
- 3: /cgn2_6/prodata/2/ina/6A.COMB.seq:*
- 4: /cgn2_6/prodata/2/ina/6B.COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/PCTUS.COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length DB	ID	Description
1	252	7.8	2551	4 US-09-290-640-1	Sequence 1, Appl
2	226	7.0	2471	1 US-08-444-231-18	Sequence 18, Appl
3	226	7.0	2471	1 US-08-152-443A-18	Sequence 18, Appl
4	226	7.0	2534	2 US-08-219-237B-1	Sequence 1, Appl
5	226	7.0	2534	4 US-08-468-560C-1	Sequence 1, Appl
6	226	7.0	2534	4 US-09-180-100-16	Sequence 16, Appl
7	79.4	2.1	7218	1 US-08-232-463-14	Sequence 14, Appl
8	67.8	2.1	7218	1 US-08-232-463-14	Sequence 14, Appl
9	59.8	1.9	35100	1 US-08-306-691B-19	Sequence 19, Appl
10	59.8	1.9	35100	5 PCT-US93-06251-19	Sequence 19, Appl
11	57	1.8	857	5 PCT-US95-17083-9	Sequence 9, Appl
12	57	1.8	920	5 PCT-US95-17083-7	Sequence 9, Appl
13	57	1.8	920	5 PCT-US95-17083-5	Sequence 9, Appl
14	57	1.8	1104	5 PCT-US95-17083-3	Sequence 3, Appl
15	57	1.8	1167	5 PCT-US95-17083-1	Sequence 1, Appl
16	51.6	1.6	556	4 US-09-018-584A-25	Sequence 25, Appl
17	50.8	1.6	370	2 US-08-332-766A-8	Sequence 8, Appl
18	50	1.6	376	2 US-08-623-906A-18	Sequence 18, Appl
19	49.8	1.6	5751	4 US-09-417-455-7	Sequence 7, Appl
20	49.2	1.5	361	4 US-09-348-942-7	Sequence 7, Appl
21	49.2	1.5	361	4 US-09-018-584A-9	Sequence 9, Appl
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23	48.4	1.5	15144	3 US-08-458-434A-6	Sequence 6, Appl
24	48	1.5	421	1 US-08-480-784-24	Sequence 24, Appl
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29	48	1.5	421	4 US-08-850-727-24	Sequence 24, Appl
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32	48	1.5	421	5 PCT-US95-10220-24	Sequence 2, Appl
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36	47.4	1.5	1679	4 US-08-880-342-11	Sequence 11, Appl
37	47.4	1.5	12141	4 US-09-488-671-10	Sequence 10, Appl
38	47.4	1.5	80246	4 US-09-078-294-4	Sequence 3, Appl
39	47.4	1.5	80595	4 US-09-078-294-3	Sequence 8, Appl
40	47.2	1.5	295	4 US-08-332-766A-11	Sequence 11, Appl
41	47.2	1.5	325	2 US-08-332-766A-11	Sequence 26, Appl
42	47.2	1.5	446	2 US-08-332-766A-26	Sequence 10, Appl
43	46.8	1.5	444	4 US-09-018-584A-19	Sequence 19, Appl
44	46.6	1.5	444	4 US-09-018-584A-19	Sequence 13, Appl
45	45.6	1.4	388	2 US-08-623-906A-13	

ALIGNMENTS

RESULT 1
US-09-290-640-1
Sequence 1, Application US/09290640
Patent No. 6204055
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2551
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (221)..(1228)
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 267
ISSUE: 15
PAGES: 10709-10715
DATE: 1992-05-25
DATABASE ACCESSION NUMBER: X63717/Genbank
DATABASE ENTRY DATE: 1996-07-19
US-09-290-640-1

Query Match 7.8%; Score 252; DB 4; Length 2551;
Best Local Similarity 100.0%; Pred. No. 5.9e-60;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-08-444-231-18
; Sequence 18, Application US/08444231
; Patent No. 5652210
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: SHAPIRO, JOHN P.
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,231
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/152,443
; FILING DATE: 15-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20006.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 195..1136
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 243
; US-08-444-231-18

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Db 121 CTCGCCGGGGTGTGTGAGACCCGCTCAGTACGAGAGTTGGGGAAGCTCTTTCATCTCGAGG 180
OY 2213 atgtctaacacacatgctggcctcctgacccctcctactctgt 2258
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RESULT 3

US-08-152-443A-18
; Sequence 18, Application US/08152443A
; Patent No. 5663070
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: SHAPIRO, JOHN P.
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,443A
; FILING DATE: 15-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20006.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 195..1136
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 243
; US-08-152-443A-18

Query Match 7.0%; Score 226; DB 1; Length 2471;
Best Local Similarity 100.0%; Pred. No. 9.9e-53;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 2153 ctccgggggttggtgagcccgctcagtaaggaagcttcaacttcgagag 2212
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QY 2213 attgctcaaacaccatctggtgacatctgagaccctcactctgt 2258
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 Db 181 ATTGCTCAACACCATGCTGGGATCTGGACCTCTACCTCTGCT 226

RESULT 4

US-08-219-237B-1
 ; Sequence 1, Application US/08219237B
 ; Patent No. 5874546
 ; GENERAL INFORMATION:
 ; APPLICANT: NAGATA, Shigekazu
 ; APPLICANT: ITOH, Naoto
 ; APPLICANT: YONEHARA, Shin
 ; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: James W. Hellwege
 ; STREET: P.O. Box 2266 Eads Station
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/219,237B
 ; FILING DATE: 28-MAR-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/872,129
 ; FILING DATE: 22-APR-1992
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: James W. Hellwege
 ; REGISTRATION NUMBER: 28,808
 ; REFERENCE/DOCKET NUMBER: 516762
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2534 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; IMMEDIATE SOURCE:
 ; LIBRARY: pCEV4
 ; CLONE: clone pF58
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 195..1202
 ; IDENTIFICATION METHOD: by similarity with known sequence or
 ; IDENTIFICATION METHOD: to an established consensus
 ; FEATURE:
 ; NAME/KEY: sig_peptide
 ; LOCATION: 195..242
 ; IDENTIFICATION METHOD: by similarity with known sequence or
 ; IDENTIFICATION METHOD: to an established consensus
 ; FEATURE:
 ; NAME/KEY: mat_peptide
 ; LOCATION: 243..1199
 ; IDENTIFICATION METHOD: by similarity with known sequence or
 ; IDENTIFICATION METHOD: to an established consensus
 ; FEATURE:
 ; NAME/KEY: polyA_site
 ; LOCATION: 1831..1836
 ; IDENTIFICATION METHOD: by similarity with known sequence or
 ; IDENTIFICATION METHOD: to an established consensus
 ; FEATURE:
 ; NAME/KEY: polyA_site
 ; LOCATION: 1831..1836
 ; IDENTIFICATION METHOD: by similarity with known sequence or
 ; IDENTIFICATION METHOD: to an established consensus

LOCATION: 2352..2357
 ; IDENTIFICATION METHOD: by similarity with known sequence or
 ; IDENTIFICATION METHOD: to an established consensus
 ; FEATURE:
 ; NAME/KEY: polyA_site
 ; LOCATION: 2518..2523
 ; IDENTIFICATION METHOD: by similarity with known sequence or
 ; IDENTIFICATION METHOD: to an established consensus
 ; US-08-219-237B-1

Query Match 7.0%: Score 226; DB 2; Length 2534;
 Best Local Similarity 100.0%; Pred No. 1e-52;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 2093 ggcactgtgacgaggaacacacccctgaagcccttgctgctcccaagcgagctgctctt 2152
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 Db 61 GGCACGTGGCAGCGAACAACACCCCTGAGGCGCAGCCCTGCTGCCAGGCGGAGCTGCTCTT 120
 QY 2153 ccccccgggttggtgagcccgctcagtaagagtgagtgaggaagctcttactcggag 2212
 |||
 Db 121 CTCGCCGGGCTTGCTGACCCGCTCAGTACGAGTGGGGAAGCTCTTTCACCTTCCGAGG 180
 QY 2213 attgctcaaacaccatctggtgacatctgagaccctcactctgt 2258
 |||
 Db 181 ATTGCTCAACACCATGCTGGGATCTGGACCTCTACCTCTGCT 226

RESULT 5

US-08-468-560C-1
 ; Sequence 1, Application US/08468560C
 ; Patent No. 6270998
 ; GENERAL INFORMATION:
 ; APPLICANT: NAGATA, Shigekazu
 ; APPLICANT: ITOH, Naoto
 ; APPLICANT: YONEHARA, Shin
 ; TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
 ; TITLE OF INVENTION: ANTIGEN
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
 ; STREET: P.O. BOX 747
 ; CITY: FALLS CHURCH
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22040-0747
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/468,560C
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURPHY JR., GERALD M.
 ; REGISTRATION NUMBER: 28,977
 ; REFERENCE/DOCKET NUMBER: 20-4393P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-205-8000
 ; TELEFAX: 703-205-8050
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2534 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA

Db 1166 YY 1225
QY 514 aatgaagaatlaaagaagaatcacatagtcgtgcttataatcacac 573
Db 1226 YY 1285
QY 574 tcaagagatcgtatcttgcattgccttcccttcttctcttccctcc 633
Db 1286 YY 1345
QY 634 atctctctcccttactctctctctctctccctccaccccttctctctctt 693
Db 1346 YY 1405
QY 694 acatttttatttaaatgaacttcatcttggaatagtttagaattcaaaaatt 753
Db 1406 YY 1465
QY 754 gcaagagata 762
Db 1466 GCATAGATA 1474

RESULT 8

US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEITLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpc-Fls
US-08-232-463-14

Query Match 2.1%; Score 67.8; DB 1; Length 7218;
Best Local Similarity 8.2%; Pred. No. 2,1e-08;
Matches 36; Conservative 227; Mismatches 174; Indels 0; Gaps 0;

QY 806 ttgtgtctatgtatgacgtcagagtggtgtcacaaagctgcagccaggtctctc 865
Db 1442 TTTGGTACRR 1363
QY 866 atggcactaacagcttactactaaagtggaacagagaacgttacaacactacaagc 925
Db 1382 RRR 1323
QY 926 tgggtgaagtcagtcagatgcacaacacaggggtgtaggaagccctcagaaggt 985
Db 1322 RRR 1263
QY 986 acctaacctagattttagggcccaacaggtcccaagaaatgcaactagaaggaagc 1045
Db 1262 RRR 1203
QY 1046 ctgaagatgaacagtcggtcgaagaaaggttataatgttataatgttgatc 1105
Db 1202 RRR 1143
QY 1106 taattgggaaggaagaggttcagagtcagatgcagagcttgtagagatccaaag 1165
Db 1142 RRR 1083
QY 1166 gaatactgaacctttagtctgctcagtcggaactcatccaatcaggtcagta 1225
Db 1082 RRR 1023
QY 1226 gatgcattatccaac 1242
Db 1022 GTGAGCGTATGCCAAC 1006

RESULT 9

US-08-306-691B-19
Sequence 19, Application US/0830691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorina & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383

```

:
: TELFAX: (215) 568-5549
:
: TELE: No. 574039e
:
: INFORMATION FOR SEQ ID NO: 19
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 35100 base pairs
:
: TYPE: nucleic acid
:
: STRANDEDNESS: double
:
: TOPOLOGY: linear
:
:
: US-08-306-691B-19

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Query Match	1.9%	Score 59.8;	DB 1;	Length 35100;
Best Local Similarity	55.6%	Pred. No. 1e-05;		
Matches 115; Conservative	0;	Mismatches 92;	Indels 0;	Gaps 0;

Qy	534	gaagatccacataatgagttgttgctataattcaacacaaagaataactgattttgt	593
Db	3806	gaggtttgcagtagtgaactgagatcagccactgacactcagcctaaaggcacaagagaaagact	3865
Qy	594	caattgcctttcccccctttttctctctccctccctccatccctctctcccttaacct	653
Db	3866	ccatccctccctccctttctttcttcttccctccctccctccctctctctctctctctcc	3922
Qy	654	tccttctccttccctcaacacccctttctcctcctcttttaacatttttaataatga	713
Db	3936	ttcccttccctccctccctccctcttcttcttcttcttcttcttcttcttcttcttcttct	3985
Qy	714	actctcatcttgaataattaga	740
Db	3986	ttctttctttttttctttctttttgaga	4012

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RESULT 10
PCT-US93-06251-19
: Sequence 19, Application PC/TUS9306251
: GENERAL INFORMATION:
: APPLICANT: WICKSTROM, Eric and Rife, Jason P.
: TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
: TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
: NUMBER OF SEQUENCES: 93
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
: STREET: 400 Garden City Plaza
: CITY: Garden City
: STATE: NY
: COUNTRY: USA
: ZIP: 11530
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/06251
: FILING DATE: 19930630
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: DiGiglio, Frank S.
: REGISTRATION NUMBER: 31,346
: REFERENCE/DOCKET NUMBER: 8586
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 516-742-4343
: TELEFAX: 516-742-4366
: TELEX: 230 901 SANS UR
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 35100 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-19

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Query Match	1.9%	Score 59.8;	DB 5;	Length 35100;
Best Local Similarity	55.6%;	Pred. No. 1e-05;		
Matches 115;	Conservative 0;	Mismatches 92;	Indels 0;	Gaps 0;

QY 534 gaatatcaactatgtagtgcgcgttaataactaactaagaagtaacgatttgt 593

Db 3806 GAGTTGCAGAGAGACTAAGTTCATGCCACATCGCACTCCAGGCTTAGGGACAGACAGACT 3865

QY 594 caattgctcttcgccctttttctctctctacccttccttcacactcctctccctacelc 653

Db 3866 CCACTCTCTCTTCCTTTCTTCTCTCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 3925

QY 654 tcccttccttcctcccaaaccccttctcctcctctctctttaaatttttaataaaga 713

Db 3926 TTCCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 3985

QY 714 actttcaatttgaatagatttaaga 740

Db 3986 TTCTTTCTTTTCTATCTTTTGAAA 4012

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RESULT 11
PCT-US95-17083-9
: Sequence 9 Application PC/TUS9517083
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGENE
: NUMBER OF SEQUENCES: 16
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/17083
: FILING DATE: CONCURRENTLY HERewith
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/371,263
: FILING DATE: 23-DEC-1994
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 857 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: PCT-US95-17083-9

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Query Match	1.8%;	Score 57;	DB 5;	Length 857;
Best Local Similarity	100.0%;	Pred. No. 5.3e-06;		
Matches 57; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

QY	2202	cactctcgaggaattgtcctaacaacacatgctggcatctgaccctctacctcgtt	2258
Db	1	CACCTCGAGGATTTGTCAACAACCATGCTGGCATCTGCACCCTTCCTAACCTTGGT	57

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12 RESULT
13 PCT-US95-17083-7
14 : Sequence 7, Application PC/TUS9517083
15 : GENERAL INFORMATION:
16 : APPLICANT:
17 : TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
18 : NUMBER OF SEQUENCES: 16
19 : CURRENT APPLICATION DATA:
20 : APPLICATION NUMBER: PCT/US95/17083
21 : FILING DATE: CONCURRENTLY HERewith
22 : CLASSIFICATION:
23 : PRIOR APPLICATION DATA:
24 : APPLICATION NUMBER: USSN 08/371,263
25 : FILING DATE: 23-DEC-1994
26 : INFORMATION FOR SEQ ID NO: 7:
27 : SEQUENCE CHARACTERISTICS:
28 : LENGTH: 920 base pairs
29 : TYPE: nucleic acid
30 : STRANDEDNESS: single

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TOPOLOGY: linear
PCT-US95-17083-7

Query Match
Best Local Similarity 100.0%; Score 57; DB 5; Length 920;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2202 cactcgagagattgtctcaacaacatgctgggcatctgagacctctactctgt 2258
DB 1 CACTTCGAGAGATTGCTCAACAACATGCTGGGCATCTGAGACCCCTACTCTGTGT 57

RESULT 13
PCT-US95-17083-5
; Sequence 5, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17083
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 975 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-17083-5

Query Match
Best Local Similarity 100.0%; Score 57; DB 5; Length 975;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2202 cactcgagagattgtctcaacaacatgctgggcatctgagacctctactctgt 2258
DB 1 CACTTCGAGAGATTGCTCAACAACATGCTGGGCATCTGAGACCCCTACTCTGTGT 57

RESULT 14
PCT-US95-17083-3
; Sequence 3, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17083
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1104 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-17083-3

Query Match
Best Local Similarity 100.0%; Score 57; DB 5; Length 1104;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2202 cactcgagagattgtctcaacaacatgctgggcatctgagacctctactctgt 2258

DB 1 CACTTCGAGAGATTGCTCAACAACATGCTGGGCATCTGAGACCCCTACTCTGTGT 57

RESULT 15
PCT-US95-17083-1
; Sequence 1, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17083
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1167 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-17083-1

Query Match
Best Local Similarity 100.0%; Score 57; DB 5; Length 1167;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2202 cactcgagagattgtctcaacaacatgctgggcatctgagacctctactctgt 2258
DB 1 CACTTCGAGAGATTGCTCAACAACATGCTGGGCATCTGAGACCCCTACTCTGTGT 57

Search completed: September 7, 2002, 18:21:05
Job time: 28759 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 10:21:46 ; Search time 13836.9 Seconds
(without alignments)
5022.158 Million cell updates/sec

Title: US-09-834-291-1
Perfect score: 3212
Sequence: 1 tgcagactcgaagaataty.....ttgcagatgcgtaacaaag 3212

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues 43959072

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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Result No.	Score	Query	Match Length	ID	Description
1	3212	100.0	3212	US-09-834-291-1	Sequence 1, Appl1
2	3193	99.4	45121	US-09-997-722-10	Sequence 10, Appl1
3	2346.6	73.1	2827	US-09-834-291-4	Sequence 4, Appl1
4	2143.4	66.7	2165	US-09-665-6118-94	Sequence 94, Appl1
5	2143.4	66.7	2165	US-09-802-669-94	Sequence 94, Appl1
6	1899.6	59.1	2880	US-09-834-291-3	Sequence 3, Appl1
7	1536.8	47.8	1608	US-08-377-522-1	Sequence 1, Appl1
8	1536.8	47.8	1608	US-08-377-522C-1	Sequence 1, Appl1
9	1536.8	47.8	1608	US-08-377-522C-1	Sequence 1, Appl1
10	799.8	24.9	3814	US-09-324-185-29531	Sequence 29531, A
11	713	22.2	720	US-09-834-291-2	Sequence 2, Appl1
12	424.2	13.2	449	US-09-404-284-674	Sequence 674, App
13	424.2	13.2	449	US-09-524-038-674	Sequence 674, App
14	387.4	12.1	1368	US-09-324-185-9888	Sequence 9888, App
15	367.8	11.5	1732	US-09-644-861-7725	Sequence 7725, App
16	367.8	11.5	1732	US-09-652-911-10283	Sequence 10283, A
17	336.2	10.5	495	US-09-652-911-4924	Sequence 4924, Ap
18	336.2	10.5	2871	US-09-652-124-8816	Sequence 8816, Ap
19	336.2	10.5	2871	US-09-717-350-4929	Sequence 4929, Ap
20	336.2	10.5	2871	US-09-726-172-2083	Sequence 2083, Ap
21	336.2	10.5	2871	US-09-726-175-3031	Sequence 3031, Ap
22	336.2	10.5	2871	US-09-726-788-5939	Sequence 5939, Ap
23	336.2	10.5	2871	US-09-726-810-2456	Sequence 2456, Ap
24	334.4	10.4	772	US-09-760-455-21	Sequence 21, App
25	334.4	10.4	772	US-09-760-485-327	Sequence 327, App
26	331.4	10.3	2641	US-09-172-373-15844	Sequence 15844, A
27	331.4	10.3	2641	US-09-213-360-1236	Sequence 1236, Ap
28	330.8	10.3	575	US-09-471-275-3315	Sequence 3315, Ap
29	327.4	10.2	458	US-09-306-350A-14682	Sequence 14682, A
30	327.4	10.2	458	US-09-909-629-14682	Sequence 14682, A
31	309.6	9.6	428	US-09-287-618-11167	Sequence 11167, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C	32	301.2	9.4	2760	25	US-09-644-869-8181	Sequence 8181, Ap
C	33	301.2	9.4	2760	25	US-09-652-124-8055	Sequence 8055, Ap
C	34	301.2	9.4	2760	25	US-09-652-127-7930	Sequence 7930, Ap
C	35	301.2	9.4	2760	25	US-09-652-816-7672	Sequence 7672, Ap
C	36	301.2	9.4	2760	25	US-09-652-911-8889	Sequence 8889, Ap
C	37	300.6	9.4	419	18	US-09-943-143-818	Sequence 818, App
C	38	300.6	9.4	419	18	US-09-943-143-818	Sequence 818, App
C	39	293.4	9.1	404	17	US-09-362-510-3927	Sequence 3927, Ap
C	40	293.4	9.1	404	17	US-09-362-510-3927	Sequence 3927, Ap
C	41	293.4	9.1	404	17	US-09-362-510-3927	Sequence 3927, Ap
C	42	292.8	9.1	1655	56	US-60-172-373-10224	Sequence 10224, A
C	43	289.8	9.0	467	56	US-60-172-360-3705	Sequence 3705, App
C	44	287.4	8.9	859	1	PCT-US00-05883-187	Sequence 187, App
C	45	287.4	8.9	859	34	US-09-925-299-187	Sequence 187, App

ALIGNMENTS

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RESULT 1
US-09-834-291-1
; Sequence 1, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Kramer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834, 291
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3212
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-1

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Query Match 100.0%; Score 3212; DB 32; Length 3212;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	tttcccgagacacagagcttcatctggttcatcacaatagattcttcaaggattcca	120
QY	121	aaggcaagaagtttggggaacagatataataattcccaaccccttgaaatgacatc	180
DB	121	aaggcaagaagtttggggaacagatataataattcccaaccccttgaaatgacatc	180
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DB	181	taaggccctcagaagtttggatgaagaagtttcaaatgaagaatgaaccagaatttt	240
QY	241	ctaagattatttgacatgaacataatgtctcccaagaacacatatctctctcctt	300
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QY	301	gaacttgaggaatgaactgaactggtgtaagggttaagggaagggtgataatgacata	360
DB	301	gaacttgaggaatgaactgaactggtgtaagggttaagggaagggtgataatgacata	360
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RESULT 2
 US-09-997-722-10
 ; Sequence 10, Application US/09997722
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, David
 ; APPLICANT: Engelhard, Eric
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
 ; FILE REFERENCE: A-71171/RMS/DCF
 ; CURRENT APPLICATION NUMBER: US/09/997, 722
 ; CURRENT FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: US 09/747, 377
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: US 09/798, 586
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 301
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 45121
 ; TYPE: DNA
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 US-09-997-722-10

Query Match 99.4%; Score 3193; DB 36; Length 45121;
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QY	1200	ctgcatcccaaatccaggttccagtaatgtatgcattatccaaacataccttctgttaaat	1255
Db	1201	ctgcatcccaaatccaggttccagtaatgtatgcattatccaaacataccttctgttaaat	1260
QY	1260	catgctaaactatacttaagagctatctctccgttccaaagcaaatgaagctttgaaacagtc	1311
Db	1261	catgctaaactatacttaagagctatctctccgttccaaagcaaatgaatgttgaacagagtc	1320
QY	1320	tcaaccagacacgaagaagaatttacaagaattttttttaaagaanaatttggccagaaatat	1375
Db	1321	tcaaccagacacgaagaagaatttacaagaattttttttaaagaanaatttggccagaaatat	1381
QY	1380	gaagtaacgaagaagacagaagaatgaattgtgaattttaaataagcttgggctatgagatttg	1435
Db	1381	gaagtaacgaagaagacagaagaatgaattgtgaattttaaataagcttgggctatgagatttg	1440
QY	1440	gcttaagttgttagagttgtgttctcccttgaagaataaatacagaagggtccctccctt	1495
Db	1441	gcttaagttgttagagttgtgttctcccttgaagaataaatacagaagggtccctccctt	1500
QY	1500	cagagcctatgtgccaacacatctgtatcttcttaatagtttaactgttccattccagaac	1555
Db	1501	cagagcctatgtgccaacacatctgtatcttcttaatagtttaactgttccattccagaac	1560
QY	1560	gtctgtgagcctctcatgttgcaagccacaacatlgagacagcccaatgcacatgccccgaag	1611
Db	1561	gtctgtgagcctctcatgttgcaagccacaacatlgagacagcccaatgcacatgccccgaag	1620
QY	1620	tctttctcctcgaattgactccaagaatttagccaagagctctgttaccagagcagacctctgc	1679
Db	1621	tctttctcctcgaattgactccaagaatttagccaagagctctgttaccagagcagacctctgc	1680
QY	1680	gctcagagcttccattctcttccaagagcttcccaacttcccaaggttgaactataagcagaa	1739
Db	1681	gctcagagcttccattctcttccaagagcttcccaacttcccaaggttgaactataagcagaa	1740
QY	1740	gacctttagaaaggcagagagccggtctcagagttctcaccctgaagtgcagatgcagcagc	1799
Db	1741	gacctttagaaaggcagagagccggtctcagagttctcaccctgaagtgcagatgcagcagc	1800
QY	1800	cactgcagagaaagcccccggagacagaaatgcccattgtgtgcaacgaacctgtactcttcc	1859

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Db	2548	gcctgtctccctctccgggaattctctctcttaagaactgtaagtcgtctgcctgaagtgtt	2607
QY	3000	catttgtttgtttcttcgtccctctctctctctctctcttttgcccttcttaagctgaact	3059
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QY	3060	ccatgtgtatcttctgtgtgctcctctgtctgggtgtgtgtaactgtttccacgcgcacag	3119
Db	2668	ccatgtgtatcttctgtgtgctcctctgtctgggtgtgtgtaactgtttccacgcgcacag	2727
QY	3120	aaccggcgccctattattgccaagaactgtagcagcctgtttgaaagtcctcgct	3179
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QY	3180	cagaaatgcagcgtctgcagatgctaatcaag	3212
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RESULT 4			
US-09-665-615B-94			
; Sequence 94, Application US/09665615B			
; GENERAL INFORMATION:			
; APPLICANT: Dean, Nicholas M.			
; APPLICANT: Marcusson, Eric G.			
; APPLICANT: Wylet, Jacqueline			
; TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling			
; FILE REFERENCE: ISPH-0502			
; CURRENT APPLICATION NUMBER: US/09/665,615B			
; PRIOR APPLICATION NUMBER: US 09/290,640			
; PRIOR FILING DATE: 1999-04-12			
; NUMBER OF SEQ ID NOS: 179			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 94			
; LENGTH: 2165			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1782)...(1813)			
; US-09-665-615B-94			
Query Match 66.7%; Score 2143.4; DB 26; Length 2165;			
Best Local Similarity 99.7%; Pred. No. 0;			
Matches 2158; Conservative 0; Mismatches 6; Indels 1; Gaps 1.			
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QY	507	gggcataatgatagtatataagtaaggaagtcacaatagtgtgtgctgctatata	566
Db	61	gggcataatgatagtatataagtaaggaagtcacaatagtgtgtgctgctatata	120
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QY	687	tctttttaatttttttatttaataagaaatttcaatttttggaatgatttagattcaa	746
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QY	747	aaaatttgcagaaataatacagaaatgcccataatacgaatccctcccttaaccacattctt	806

D	b	301	aaaatlgaagagataaatacagaatgcccataataccatcccttaaccctctctt	360
Q	y	807	ttgtgtctctatagatgctcagaagtggtgtgcacaagaagcttgcacgcccagggtctctccca	866
D	b	361	ttgtgtctctatagatgctcagaagtggtgtgcacaagaagcttgcacacccagggtcttccctca	420
Q	y	867	tggcactaagactactatctyaaaaggtgtgaaacagagacagaagctatacaacactcaagact	926
D	b	421	tggcactaagactactactctyaaaaggtgtgaaacagagacagaagctatacaacactcaagact	480
Q	y	927	ggtgtgaagtgtcagtgacagcagatgtcacaacacaggggtgtagtggaaagccctcagaagggtaa	986
D	b	481	ggtgtgaagtgtcagtgacagcagatgtcacaacacaggggtgtagtggaaagccctcagaagggttaa	540
Q	y	987	cctaaccctgattttagagggccc-aacagagctcccaagagaagaaatgtcacaactyaaaggaagc	1045
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Q	y	1046	cctgaagagatgaacaagtgtggcctlaagcaaaaggtattataatgtgtataatlaabtggttgaatc	1105
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Q	y	1106	taattvggagaaggagagagagtgacagagtgtgaagtgtcagaagcttgggtgtgaaagatgtccaaag	1165
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Q	y	1166	gaatactgaacaactttaagtggtgtgtccaggtctcggagacagatcccaaatccaagttccaagat	1225
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Q	y	1226	gatlgtcattatcccaacaacatacctctcgtlaaaattcatagtcaaacactcaagactaagactatct	1285
D	b	781	gatlgtcattatcccaacaacatacctctcgtlaaaattcatagtcaaacactcaagactaagactatct	840
Q	y	1286	accggtccsaagaacatagtgactttgaaacagtggttcaacagacagaaagaaattataaag	1345
D	b	841	accggtccsaagaacatagtgactttgaaacagtggttcaacagacagaaagaaattataaag	900
Q	y	1346	attttttttaagaagaaatttggccsaagaaataatgtgaacaggaagcaagaaataatgt	1405
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Q	y	1406	tgaatgtttaataataagctcgggggtcataagcagatttggccttaagttgttagccttgttccct	1465
D	b	961	tgaatgtttaataataagctcgggggtcataagcagatttggccttaagttgttagccttgttccct	1020
Q	y	1466	cttgagaataataaaactaagaaggggccctcccttccagagcccttaatgtggcacaactctgtca	1525
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Q	y	1526	ctttttcataatggtttacgttgcattctccagaaagcgtctgtgagacccttcagttgttcagacc	1585
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Q	y	1766	tctcgaaggtcctcaacctgaagaatgagcaatgccaagccacatgcaagaagcccccggagacaaga	1825
D	b	1321	tctcgaaggtcctcaacctgaagaatgagcaatgccaagccacatgcaagaagcccccggagacaaga	1380
Q	y	1826	atgcacattgtgtgcaagaaacccctgaactctctccaaacctgacttctccctccctac	1885

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 Db 1381 atgcccattgttgaagaacccctgactccttccacactgacttccctccctccac 1440
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 Db 1501 gaagcttccctccatcctcctgacacacggggttctcgtgagctgtctctgactcg 1560
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 Db 1561 cgcagaaggtacacacaggtgttcaagaacgcttctgggaggttggggaagcggttacc 1620
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 RESULT 6
 US-09-834-291-3
 ; Sequence 3. Application US/09834291
 ; GENERAL INFORMATION:
 ; APPLICANT: Krammer, Peter
 ; APPLICANT: Muller-Schilling, Martina
 ; APPLICANT: Oren, Moshe
 ; TITLE OF INVENTION: p53 Binding Areas
 ; FILE REFERENCE: 4121-122
 ; CURRENT APPLICATION NUMBER: US/09/834,291
 ; CURRENT FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: PCT/DE99/03343
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: DE 198 47 779.1
 ; PRIOR FILING DATE: 1998-10-16
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 3
 ; LENGTH: 2380
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; US-09-834-291-3

 Query Match 59.1%; Score 1899.6; DB 32; Length 2380;
 Best Local Similarity 84.9%; Pred. No. 0;
 Matches 2348; Conservative 0; Mismatches 24; Indels 394; Gaps 4;

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QY 2007 gcaagatggaacacacagatgttccaagaacgctctctgtggaatgaggaagcgtttaca 2066
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QY 2247 cctacccctgtgtatccctctccctcccggtgtggaaggttaacccgtttagtccgggg 2306
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Db 1741 ----- 1740
QY 2307 ataggcaagtggtggcggtggcgagcggtgagatgtgagcggtgagcggtgagcggtgagcg 2366
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Db 1741 atgtgcaagtggtggcggtgagcggtgagatgtgagcggtgagcggtgagcggtgagcg 1765
QY 2367 ggcacccgtggagcggtggcggtgagcggtgagcggtgagcggtgagcggtgagcggtg 2426
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Db 1766 -----aa 1765
QY 2427 aggaactcctcccaagcccggtgtctcagaacgagtgaggaacttcttcttgggcct 2486
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Db 1766 ----- 1765
QY 2487 gatgcgaagtgtgatacccgctgtggcagggcgagctccggtcctccgagagacaa 2546
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QY 2547 tgggtcccaagtgtaagtggtggcggtggggcggaagatgtgaagcggaaagctgtgaa 2606
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Db 1766 -----aa 1767
QY 2607 gcttaaggtctgctgtggaaggggagcccggttggaagaggaagcgaactcctgtgagaacg 2666
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Db 1768 gcttaaggtctgctgtggaaggggagcccggttggaagaggaagcgaactcctgtgagaacg 1827
QY 2667 cctgacaagggccaagccaaggtccggtccggcggtgtggtgagtggtgagtggtgagtggt 2726
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Db 1828 cctgacaagggccaagccaaggtccggtccggcggtgtggtgagtggtgagtggtgagtggt 1887
QY 2727 gggggcggggaagagcctcaagcctcaagacacataatgtctcaatttctgtgaggttct 2786
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Db 1888 gggggcggggaagagcctcaagcctcaagacacataatgtctcaatttctgtgaggttct 1947
QY 2787 cagaacgtaagaaataagtcagacacgaagcagtggttaagccggaggggtcctgaaagaacg 2846
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Db 1948 cagaacgtaagaaataagtcagacacgaagcagtggttaagccggaggggtcctgaaagaacg 2007
QY 2847 gcaaccttctctctcogaanaagttataatgggggtgaaatgagctctgtgaggtctgtt 2906
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Db 2008 gcaaccttctctctcogaanaagttataatgggggtgaaatgagctctgtgaggtctgtt 2067
QY 2907 accgttttatgttacaagaagaagaagaactgtgtctgtctcctcccggaattcct 2966
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Db 2068 accgttttatgttacaagaagaagaagaactgtgtctgtctcctcccggaattcct 2127
QY 2967 ccttaagactgttaagtcgctgtgaggtgttcaattgtgttggtttctgcccctct 3026
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Db 2128 ccttaagactgttaagtcgctgtgaggtgttcaattgtgttggtttctgcccctct 2187
QY 3027 ctttctcttctgccccttcttaagcttgaaatcccaatgtgaattctgtgtgtctcgt 3086
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Db	2188	cttctctcttctgccccttcttcttagctgtacatcccatagtgatcttctgttgcctc	224
Qy	3087	cttgggcttggttgtactcgtctccacgcgcagacagaccggcgccctctatttggccaagaa	314
Db	2248	cttgggcttggttgtactcgtctccacgcgcagacagaccggcgccctctatttggccaagaa	230
Qy	3147	acttgagcagccctgttttggaaagctccctgcgtcagaaatgcagcttgcagatgctaa	320
Db	2308	acttgagcagccctgttttggaaagctccctgcgtcagaaatgcagcttgcagatgctaa	236
Qy	3207	tcaaaag 3212	
Db	2368	tcaaaag 2373	
RESULT 7			
US-08-377-522-1			
Sequence 1, Application US/08377522			
GENERAL INFORMATION:			
APPLICANT: Mountz, John D.			
APPLICANT: Liu, Changdan			
APPLICANT: Cheng, Jianhua			
APPLICANT: Koopman, William J.			
APPLICANT: Zhou, Tong			
TITLE OF INVENTION: Human Fas Gene Promoter Region			
NUMBER OF SEQUENCES: 2			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Arnold, White & Durkee			
STREET: P.O. Box 4433			
CITY: Houston			
STATE: Texas			
COUNTRY: US			
ZIP: 77210			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patentin Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/377,522			
FILING DATE: 20-JAN-1995			
CLASSIFICATION: 435			
ATTORNEY/AGENT INFORMATION:			
NAME: Setlich, Gary J.			
REGISTRATION NUMBER: 34,430			
REFERENCE/DOCKET NUMBER: UOAB:034/SER			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 512/418-3000			
TELEFAX: 512/474-7577			
TELEX: N/A			
INFORMATION FOR SEQ ID NO: 1:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 1608 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: DNA (genomic)			
FEATURE:			
NAME/KEY: CDS			
LOCATION: 1467..1496			
US-08-377-522-1			
Query Match			
Best Local Similarity 47.8%; Score 1536.8; DB 7; Length 1608;			
Matches 1582; Conservative 0; Mismatches 17; Indels 5; Gaps			
Qy	767	agagaatgcccataacatccctccatccaccctcttcttggctatgatgctca 826	
Db	7	ACAGAGGAGCCCTTACCATCCTTATCCCACTCTTTTGTGCTATTAGATGCTCA 66	
Qy	827	gagtgctgacacaaggctcggaagcccaaggctcttctctatgacataaagctactga 886	

Db	67	GAGTGTGGCAACAAAGGCTGGCGACGGCCAGGCGCTTCCTCATGTGGCCATACAGCTACTGA	126
QY	887	aagtgtagaagcagagcaagcgcctatcaaacccctcaaacgaacttggtgtraaatgcaagtacag	946
Db	127	AAGGTGGAACACAGACAAGCCCTATCAACACCTTCAAGACTGGTGGTAAGTCAGTACAG	186
QY	947	atgcaaacacacagggatgatatgaaagccctcaagaggtgtaacctaaactagattgagggc	1006
Db	187	ATGCAAACACACGGGTGATGGAAGGCCCTCAGAGGGGTAACTAACCTAGATTGAGGGC	246
QY	1007	cc-aacagagctccagaagaanaatlgtcaactgagaggaaagcctgaagatgacagtgggc	1065
Db	247	CCAAACAGGCTCCACAAGAAATGTCACTGAGAGGAAACCTGAAGATGAACAGTGGCG	306
QY	1066	taagaagaaggtatataatgattgatttaatggttgaaactciaatitgggaagggaagag	1125
Db	307	TAAGCAAAAGGTTATTAATGTATTATTAATGGTTAAATCTAATTTGGAGGGAGAGAGG	366
QY	1126	ttgcaagatgaaagtgcgaagccttggtgagcgaatgccaagaagtaactgaacctttagt	1185
Db	367	TTGCAGAGTGAAGCTGCAGAGCTTTGGTGGACGANTGCCAAAGAAATACTGAACCTTTAGTG	426
QY	1186	tgtccagctgtgaaactgcatccaanaatlccaggtcagtaatgaltgltcaatlacccaacata	1245
Db	427	TGTCCAGTGTGAACGTGCATCCCAAAATTCAGTTCACTAATGATGTCATATCCAAACATA	486
QY	1246	ccctctgtataaatcatgcttaaacctccaaagcctatctacccgttccaaagaactagtg	1305
Db	487	CCCTTGTAATAATTCATGTGTAACTACCTTAAGAGCTATCACGGTTCCAAAGCAATATGTG	546
QY	1306	actttgaaacagtggttcaacagagcaacgaagaattcaacgaatttttlltaagaanaat	1365
Db	547	ACTTTGAAACAGTGTTCACCAGACACGAAGAATTTACAGATTTTTTTTAAAGAAATTT	606
QY	1366	ggccaggaataatgaglaacgaagaagcaggaagtatgltgaatglttaataatgctgg	1425
Db	607	GGCCAGGAATATATGATGTAAACGAAGACAGGAAGTAAATTTGTAATGTTTAATATACGTG	666
QY	1426	ggctatgagatttgctctaagtgtgtaagcttggttttctcctctggagaataaaaaactaag	1485
Db	667	GGCTATGACATTTGGCTTTAAGTTGTTAGCTTTTTCCTTGAGAAATTAATAAATCTAAG	726
QY	1486	ggggccctccttltgaagccctatgaggcaacatcgtatccttltcatatgttlaactg	1545
Db	727	GGGGCCTCCTTTTCAGAGCCCTATGGCGCAACATCTGTACTTTTCATATGTTAGTACTG	786
QY	1546	tccattccagaaagctctgtgagcctctcaatglttgagccacaacaatgagcccaagc	1605
Db	787	TCCATTCCAGGAACGTCGTGAGACCTCTCATGTTGACGCCACAAGATGGACAGCCCACTG	846
QY	1606	aaatgcccgcgaagttcttctctgagtgactccagcaaatgaagcaagctccgttaccca	1665
Db	847	AAATGCCCCGCAAGTCTTTCTCTGAATGACTCCAGCAATTAAGCCAAAGCTCTGTACCA	906
QY	1666	ggcaggaaccttbgcgtcttgaagctcatcttccttcaagaccctccccaacttcccaagtt	1725
Db	907	GGAGGAACCTCTCGCTCTGAAGCTCATTTCTTCAAGACCTTCCCAACTTCCCAAGTT	966
QY	1726	gaactccagcagaagcctttagaagaaggcagagagccgggtctclogaggttccactgaa	1785
Db	967	GAACTACAGACGAAGGCTTTAGAAAGGCGAGAGGCCGGCTTCGAGGTCCTCACTGAA	1026
QY	1786	gtgagcatgcccagcaactgcaagaaagcccgaggaaacagaaatgcccattgtgtcaacgaa	1845
Db	1027	GTGAG-ATGCCACCACTGTCAGGAAGCCCGCGGACAGGAATGCCCATTTGTCAACGAA	1085
QY	1846	cttgagctcttcttaaccttgaagcttccacctccctacccggcggcagggcaagatgac	1905
Db	1086	CCCTGACTCCTTCTCAACCTGACTTCTCCCTCTTACCCTGGCCAGGCCAAGTTGC	1145
QY	1906	tgaatcatgagaccttcccaaacccggaggttccccagcagagcttcccttccatctc	1965
Db	1146	TGATTAATGAGACCTCCCAACCGGGGGTTCCCAAGGAGGCTTCCTTCCATCCTC	1205

QY 1966 ctgacacccggggtcttctgctgagctcgtctcgtatctcgcgcaagtgacacacaggt 2025
 Db 1206 ctgacacacccggggtcttctgctgagctcgtctcgtatctcgcgcaagtgacacacaggt 1265
 QY 2026 gtccaaagacgctcttcggggaagtgaggaagcggtttacagatgacttgctgagacgtc 2085
 Db 1266 gtccaaagacgctcttcggggaagtgaggaagcggtttacagatgacttgctgagacgtc 1325
 QY 2086 agggcgagcactgtgacaggaacacacacccctgagccctgagctcgcgcaagtgagacgt 2145
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 QY 2146 gacctcttcctccggggtgtgtgtgagccgctcagtgacgaggttgagggaagctcttcaact 2205
 Db 1386 gacctcttcctccggggtgtgtgtgagccgctcagtgacgaggttgagggaagctcttcaact 1445
 QY 2206 tggagagatgtctcaaac 2265
 Db 1446 tggagagatgtctcaaac 1505
 QY 2266 ctctctgccccgggttgagagcttaccctcttaagtcctccgggagatagcaaaagtggggcg 2325
 Db 1506 ctctctgccccgggttgagagcttaccctcttaagtcctccgggagatagcaaaagtggggcg 1565
 QY 2326 cgggggagcgctgctgaggttgctgagcgagcgagcgagcgagcgagcgagcgagcgagcg 2369
 Db 1566 cgggggagcgctgctgaggttgctgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 1606

RESULT 8

US-08-377-522C-1

Sequence 1, Application US/08377522C

GENERAL INFORMATION:

APPLICANT: Mounitz et al.

TITLE OF INVENTION: Human Fas Gene Promoter Region

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.

STREET: 8011 Candle Lane

CITY: Houston

STATE: TX

ZIP: 77071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch floppy

OPERATING SYSTEM: Macintosh

SOFTWARE: Microsoft Word for Macintosh

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08377,522C

FILING DATE: January 20, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benjamin Aaron Adler, Ph.D., J.D.

REGISTRATION NUMBER: 35,423

REFERENCE/DOCKET NUMBER: D5919

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 777-2321

TELEFAX: (713) 777-6908

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1608 bp

TYPE: nucleic acid

STRANDEDNESS: double-stranded

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

HYPOTHETICAL: no

ANTI-SENSE: no

FRAGMENT TYPE:

ORIGINAL SOURCE:
 ORGANISM: human
 TISSUE TYPE: placental
 IMMEDIATE SOURCE:
 LIBRARY: (FIXIT); EMBL-Spe/77
 CLONE: FIX1, FIX2, FIX3; EMBL1, EMBL2, EMBL3
 POSITION IN GENOME:
 FEATURE:
 PUBLICATION INFORMATION:
 US-08-377-522C-1

Query Match 47.8%; Score 1536.8; DB 7; Length 1608;
 Best Local Similarity 98.6%; Pred. No. 0;
 Matches 1582; Conservative 0; Mismatches 17; Indels 5; Gaps 3;

QY 767 agagaatgccatataccaatccctccttaaccactcttcttgctatgaatgctca 826
 Db 7 ACAGAGATGCCCTATACCAATCCCTTATCCCACTTCTTTTGTGCTATAGATGCTCA 66
 QY 827 gaagtgtgcaagaagctgagcagccagagcttctcctcaatgacataagctactga 886
 Db 67 GAGTGTGTGACAAAGGCTGTGGACGGCCAGGGTCTTCTCATAGGCACTTAACAGCTACTGA 126
 QY 887 aagtggaacagagaacagccctacaacacacacacacacacacacacacacacacacacac 946
 Db 127 AAGGTGGAACAGAGACAAAGCTATACACACCTACAAAGACTGTGTGTAAGTGCAGTACAG 186
 QY 947 atgcaaaacacagaggtgtatggaagccctcaggaaggttaacctagatttgaagcg 1006
 Db 187 ATGCAAAACACAGSGGTGTATGGAAGCCCTCAGAGAGGTAACCTAACCTAGATTGAGGCC 246
 QY 1007 cc-aacagctccagaagaagaatgtcactgtgaggaagcccggaaggtgaagaagcgagcg 1065
 Db 247 CCAAAAGAGCTCCAGAAAGAAATGTCAACTGAGAGAAACCTGTAAAGATGAACAGTGGCC 306
 QY 1066 taagcaaaagggttaataatggttaataatggttaataatggttaataatggttaataatg 1125
 Db 307 TAAGCAAAAGGCTTATTAATGTATTAATGATGATGATGATGATGATGATGATGATGATG 366
 QY 1126 ttgcaagtgaggtgagcaagcttggtgagcgtgccaagaagatactgaaccttaagt 1185
 Db 367 TTGCAAGTGAAGTGCACAGCTGGTGGACGATGGCAAGAAAGTAACCTTAACTGAGT 426
 QY 1186 tttccagcttggaactgcatccaatctcaaggttcaagtaatgagtcattatccaacata 1245
 Db 427 TGTCCAGCTGTGAAGTGCATCCAATTCAGGTTCAGTATGATGATGATGATGATGATGATG 486
 QY 1246 ccttcgttaaaatcaatgctaaactaaagatacttaacggttccaagaataagt 1305
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 QY 1306 acctgaacagtgctaccagaagacaggaagaataatgaagaattttttaaagaagaatt 1365
 Db 547 ACTTTGAACAGTGTTCACCAAGACGACGAAGAAATTAAGATTTTTTTTAAAGAAATTT 606
 QY 1366 gggcaggaataatgagtaagtaaggaaggaagaagaatgtaagttaatatagctg 1425
 Db 607 GGCAGGAATTAATGAGTAAGTAAGGAAGACAGGAAGTAATTTGTAAGTATAGCTGG 666
 QY 1426 ggcatacgatgtggttaagtgttagctgtttccctccttggaataaataaataag 1485
 Db 667 GGCATATCGATTGGCTTAATGCTTAACTGTTGTTTCTCTTGGAATTAATAAAGCTAAG 726
 QY 1486 gggccctccctttcagagccttctgagcaacacacacacacacacacacacacacacac 1545
 Db 727 GGGCCCTCCCTTTTCAAGGCCCTATGGGACACATGCTACTTTTCTATATGTTAACTGG 786
 QY 1546 tccattccagaagaagcttgtagccttcatgtgtgcaagcacaacatggaagcccaatc 1605
 Db 787 TCCATTCCAGGAAGCTGTGAGACCTCTCAAGTGTGCAAGCCCAAGATGAGACGCCCAATC 846
 QY 1606 aaatgccccgaagcttcttctctgagtgactcaagcaatgaagcaagcctctctgaacca 1665

Db	847	AATGCCCCGCAAGTCTTCTCTGAGTACTGCACCAATFAGCCAAAGGCTCTGACCCA	906
Qy	1666	ggcaggacctctgagctctgagctccatcttccttcaagacctcccaattcccaagtt	1725
Db	907	GGCAGGACCTCTGCGCTCTGACCTCCATCTCTTCAAGACCTCCCCCAACTCCAGATT	966
Qy	1726	gaacttcagcaagaagcctttagaaggagcaaggccgagctctgagttcctcaacttga	1785
Db	967	GAACCTACAGCAGAGACCTTTTAAAAAAGGCGAGAGAGCCGCGCTCTGAGTCTCTACCTGAA	1026
Qy	1786	gttagatcgtccagccactgtcaagaaacgcccggagcaagaatgccaattgttgaacgaa	1845
Db	1027	GTGAG-ATGCGAACCCACTGCAGGAAGCGCCCGGAGACAGAAATGCCATTGTGCAACGAA	1085
Qy	1846	ccctgagctcttcttcaacctgactttccctctcccttcaaccggcgagagccaaagtgc	1905
Db	1086	CCCTGACTCTTCTCTACCCCTGACTCTTCTCCCTCCCTCAACCGCGGACGCAAGATTGC	1145
Qy	1906	tgaatcaatgtagacccttccccaaccggcgctgtccccaagcagaggtttcccttccatccctc	1965
Db	1146	TGATCAATAGAGACCTCTCCCAACCGGGCGATTCCCAAGCGAGGCTCTTCCCATCTCTC	1205
Qy	1966	ctgacccaacggggacttttcgttagctcgtctccttgatctcgcgcgaagatgaaacagagt	2025
Db	1206	CTGACCAACCGGGGCTTTTGCTGAGCTCGTCTTGATCTGCGCCCAAGCTGACACACAGT	1265
Qy	2026	gttcaagaagcgtctctggaggatgaaggagacggtttacgaatgagcttggactggagcctc	2085
Db	1266	GTTCAAAGACGCTTCTGGGAGAGTGAAGGAAGCGGTTTACGAGATGACTTGGCTGGAGCTTC	1325
Qy	2086	aggaggcggacatgtgcacggaacaaccccttgagcccaagccttggtgtgccagcgagact	2145
Db	1326	AGGGGCGGCGACTGCGACGGAACACACCTGTAGAGGCGACGCTCGCTGCGCCACGCGAGACT	1385
Qy	2146	ggctcttctccggcggtttgtgtgaccgcgctgaagcagagtctggaggaaagctcttgaat	2205
Db	1386	GCCCTCTCTCCCGGGGTTGGTGGACCCGCTCAGTACGAGATTGGGAGAGCTCTTTCACT	1445
Qy	2206	tcggaagattgtcccaacaacaacatgctcgtggacatctggaacctctcaactctgtgtacct	2265
Db	1446	TGGAGGATTGTCAACAACACATGCTGGGACATGTGAGACCTCTCTACCTGTGGTAGCCCT	1505
Qy	2266	ctctctccgggtgtgagaggttaccgcgctttagtcccgaggatagcaaatgtgggcygg	2325
Db	1506	CTCTCGCCCGGGGTGGAGGCTTACCCGCTTGTAGTCCCGGGGATTAGGCAAAAGTGGGGCGGG	1565
Qy	2326	cgcggacgcgtctgagattgcggcgcaagcgcgacgcggagc 2369	
Db	1566	CGCGGGACG---GCGGGATTGCGCGCGGCGACGCGCACCGCGGGC 1606	
RESULT 9			
US-08-377-522D-1			
Sequence 1, Application US/08377522D			
GENERAL INFORMATION:			
APPLICANT: Mountz et al.			
TITLE OF INVENTION: Human Fas Gene Promoter Region			
NUMBER OF SEQUENCES: 27			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.			
STREET: 8011 Candle Lane			
CITY: Houston			
STATE: TX			
ZIP: 77071			
COUNTRY: USA			
COMPUTER READABLE FORM:			
MEDIUM TYPE: 3.5 inch floppy			
COMPUTER: Apple Macintosh			
OPERATING SYSTEM: Macintosh			
SOFTWARE: Microsoft Word for Macintosh			
CURRENT APPLICATION DATA:			
US/08/377,522D			

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? FILING DATE: January 20, 1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Benjamin Aaron Adler, Ph.D., J.D.
? REGISTRATION NUMBER: 35,423
? REFERENCE/DOCKET NUMBER: D5919
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (713) 777-2321
? TELEFAX: (713) 777-6908
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1608 bp
? TYPE: nucleic acid
? STRANDEDNESS: double-stranded
? TOPOLOGY: linear
? MOLECULE TYPE:
? DESCRIPTION: genomic DNA
? HYPOTHEITICAL: no
? ANTI-SENSE: no
? FRAGMENT TYPE:
? ORIGINAL SOURCE:
? ORGANISM: human
? TISSUE TYPE: placental
? IMMEDIATE SOURCE:
? LIBRARY: (FIXI); EMBL-SP6/77
? CLONE: FIX1, FIX2, FIX3; EMBL1, EMBL2, EMBL3
? POSITION IN GENOME:
? FEATURE:
? PUBLICATION INFORMATION:
US-08-377-522D-1

Query Match          47.8%; Score 1536.8; DB 7; Length 1608;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1582; Conservative 0; Mismatches 17; Indels 5; Gaps 3

QY      767 agagaatgcccatataccactcctccttaccacattcttttgtgtcattagatgctca 826
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DB       7 ACAGGATGGCCCTTAACCACTCCTCTTATCCCATCTTTTGTCATTGTGATGATCCTCA 66
QY      827 gagtgtygcacaagaagcgctggcacgcccgaagrgcttcctccatgacaaacagtctactga 886
        |||||||
DB      67 GAGTGTGTGCACAAGAAGCGCTGGCACGCCACAGGCTCTTCTCATGGCACTAACAGCTACTGA 126
QY      887 aaggtggacacagagacaagcctcatacaacacctacaagacttgtytgaatgycaglyaacg 946
        |||||||
DB     127 AAGGTGGAAACAAGACAAGCCTATCAACACCTAACAAGACTGGGHTGAAGTGCAGTAGACAG 186
QY     947 atgcaaaaacacagggtgtatgtgaagaagccctcagagggttaactaactagatttgaggcg 1006
        |||||||
DB     187 ATGCAAAAACACAGGGGTGAGTGAAGAACGCCCTCAGGAGGGTAACTTAACCTTGATTGAGGGC 246
QY    1007 cc-aacagcgctccagaagaanaaatgtcaactltgagaggaagccgtgaagaagtgaacagtgygc 1065
        |||||||
DB     247 CCAACACAGGCTCCAGAACAGAAATGTCAACTGAGAGSAAAGCCTGAAGATGAACAGTGGGCG 306
QY    1066 taagcaaaaggttatctaattgtttaaattgaggttgaatctaaattgaggaaaggagagag 1125
        |||||||
DB     307 TAAGCAAAGAGCTTATTAAATGCTGTTATTATAATGAGGTGAATCTAATTTGGAAAGGAGAGAGG 366
QY    1126 ttgcagagtggaagtgtagagagcttggtyggacagatlgccaagaagaaactgtaaacctttaagt 1185
        |||||||
DB     367 TTGCAAGAGTGAAGGTGACAGCTTTGGTGGACGATGCCAAAGGAATTAATGAAACCTTTTAACTG 426
QY    1186 tgtccagtgctggaactgca lccaattcaggttcagtaatgatlytcatlataccaacata 1245
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DB     427 TGTCCAGTGTGGAACGTGCATCCAAATTCAGGTTCAGTAAATGATGTATTAATCCAACATFA 486
QY    1246 ccttctgtataaattcatgtctaactccctaaagagctatctaccgttccaaagcaatagtg 1305
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Db 487 CCTTCTGTAATTCATGCTAACTACCTTAAGAGCTATCTACCGTTCCAAAGCAATAGTG 546
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 Db 547 ACTTGAACAGTGTTCACGAGACAGAAAGATTACAGATTTTTTTAAAGAAATT 606
 QY 1366 ggcgaagaaataatgagtaacagagacaggaagtaattgtgaatttaataatgctg 1425
 Db 607 GGCAGAGAAATATGATTAACGAAAGACAGAACTAATTGGAATGTTTATATAGCTGG 666
 QY 1426 ggcatacgagatttgagtaattgattgatttcttcccttgaagaataaataactag 1485
 Db 667 GGGTATGCGATTGGCTTAGTGTGTTGCTTTGTTCTTCTTGAAGATTAATAAGTAAG 726
 QY 1486 gggccctcccttccagagccttataggcgcaacatcgtacttcttataatgtaactg 1545
 Db 727 GGGCCCTCCCTTTTCAGAGCCCTATGCGCAACATCTGTACTTTTCATATAGGTTAATG 786
 QY 1546 tccattccagaaacgtctgtgagccttctatgttgcagcaacaatgagaccagtc 1605
 Db 787 TCCATTCCAGAAAGTCTGTGAGCCCTCTCATGTTGACGCAACAAAGATGAGACGCCAGTC 846
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 Db 1027 GTGAG-ATGCCAGCCACTGACAGAACGCCCGGAGACAGAAATCCCTTGTGCAAGAA 1085
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RESULT 10
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 ; Sequence 29531, Application US/60324185
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, MacDonald
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Diep, Dinh
 ; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
 ; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
 ; FILE REFERENCE: GX-0019-1 P
 ; CURRENT APPLICATION NUMBER: US/60/324,185
 ; NUMBER OF SEQ ID NOS: 35862
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 29531
 ; LENGTH: 3814
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; OTHER INFORMATION: Incyte ID No: 415714.1
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 Best Local Similarity 99.6%; Pred. No. 8,6e-163;
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Total number of hits satisfying chosen parameters: 4073328

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	3193	99.4	45121	US-10-035-832-1262	Sequence 1262, App
2	424.2	13.2	449	US-10-011-154-674	Sequence 674, App
3	334.4	10.4	772	US-10-211-364-477	Sequence 477, App
4	334.4	10.4	772	US-10-143-906-21	Sequence 21, App
5	252	7.8	2551	PCT-US02-10824-85	Sequence 85, App
6	252	7.8	2551	PCT-US02-25766-9394	Sequence 9394, App
7	252	7.8	2551	PCT-US02-10824-85	Sequence 1263, App
8	252	7.8	2551	US-10-007-926A-143	Sequence 143, App
9	226	7.0	2534	US-09-053-375B-233	Sequence 233, App
10	67.8	2.1	55966	US-10-035-832-1259	Sequence 1259, App
11	60.8	1.9	816	US-10-027-632-145670	Sequence 145670, App
12	60	1.9	2435	US-10-113-872-796	Sequence 796, App
13	60	1.9	2821	US-10-113-872-1669	Sequence 1669, App
14	59.2	1.8	542	US-10-027-632-91808	Sequence 91808, App
15	59.2	1.8	542	US-10-027-632-304597	Sequence 304597, App
16	59.2	1.8	639	US-10-027-632-134015	Sequence 134015, App
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18	59.2	1.8	639	US-10-027-632-134016	Sequence 134016, App
19	58	1.8	43599	PCT-US02-25766-10281	Sequence 10281, App
20	57.6	1.8	1350	US-10-011-154-201	Sequence 201, App
21	57	1.8	920	PCT-US02-25766-10795	Sequence 10795, App
22	56.2	1.7	975	US-09-954-531-998	Sequence 998, App
23	56.2	1.7	2892	PCT-US02-19457-103	Sequence 103, App
24	56.2	1.7	2892	US-10-175-523-103	Sequence 103, App
25	56	1.7	822	US-10-098-754-2303	Sequence 2303, App

26	55.8	1.7	1140	US-10-027-632-253750	Sequence 253750, App
27	55.8	1.7	1140	US-10-027-632-253751	Sequence 253751, App
28	55.2	1.7	443	US-10-027-632-64316	Sequence 64316, App
29	55.2	1.7	443	US-10-027-632-64317	Sequence 64317, App
30	55.2	1.7	443	US-10-027-632-296990	Sequence 296990, App
31	55.2	1.7	443	US-10-027-632-296991	Sequence 296991, App
32	54.8	1.7	1191139	US-09-811-352B-1	Sequence 1, App
33	54.8	1.7	1191139	US-10-140-924-1	Sequence 1, App
34	54.6	1.7	1527	US-10-011-154-202	Sequence 202, App
35	54.6	1.7	2501	US-10-027-632-103140	Sequence 103140, App
36	54.6	1.7	48763	PCT-US02-23268-3	Sequence 3, App
37	54.4	1.7	551	US-10-027-632-71673	Sequence 71673, App
38	54.4	1.7	1076	US-10-098-754-1296	Sequence 1296, App
39	54.4	1.7	44990	US-10-052-482-217	Sequence 1229, App
40	54.4	1.7	44990	US-10-052-482-217	Sequence 12, App
41	54.2	1.7	113585	US-10-188-470-12	Sequence 111688, App
42	54	1.7	2759	US-10-027-632-111688	Sequence 1328, App
43	54	1.7	27827	US-10-035-832-1338	Sequence 329, App
44	53.8	1.7	375	PCT-US02-09239-339	Sequence 331, App
45	53.8	1.7	375	PCT-US02-09239-331	Sequence 331, App

ALIGNMENTS

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Sequence 1262, App	GENERAL INFORMATION:	Sequence 1262, App	Application US/10035832
APPLICANT: Engelhard, Eric	FILE REFERENCE: A-71249/RMS/DCF	APPLICANT: Engelhard, Eric	FILE REFERENCE: A-71249/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/035, 832	CURRENT FILING DATE: 2002-07-22	CURRENT APPLICATION NUMBER: US/10/035, 832	CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747, 377	PRIOR FILING DATE: 2000-12-22	PRIOR APPLICATION NUMBER: US 09/747, 377	PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798, 586	PRIOR FILING DATE: 2001-03-02	PRIOR APPLICATION NUMBER: US 09/798, 586	PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613	SOFTWARE: PatentIn version 3.1	NUMBER OF SEQ ID NOS: 1613	SOFTWARE: PatentIn version 3.1
SEQ ID NO 1262	LENGTH: 45121	SEQ ID NO 1262	LENGTH: 45121
TYPE: DNA	ORGANISM: Homo sapiens	TYPE: DNA	ORGANISM: Homo sapiens
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Query Match	99.4%	Score 3193	DB 6; Length 45121
Best Local Similarity	99.8%	Pred. No. 0	Mismatches 5; Indels 1; Gaps 1
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/ ORGANISM: Homo sapiens
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/ NAME/KEY: misc_feature
/ LOCATION: (593)
/ OTHER INFORMATION: n equals a,t,g, or c
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/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PTZ/OCIN
/ CURRENT APPLICATION NUMBER: US/10/143,906
/ PRIOR FILING DATE: 2002-05-14
/ PRIOR APPLICATION REMOVED - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 96
/ SOFTWARE: Patentl Ver. 2.0
/ SEQ ID NO 21
/ LENGTH: 772
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (593)
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/ NAME/KEY: misc_feature
/ LOCATION: (704)
/ OTHER INFORMATION: n equals a,t,g, or c
US-10-143-906-21
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Query Match 10.4%; Score 334.4; DB 7; Length 772;
Best Local Similarity 99.7%; Pred. No. 1.8e-61;
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1923 ccccaaccgagcggttcccccagagagcttccatccctctcagccacccgggctt 1982
Db 9 cgcacaccgagcggttcccccagagagcttccatccctctcagccacccgggctt 68
OY 1983 tcgtagctcgctctctgactcgcgcaagagtgacacacagtggttcaagaagcttcg 2042
Db 69 tcgtagctcgctctctgactcgcgcaagagtgacacacagtggttcaagaagcttcg 128
OY 2043 gggagtgagggagcggtttacagagtgacttgctgagagcctcagggcgagcttgca 2102
Db 129 gggagtgagggagcggtttacagagtgacttgctgagagcctcagggcgagcttgca 188
OY 2103 cggacacacaccttgagcgccctgctgctccacagcgagctgctctctcccgcg 2162
Db 189 cggacacacaccttgagcgccctgctgctccacagcgagctgctctctcccgcg 248
OY 2163 ttgttgagcccgctcagtaagagtggtggagctcttccacttggaagattgtcaca 2222
Db 249 ttgttgagcccgctcagtaagagtggtggagctcttccacttggaagattgtcaca 308
OY 2223 aaccatgctgggcatctggaacctctactctgt 2258
Db 309 aaccatgctgggcatctggaacctctactctgt 344
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RESULT 5
PCT-US02-10824-85
/ Sequence 85, Application PC/TUS0210824
/ GENERAL INFORMATION:
/ APPLICANT: Origene Technologies
/ TITLE OF INVENTION: Prostate Cancer Expression Profiles
/ FILE REFERENCE: 90 206 PCT
/ CURRENT APPLICATION NUMBER: PCT/US02/10824
/ PRIOR FILING DATE: 2002-04-08
/ PRIOR APPLICATION NUMBER: US 60/281,732
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: US 60/281,731
/ PRIOR FILING DATE: 2001-04-06
/ NUMBER OF SEQ ID NOS: 211
/ SOFTWARE: Patentl version 3.1
/ SEQ ID NO 85
/ LENGTH: 2551
/ TYPE: DNA
/ ORGANISM: Homo sapiens
PCT-US02-10824-85
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Query Match 7.8%; Score 252; DB 1; Length 2551;
Best Local Similarity 100.0%; Pred. No. 9.4e-44;
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Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2007 gcaagagtgacacacaggttccaagaagcttctgggagtgagggagcggttaca 2066
Db 1 gcaagagtgacacacaggttccaagaagcttctgggagtgagggagcggttaca 60
OY 2067 gtaacttgctgagcctcagggcgagcctgcaacgacacacacctgaagccacc 2126
Db 61 gtaacttgctgagcctcagggcgagcctgcaacgacacacacctgaagccacc 120
OY 2127 tggctgccagcgagagctcctctcccgcgagtggttgagccgcctcagagag 2186
Db 121 tggctgccagcgagagctcctctcccgcgagtggttgagccgcctcagagag 180
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QY	2187	181	2247	241	QY	2247	241
Db	tttgggaagctcttctactcgtgagattgtctcaacaacatgctgggcatctgaccc	tttgggaagctcttctactcgtgagattgtctcaacaacatgctgggcatctgaccc	tttgggaagctcttctactcgtgagattgtctcaacaacatgctgggcatctgaccc	tttgggaagctcttctactcgtgagattgtctcaacaacatgctgggcatctgaccc	Db	tttgggaagctcttctactcgtgagattgtctcaacaacatgctgggcatctgaccc	tttgggaagctcttctactcgtgagattgtctcaacaacatgctgggcatctgaccc
QY	2187	181	2247	241	QY	2247	241
Db	tttgggaagctcttctactcgtgagattgtctcaacaacatgctgggcatctgaccc	tttgggaagctcttctactcgtgagattgtctcaacaacatgctgggcatctgaccc	tttgggaagctcttctactcgtgagattgtctcaacaacatgctgggcatctgaccc	tttgggaagctcttctactcgtgagattgtctcaacaacatgctgggcatctgaccc	Db	tttgggaagctcttctactcgtgagattgtctcaacaacatgctgggcatctgaccc	tttgggaagctcttctactcgtgagattgtctcaacaacatgctgggcatctgaccc

RESULT 6
PCT-US02-25766-9394

```

Sequence 9394. Application PC/TUS0252766
GENERAL INFORMATION:
APPLICANT: GENE LOGIC, INC.
APPLICANT: MONGER, William E
APPLICANT: FAULK, Ronald
APPLICANT: SUN, Hongwei
APPLICANT: SASAI, Hitoshi
APPLICANT: WAGA, Iwao
APPLICANT: YAMAMOTO, Jun
TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
FILE REFERENCE: 44921-5068-WO
CURRENT APPLICATION NUMBER: PCT/US02/25766
PRIORITY FILING DATE: 2002-08-14
PRIORITY APPLICATION NUMBER: US 60/311,837
PRIORITY FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 13946
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9394
LENGTH: 2551
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. X63717
PCT-US02-25766-9394

```

Query Match	7.8%	Score 253	DB 1:	Length 2551
Best Local Similarity	100.0%	Pred. NO.	9.4e-44	
Matches 252	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0

QY	2007	gctgagagagacacacacaggtgttcacaaagacgtctctgagagatgtagggaaacggtttacga	2066
Db	1	gcaaaagatgacacacacagagtgcttcaaaagacgtctctctgagagatgtagggaaacggtttacga	60
QY	2067	gtgaactctgctgtagagaccttcacagagcgcgagctctgtagcagacacacaccccttgagcgacgccc	2126
Db	61	gtgaactctgctgtagagaccttcacagagcgcgagctctgtagcagacacaccccttgagcgacgccc	120
QY	2127	tggctgcacacagacgagacgtcgtcctctctcccgagggtttgtgacccgcgtcagtagcagag	2186
Db	121	tggctgcacacagacgagacgtcgtcctctctcccgagggtttgtgacccgcgtcagtagcagag	180
QY	2187	tctggtggaagcctcttccactctcgagagatctgcttcaacaacacatctctgggcatctgagacct	2246
Db	181	tctggtggaagcctcttccactctcgagagatctgcttcaacaacacatctctgggcatctgagacct	240
QY	2247	cctacctctggt 2258	
Db	241	cctacctctggt 252	

RESULT 7
US-10-035-

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: Sequence 1263, Application US/10035832
:
: GENERAL INFORMATION:
:
: APPLICANT: Morris, David
: APPLICANT: Engelhard, Eric
:
: TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
:
: FILE REFERENCE: A-711249/RMS/DCF
:
: CURRENT APPLICATION NUMBER: US/10/035,832
:
: CURRENT FILING DATE: 2002-07-22
:
: PRIOR APPLICATION NUMBER: US 09/747,377

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? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: US 09/796,586
? PRIOR FILING DATE: 2001-03-02
? NUMBER OF SEQ ID NOS: 1613
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 1463
? LENGTH: 2551
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-10-035-832-1263

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Query Match	7.8%;	Score 253;	DB 6;	Length 2551;
Best Local Similarity	100.0%;	Pred. No. 9,4e-44;		
Matches 252;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	2007	gcaagaaatgacacacacagatgttcaaaagacgctctctgagagatgaagaaacgagtttaaga	2066
Db	1	gcaaaagatgacacacacagatgttcaaaagacgctctctctgagagagagaaagcagtttaaga	60
QY	2067	gtgaacttgagctctcagagggcaggaactgagcaacgaaacacacccctgaagccagccc	2126
Db	61	gtgaacttgagctctcagagggcaggaactgagcaacgaaacacacccctgaagccagccc	120
QY	2127	tggctgacacagggcagagctctcctctctcccgagggatggtagaacgctctcaagtaacgag	2186
Db	121	tggctgacacagggcagagctctcctctctcccgagggatggtagaacgctctcaagtaacgag	180
QY	2187	ttaggggaagctcttctcaatctcagagagatgtctcaaaacacatgctgagcatctgagccct	2246
Db	181	ttaggggaagctcttctcaatctcagagagatgtctcaaaacacatgctgagcatctgagccct	240
QY	2247	cctacactctggt 2258	
Db	241	cctacactctggt 252	

RESULT 8
US-10-007-

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: Sequence 143, Application US/10007926A
: GENERAL INFORMATION:
: APPLICANT: BERTUCCI, FRANCOIS
: APPLICANT: HOULGAITE, REMI
: APPLICANT: BIRNBAUM, DANIEL
: APPLICANT: NGUYEN, CATHERINE
: APPLICANT: VIENS, PATRICE
: APPLICANT: FERT, VINCENT
: TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
: TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
: FILE REFERENCE: 1546-R-00
: CURRENT APPLICATION NUMBER: US/10/007,926A
: CURRENT FILING DATE: 2001-12-07
: PRIOR APPLICATION NUMBER: 60/254,090
: PRIOR FILING DATE: 2000-12-08
: NUMBER OF SEQ ID NOS: 468
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 143
: LENGTH: 2551
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: tumor necrosis factor receptor superfamily,
: OTHER INFORMATION: member 6 (TNFRSF6) gene.
US-10-007-926A-143

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Query Match 1	7.8%	Score 252	DB 7	Length 2551
Best Local Similarity	100.0%	Pred. No.	9.4e-44	
Matches 252; Conservative	0	Mismatches	0	Indels 0
				Gaps 0

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Qy      207  gcaagagtgcacacacagtggttcaaagaacgctctctggagtgatgaaggaaagcggtttcga   2066
|||||
Db       1  gcaagagtgcacacacagtggttcaaagaacgctctctggagtgatgaaggaaagcggtttcga   60
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 10:21:41 ; Search time 8462.63 Seconds
(without alignments)
5122.783 Million cell updates/sec

Title: US-09-834-291-1
Sequence: 1 ttgagactctcagaataatg.....ttgcagatgctcaatcaag 3212

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:*
1: em_estbta:*
2: em_estchm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	710	22.1	793	10	BI763679 603049567
C 2	453.4	14.1	467	9	AA704610 zj19h02.s
C 3	386.6	12.0	899	9	AL540709
C 4	386.4	12.0	506	10	BG659530 TEGSTY2
C 5	357.8	11.1	599	10	BF659266 602185634
C 6	340.6	10.6	1140	10	BG121070 602352793
C 7	328.2	10.2	617	9	AV695647 AV695647
C 8	291.4	9.1	603	9	AA058563 zf55b04.s
C 9	287.4	8.9	577	9	AA056275 zf53q03.s
C 10	280.4	8.7	547	9	AA047220 zf49e11.s
C 11	279.4	8.7	442	9	AA011028 ze34d02.s
C 12	278.4	8.7	447	9	AA057418 z159h03.s
C 13	276.4	8.6	467	9	AA020992 ze65f07.s
C 14	263	8.2	376	10	H84298 ys95e09.s1
C 15	257	8.0	398	10	H86126 ys94d08.s1
C 16	256.4	8.0	429	9	AW239285 xh38d02.y
C 17	254.4	7.9	297	9	AA018441 ze50a08.s

C 18	253	7.9	381	10	H86544 yT04F01.s1
C 19	215.4	6.7	359	9	AV692383
C 20	214.4	6.7	1339	10	BG288747 602385566
C 21	214	6.7	932	9	AL542093 AL542093
C 22	210.4	6.6	300	9	AU100132 AU100132
C 23	202.4	6.3	1052	10	BM455788 BM455788
C 24	191	5.9	800	10	BI463384 BI463384
C 25	190	5.9	419	10	R83827
C 26	185.2	5.8	928	9	AV715411
C 27	181.8	5.7	828	10	BI838027
C 28	135	4.2	577	10	BM310113
C 29	124.4	3.9	291	9	AA383161
C 30	114.4	3.6	341	9	AA375635
C 31	96	3.0	285	10	BM090262
C 32	80.4	2.5	1101	12	CNS00396
C 33	67	2.1	1101	12	CNS00396
C 34	66.4	2.1	993	12	AG090948
C 35	66	2.1	1101	12	CNS01523
C 36	65.2	2.0	932	12	CNS00720
C 37	63.8	2.0	1027	12	CNS01677
C 38	63.6	2.0	306	9	AA668797
C 39	63.6	2.0	549	9	AA521324
C 40	63.6	2.0	583	9	AA521406
C 41	63.4	2.0	699	10	BG076530
C 42	63.2	2.0	1101	12	CNS0182P
C 43	63	2.0	698	12	A2184604
C 44	63	2.0	1201	12	CNS0165X
C 45	62.8	2.0	987	12	CNS016F1

ALIGNMENTS

RESULT 1
BI763679 793 bp mRNA linear EST 25-SEP-2001
603049567F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5189752 5',
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NIH-MGC http://imgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM11474 row: e column: 17
High quality sequence stop: 786.
Location/Qualifiers
1.793
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5189752"
/clone.lib="NIH_MGC_116"
/lab.host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 52 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is


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Db 241 AGTCAGTACAGATGACAAACACAGGGTGATGAAAGCCCTCAGGAGGTAACCTAAC 300
Qy 994 tagatttgaagggccc-aacaggtcccaagaagaatgtcaactgaagaagcctgaag 1052
Db 301 TAGATTTAGGGCCCAACAGGCTCCAGAAAGAAATGTCACACTGAGAGAGCTGAGG 360
Qy 1053 atgaacagtgggctaaagaagaaggtatattatgtgttattatgaatgaatcttgg 1112
Db 361 ATGACACTGGGCTTAAGCAAGAGGTTATTAATGTTATTAATGCTTGAACTAATAGG 420
Qy 1113 gaaggaagaagaaggtgtcgaagtgatgaagctgtgtggaacatg 1159
Db 421 GAAGGAGAGAGAGGTTGACAGAGTGAGGTCAGAGCTGTGAGCAGAG 467

RESULT 3
LOCUS AL540709 899 bp mRNA linear EST 16-FEB-2001
DEFINITION AL540709 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE002YN18 5 prime
, mRNA sequence.
ACCESSION AL540709
VERSION AL540709.1 GI:12871113
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 899)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Source
1. 899
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DE002YN18"
/clone_1lb="LTI_FL002_PL1"
/lab_host="DH10B"
/note="Organ: Placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-Oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by life
technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 192 a 288 c 245 g 170 t 4 others
ORIGIN

Query Match 12.0%; Score 386.6; DB 9; Length 899;
Best Local Similarity 99.0%; Pred. No. 3,1e-58;
Matches 397; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 2289 cccgtcttagtcccgaggatagcaaaagtggcgcgagcgagcgctgcgagatgcg 2348
Db 400 CCCGCTTAGTCCCGGGAGATAGCAAAAGTGGCGCGGC -CGGAGCGCTCGCGGATTCG 342
Qy 2349 gcggcagcgcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcg 2408
Db 341 GCGGCAAGCGGCGACGCGGCGACCTGGAGCGGCGGCTGCTGGGAGGCGGCTTGAGAC 282
Qy 2409 tggctcccgaggcgctgttagaacctccctcaagcccggtgtctcaagaacatgagag 2468
Db 281 TGCGTCCCGGGGCGCTKTITAGACCTTCCCTCAGGCGCGGCGGTGTGAGAACCTGAGAGAC 222
Qy 2469 ttgctttcttgagccttgatgcgaagtgtctgatacccgctggcgagcgagcgagcctcg 2528

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Db 221 TTTGCTTTCTTGGGCTTGATGCGAGTGTGATCCCGTGGGCGAGCGGCGAGTCCG 162
Qy 2529 ggcctcctcgagagacacatgcgtccacgttgaagtggtggcggtggcgagcagaat 2588
Db 161 GCGCTCCTCGGAGACACTGCGCTCAGCTTGAGGTGGCGGTGGGCGGCGAGAGAT 102
Qy 2589 gaagcgaagatctgggaagcttgaagtcgctgtgagggagaccgggttggagagagag 2648
Db 101 GAAGCGAAGTCTGTGGAAGCTTTAGGCTGCGTGAGGGGAGCCCGGTTGAGAGAGAG 42
Qy 2649 cggaactcttgagacagccctgacagcagcagcagcagcagcagcagcagcagc 2689
Db 41 CGGAAGCTCTGAGACAGCCCTGACAGCCAGCCAGCCAGAGGTC 1

RESULT 4
LOCUS BG659530 506 bp mRNA linear EST 11-MAY-2001
DEFINITION BG659530
TgSTzya24g01.y1 TgYEG118 Tachyzoite cDNA library Toxoplasma gondii
cDNA clone TgSTzya24g01.y1 5' similar to TR:063030 Q63030 RAT
ALPHA-SMOOTH MUSCLE ACTIN MRNA FRAGMENT ;, mRNA sequence.
ACCESSION BG659530
VERSION BG659530.1 GI:13801991
KEYWORDS EST.
SOURCE Toxoplasma gondii.
ORGANISM Toxoplasma gondii.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
REFERENCE 1 (bases 1 to 506)
AUTHORS Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajjoka, J.A., White, M.,
Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M.,
Hillier, L., Kucaba, T., Theising, B., Bowers, T., Gibbons, M., Rutter,
E., Bennett, J., Franklin, C., Tsagaris, H., R., Ronko, I., Kennedy,
S., Maguire, L., Waterston, R. and Wilson, R.
TITLE Toxoplasma EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxo@wustl.wustl.edu
Contact David Sibley (toxost@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40RP from Gibco
High quality sequence stop: 371.
Location/Qualifiers
1. 506
/organism="Toxoplasma gondii"
/strain="VR6"
/db_xref="taxon:5811"
/clone="TgSTzya24g01.y1"
/clone_1lb="TgYEG118 Tachyzoite cDNA library"
/dev_stage="Tachyzoite"
/lab_host="DH10B"
/note="Vector: pBluescript SK; Site-1: EcoRI; Site-2: XhoI
; This library was constructed by Keliang Tang, Robert
Cole, and L. David Sibley at Washington University. cDNAs
were synthesized and directionally cloned into the Uni-ZAP XR
lambda vector (Stratagene). The primary library was mass
excised as phagemids and rescued from the SOLR cells and
transformed in mass into DH10B (GeneHog, Research Genetics
, Inc.) for sequencing. WARNING: This library may contain
a small percentage contaminants from human fibroblast
cells."

BASE COUNT 86 a 191 c 140 g 89 t
ORIGIN

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VERSION AA047220.1 GI:1525120
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 547)
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B., Chisoso, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W., Hawkins, M., Hollman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Martins, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierly-Meg, J., Trevasakis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL Genome Res. 6 (9), 807-828 (1996)
 MEDLINE 97044478
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 893 Std Error: 0.00
 Seq primer: -40M13 fwd. from Amersham
 High quality sequence stop: 471.
 Location/Qualifiers
 1..547
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 /db_xref="GDB:128857"
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 /clone_1ib="Soares retina N2b4HR"
 /sex="male"
 /tissue="retina"
 /dev_stage="55 year old"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: eye; Vector: pRT3D (Pharmacia) with a modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACATCTGAGTGGAGGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 131 a 128 c 125 g 158 t 5 others
 ORIGIN
 Query Match 8.7%; Score 280.4; DB 9; Length 547;
 Best Local Similarity 99.3%; Pred. No. 1.6e-39;
 Matches 292; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 2920 gtacacagaagaagaaactgcctgtctccctccgggaattctcttaagactga 2979
 DB 1 gtcacacagaaagaaactgcctgtctccctccgggaattctcttaagactga 60
 QY 2980 agtcgctgcctgaagttcatttttttttttttttttttttttttttttttt 3039
 DB 61 agtcgctgcctgaagttcatttttttttttttttttttttttttttttttt 120
 QY 3040 ccccttctgctgctgctccatgctgctgctgctgctgctgctgctgctgctg 3099
 DB 121 ccccttctgctgctgctccatgctgctgctgctgctgctgctgctgctgctg 180
 QY 3100 tactcgttccacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3159

DB 181 TACTGCTCCACACGACAGAACCGCGCCCTATTATTGCGCAAGAACTTGACGACCT 240
 QY 3160 gtttgaagtcctcgtcctcagaaatgccaagcttgc-agaatgctaatcaag 3212
 DB 241 GTTTGAAAGTCCCTCCCTCAGAAATGCGACCTTGCAAGATGGCTAATCAAG 294
 RESULT 11
 AA011028 442 bp mRNA linear EST 29-NOV-1996
 LOCUS z34402.s1 Soares retina N2b4HR Homo sapiens cDNA clone
 DEFINITION IMAGE:360867 3', mRNA sequence.
 AA011028
 VERSION AA011028.1 GI:1472055
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 442)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hollman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 JOURNAL
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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 High quality sequence stop: 372.
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 /clone_1ib="Soares retina N2b4HR"
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 /dev_stage="55 year old"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: eye; Vector: pRT3D (Pharmacia) with a modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACATCTGAGTGGAGGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 92 a 107 c 103 g 138 t 2 others
 ORIGIN
 Query Match 8.7%; Score 279.4; DB 9; Length 442;
 Best Local Similarity 99.0%; Pred. No. 2.4e-39;
 Matches 291; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 2920 gtacacagaagaagaaactgcctgtctccctccgggaattctcttaagact-gt 2978
 DB 1 gtcacacagaaagaaactgcctgtctccctccgggaattctcttaagactggt 60

[illegible]

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (pages 1 to 447)
REFERENCE	Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman Rifkin, L., Kohlfing, T., Soares, M., Tan, F., Tevaskis, E., Waterston N., Williamson, A., Wohlmann, P. and Wilson, R. The WashU-Merck EST Project
TITLE	Unpublished (1995)
JOURNAL	Contact: Wilson RK
COMMENT	

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estwatson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -40M13 fwd. from Arnhem
High quality sequence stop: 339.

FEATURES	Location/Qualifiers
SOURCE	1. .447

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/sex="male"
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/dev_stage="55 year old"
/lab_host="DH10b (ampicillin resistant)"
/notes="Organ: eye; Vector: p773D (Pharmacia) with a
modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
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TGTTCACATCGACGACGACGACGACGACGACGCGCTTTTCTTTTCTTTTCTT
3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p773 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M.Patima Bonaldo."
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				Gaps 1
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Qy 2980	agtcgtgcctgaagtggtttcaattgtttgttttctgcacctctcttctcttgg	3039		
Db 61	agtcgtgcctgaagtggtttcaattgtttgtttgtttgttcgccctctcttctcttng	120		
Qy 3040	cccttcttaagttgaactcccatggtgattctc-gcttggtctccctgtaggtgagtg	3098		
Db 121	cccttcttaagttgaactcccatggtgattctc-gcttggtctccctgtaggtgagtg	180		
Qy 3099	gtacatcgttcccaacgcagcaagaaccggcgacctattatggccaagaacttgacaagc	3158		
Db 181	gtacatcgttcccaacgcagcaagaaccggcgacctattatggccaagaacttgacaagc	240		
Qy 3159	tgttttgaagaagtcctctgctcaagaatgcaagctctgcaagatgagtaatacaag	3212		
Db 241	tgttttgaagaagtcctctgctcaagaatgcaagctctgcaagatgagtaatacaag	294		

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LOCUS	467 bp mRNA linear EST 30-JAN-1997
DEFINITION	z65f07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363877 3' similar to contains Alu repetitive element; mRNA sequence.
ACCESSION	AA020992
VERSION	AA020992.1 GI:1484745
KEYWORDS	EST.
SOURCE	human.

ORGANISM	REFERENCE
HOMO sapiens	Hillier L., Lennon, G., Becker, M., Bonaldo, M.F., Chippelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, J., Hultman, M., Kucaba, T., Lacy, M., Le, N., Marks, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaszki, E., Underwood, K., Wohlmann, P., Waterson, R., Wilson, R. and Marra, M.
TITLE	Generation and analysis of 280,000 human expressed sequence tags
JOURNAL	Genome Res. 6 (3), 807-828 (1996)
MDLINE	9704407

HEADLINE
 COMMENT
 5/0444/0
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewartson.wustl.edu
 This clone is available royalty-free through LLNLU ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
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 Seq primer: -40M13 fwd. from Amersham
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 Location/Qualifiers
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/sex="male"
/tissue_type="retina"
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pUT3D (Pharmacia) with a
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Db 2	gtcacacagaaaagaaactgcctgctctccctcccggaattcctcttaagactga	61
QY 2980	agtcgctctccgagtggttcaattgtttgttttccctctctctcttcttcttg	3039
Db 62	agtcgctctccgagtggttcaattgtttgttttccctctctctcttcttcttg	121
QY 3040	cccttctctagcttgcaatcccatgtatattctgctgctctcctgcttgagttg	3099
Db 122	cccttctctagcttgcaatcccatgtatattctgctgctctcctgcttgagttg	181
QY 3100	tactcgttccacgcgcacagaaacccgcgcctatattgcccagaacttgagcagct	3159
Db 182	tactcgttccacgcgcacagaaacccgcgcctatattgcccagaacttgagcagct	241
QY 3160	gtttgaaagtcctcgctcagaaaatccgacgttga	3197
Db 242	gtttgaaagtcctcgctcagaaaatccgacgttga	279
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LOCUS	Y959e09.s1 Soares retina N2b5hr Homo sapiens CDNA clone	
DEFINITION	IMAGE:222568 3', mRNA sequence.	
ACCESSION	H84298	
VERSION	H84298.1 GI:1062969	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE	1 (bases 1 to 376)	
JOURNAL	Haller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman	
COMMENT	M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,	
	Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston	
	R., Williamson, A., Wohldmann, P. and Wilson, R.	
	The Wash-Merck EST Project	
	Unpublished (1995)	
	Contact: Wilson RK	
	Washington University School of Medicine	
	444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
	Tel: 314 286 1800	
	Fax: 314 286 1810	
	Email: est@wustl.edu	
	High quality sequence stops: 364	
	Source: IMAGE Consortium, LML	
	This clone is available royalty-free through LML; contact the	
	IMAGE Consortium (info@image.lml.gov) for further information.	
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	High quality sequence stop: 364.	
	Location/Qualifiers	

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/lab_host="DH10B (ampicillin resistant)"
/notice="Organ eye: Vector: pT73D (Pharmacia) with a modified polylinker. Site:1: Not I; Site:2: Eco RI. 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5 TGGTACATCTGAAGTGAGCGGCCGCCTTTTGTTTTTTTTTTTT 3'] , double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo."

```

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Db	1 CCTTCGGGGAATCTCCTTTAAGACTGTAAAGTCCCTGCCTGACAGTGATTTCATTTTGTTT 60 		
QY	3010 tgtttctcgcctctctcttcttcttlltgcccttcttaagtgcactccacvtgtgat 3069 		
Db	61 TGTWTTCCTGCCCTTCCTCTTCTTCCTTTTGCCCTTTCTTAGCTTCACATCCCATGGTGTAT 120 		
QY	3070 ttctgccttgatgctcctgtctgtggatgtgfatcgtcttccaccgccacaagaacccggagcc 3129 		
Db	121 TTCGCTGTCGTCCTCGCTCGGGGTTGGTGACTGTGTTCCACCGCACAGAACC GGCGCC 180 		
QY	3130 ctattatltggccaagaacctgtagcagcgctglttlrgaaaagtccttcgctgcataaatgcc 3189 		
Db	181 CTATTATTGGCCCAAGAACACTTGAGCAGCGCTGTTTGAAAAGTCCCTCGCTCAGAAATGCC 240 		
QY	3190 agcettgcagatlgcctaatacaag 3212 		
Db	241 AGCTTGCAGATGCGCTTAATCAAAG 263 		
RESULT 15			
H86126		398 bp	mRNA linear EST 21-NOV-1995
LOCUS	H86126		
DEFINITION	ys94q08.s1 Soares retina N2bHR Homo sapiens cDNA clone		
ACCESSION	IMAGE:222494 3', mRNA sequence.		
VERSION	H86126		
KEYWORDS	H86126.1 GI:1067705		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 398) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman, 'M., Hultman,M., Kucada,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,D., Rohlfing,T., Soares,M., Tan,F., Tevaskis,E., Waterston ,R., Williams,A., Wohlmann,P. and Wilson,R. The WashU-Merck EST Project Unpublished (1995)		
TITLE	JOURNAL		
COMMENT	Contact: Wilson RK		
	Washington University School of Medicine		

; APPLICANT: SUZ

APPLICANT: SUN, HONGWEI

```

; APPLICANT: SASAI, Hitoshi
; APPLICANT: WAGA, Iwao
; APPLICANT: YAMAMOTO, Jun
; TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
; FILE REFERENCE: 44921-5068-WO
; CURRENT APPLICATION NUMBER: PCT/US02/25766
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/311,837
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 13946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3153
; LENGTH: 4657
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. L36818
PCT-US02-25766-3153
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RESULT 3
US-10-018-407A-1
; Sequence 1, Application US/10018407A
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-2 EXPRESSION
; FILE REFERENCE: RSP-0039
; CURRENT APPLICATION NUMBER: US/10/018,407A
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/339,964
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
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; TYPE: DNA
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(3988)
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PCT-US02-23766-55/C
; Sequence 55, Application PC/TUS0223766
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; GENERAL INFORMATION:
; APPLICANT: Le, Wei-dong
; APPLICANT: Vassiliadis, Demetrios K
; TITLE OF INVENTION: Mutant Nurrl Gene in Parkinson's Disease
; FILE REFERENCE: P02512W01
; CURRENT APPLICATION NUMBER: PCT/US02/23766
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,294
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
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; TYPE: DNA
; ORGANISM: Human
PCT-US02-23766-55
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; Sequence 55, Application US/10205951
; GENERAL INFORMATION:
; APPLICANT: Le, Wei-dong
; APPLICANT: Vassiliadis, Demetrios K
; TITLE OF INVENTION: Mutant Nurrl Gene in Parkinson's Disease
; FILE REFERENCE: P02512W01
; CURRENT APPLICATION NUMBER: US/10/205,951
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,294
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 10883
; TYPE: DNA
; ORGANISM: Human
US-10-205-951-55
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Best Local Similarity 60.2%; Pred. No. 14;
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RESULT 6
US-10-137-113-12/C
; Sequence 12, Application US/10137113
; GENERAL INFORMATION:
; APPLICANT: Kepur, Vivek
; APPLICANT: Bannantine, John P.
; TITLE OF INVENTION: Mycobacterial Diagnostics
; FILE REFERENCE: 09351-112001
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; SOFTWARE: PATERLIN VET
; SEQ ID NO 178
; LENGTH: 3265
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-646-569-178

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:32:03 ; Search time 13836.9 Seconds
(without alignments)
195.445 Million cell updates/sec

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Perfect score: 125
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

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Minimum DB seq length: 0
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Listing first 45 summaries

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2	125	100.0	318	US-09-652-127-280	Sequence 2780, Ap
3	125	100.0	324	US-09-396-087-4122	Sequence 4122, Ap
4	125	100.0	720	US-09-834-291-2	Sequence 2, Appl
5	125	100.0	1368	US-60-324-185-9888	Sequence 9888, Ap
6	125	100.0	1732	US-09-644-867-7725	Sequence 7725, Ap
7	125	100.0	1732	US-09-652-911-10283	Sequence 10283, A
8	125	100.0	3212	US-09-834-291-1	Sequence 10, Appl
9	125	100.0	45121	US-09-997-722-10	Sequence 818, App
10	123.4	98.7	419	US-09-489-036-818	Sequence 818, App
11	123.4	98.7	419	US-09-943-143-818	Sequence 818, App
12	123.4	98.7	404	US-09-471-275-3315	Sequence 3315, Ap
13	121.8	97.4	575	US-09-362-510-3927	Sequence 3927, Ap
14	121.8	97.4	404	US-09-362-510A-3927	Sequence 3927, Ap
15	121.8	97.4	404	US-09-904-013-9927	Sequence 3927, Ap
16	121.4	89.9	1555	US-60-172-373-10224	Sequence 10224, A
17	112	89.6	495	US-09-652-911-4824	Sequence 94, Appl
18	109.4	87.5	2165	US-09-665-615B-94	Sequence 94, Appl
19	109.4	87.5	2165	US-09-802-669-94	Sequence 847, App
20	101.8	81.4	362	US-09-522-303-847	Sequence 847, App
21	101.8	81.4	362	US-09-617-081-898	Sequence 898, App
22	95	76.0	443	US-09-522-303-1341	Sequence 1341, Ap
23	89.2	71.4	2760	US-09-644-865-8181	Sequence 8181, Ap
24	89.2	71.4	2760	US-09-652-124-8035	Sequence 8055, Ap
25	89.2	71.4	2760	US-09-652-127-7930	Sequence 7930, Ap
26	89.2	71.4	2760	US-09-652-816-7672	Sequence 7672, Ap
27	89.2	71.4	2760	US-09-652-911-8889	Sequence 8889, Ap
28	85	68.0	355	US-09-431-517-12091	Sequence 12091, A
29	85	68.0	355	US-09-431-517-12154	Sequence 12154, A
30	85	68.0	371	US-09-489-036-24990	Sequence 24990, A
31	85	68.0	371	US-09-943-143-24990	Sequence 24990, A

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 32 63 50.4 408 16 US-09-289-768-1798 Sequence 1798, Ap
C 33 63 50.4 408 35 US-09-939-397-1798 Sequence 1798, Ap
C 34 38.4 30.7 51 56 US-09-172-373-10226 Sequence 10226, A
C 35 38.2 30.6 786 25 US-09-652-128-9418 Sequence 9418, Ap
36 37.8 30.2 438 17 US-09-306-350A-34407 Sequence 34407, A
37 37.8 30.2 438 17 US-09-306-350A-34407 Sequence 34407, A
38 37.2 29.8 396 17 US-09-359-067-35264 Sequence 35264, A
39 36.6 29.3 360 17 US-09-359-067-35264 Sequence 35264, A
40 36.6 29.3 423 17 US-09-362-510-36229 Sequence 36229, A
41 36.6 29.3 423 17 US-09-362-510-36229 Sequence 36229, A
42 36.6 29.3 423 34 US-09-504-013-36229 Sequence 36229, A
43 36.6 29.3 475 17 US-09-359-067-35265 Sequence 35265, A
44 36.6 29.3 2963 30 US-09-760-475-1176 Sequence 1176, Ap
45 36.6 29.3 4657 11 US-08-731-233A-1 Sequence 1, Appli
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ALIGNMENTS

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RESULT 1
US-09-834-291-32
; Sequence 32, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834, 291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 266
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-32
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Query Match 100.0%; Score 125; DB 32; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 gatcccgctgggagcgagcgagctccgctcctcggagaccactgctccacgtt 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 gatcccgctgggagcgagcgagctccgctcctcggagaccactgctccacgtt 60
OY 61 gaggtggcgctgggagcgagcgagctccgctcctcggagaccactgctccacgtt 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 gaggtggcgctgggagcgagcgagctccgctcctcggagaccactgctccacgtt 120
OY 121 tggag 125
| | | | |
Db 121 tggag 125
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RESULT 2
US-09-652-127-2780/c
; Sequence 2780, Application US/09652127
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1183-001
; CURRENT APPLICATION NUMBER: US/09/652, 127
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,134
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 10475
```

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2780
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-127-2780
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Query Match 100.0%; Score 125; DB 25; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 gatcccgctgggagcgagcgagctccgctcctcggagaccactgctccacgtt 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 159 gatcccgctgggagcgagcgagctccgctcctcggagaccactgctccacgtt 100
OY 61 gaggtggcgctgggagcgagcgagctccgctcctcggagaccactgctccacgtt 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 99 gaggtggcgctgggagcgagcgagctccgctcctcggagaccactgctccacgtt 120
OY 121 tggag 125
| | | | |
Db 39 tggag 35
```

```
RESULT 3
US-09-396-087-4122/c
; Sequence 4122, Application US/09396087
; GENERAL INFORMATION:
; APPLICANT: Gearling, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: MLN98-39pm
; CURRENT APPLICATION NUMBER: US/09/396, 087
; CURRENT FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: 60/100,260
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: 60/107,226
; EARLIER FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: 60/131,810
; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5220
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4122
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-396-087-4122
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Query Match 100.0%; Score 125; DB 17; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 gatcccgctgggagcgagcgagctccgctcctcggagaccactgctccacgtt 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 149 gatcccgctgggagcgagcgagctccgctcctcggagaccactgctccacgtt 60
OY 61 gaggtggcgctgggagcgagcgagctccgctcctcggagaccactgctccacgtt 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 89 gaggtggcgctgggagcgagcgagctccgctcctcggagaccactgctccacgtt 120
OY 121 tggag 125
| | | | |
Db 29 tggag 25
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```
RESULT 4
US-09-834-291-2
; Sequence 2, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
```



```
QY 1 gatcccgctggcgaagcgagcgtccgcgtctcctcgagacacatgctccacgtt 60
    |||||||
Db 178 gatcccgctggcgaagcgagcgtccgcgtctcctcgagacacatgctccacgtt 119

QY 61 gaagtgagcgttgaggggcgagacagaattgaagcggaaagtctctggaagctttaggtcgc 120
    |||||||
Db 118 gacgtggcgctggggggcgagacagaattgaagcggaaagtctctggaagctttaggtcgc 59

QY 121 tggag 125
    |||||
Db 58 tggag 54

RESULT 8
US-09-834-291-1
; Sequence 1 Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3212
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-1

Query Match 100.0%; Score 125; DB 32; Length 3212;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcccgctggcgaagcgagcgtccgcgtctcctcgagacacatgctccacgtt 60
    |||||||
Db 2500 gatcccgctggcgaagcgagcgtccgcgtctcctcgagacacatgctccacgtt 2559

QY 61 gaagtgagcgttgaggggcgagacagaattgaagcggaaagtctctggaagctttaggtcgc 120
    |||||||
Db 2560 gaagtgagcgttgaggggcgagacagaattgaagcggaaagtctctggaagctttaggtcgc 2619

QY 121 tggag 125
    |||||
Db 2620 tggag 2624

RESULT 9
US-09-997-722-10
; Sequence 10 Application US/09997722
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RME/DCP
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 10
; LENGTH: 45121
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```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-997-722-10

Query Match 100.0%; Score 125; DB 36; Length 45121;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcccgctggcgaagcgagcgtccgcgtctcctcgagacacatgctccacgtt 60
    |||||||
Db 10494 gatcccgctggcgaagcgagcgtccgcgtctcctcgagacacatgctccacgtt 10553

QY 61 gaagtgagcgttgaggggcgagacagaattgaagcggaaagtctctggaagctttaggtcgc 120
    |||||||
Db 10554 gaagtgagcgttgaggggcgagacagaattgaagcggaaagtctctggaagctttaggtcgc 10613

QY 121 tggag 125
    |||||
Db 10614 tggag 10618

RESULT 10
US-09-489-036-818
; Sequence 818 Application US/09489036
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 783
; CURRENT APPLICATION NUMBER: US/09/489,036
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 35324
; SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 818
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-489-036-818

Query Match 98.7%; Score 123.4; DB 18; Length 419;
Best Local Similarity 99.2%; Pred. No. 7.1e-21;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gatcccgctggcgaagcgagcgtccgcgtctcctcgagacacatgctccacgtt 60
    |||||||
Db 107 gatcccgctggcgaagcgagcgtccgcgtctcctcgagacacatgctccacgtt 166

QY 61 gaagtgagcgttgaggggcgagacagaattgaagcggaaagtctctggaagctttaggtcgc 120
    |||||||
Db 167 gaagtgagcgttgaggggcgagacagaattgaagcggaaagtctctggaagctttaggtcgc 226

QY 121 tggag 125
    |||||
Db 227 tggag 231

RESULT 11
US-09-943-143-818
; Sequence 818 Application US/09943143
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 783
; CURRENT APPLICATION NUMBER: US/09/943,143
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/489,036
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 35324
; SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 818
```

LENGTH: 419
TYPE: DNA
ORGANISM: Homo sapiens
US-09-943-143-818

Query Match 98.7%; Score 123.4; DB 35; Length 419;
Best Local Similarity 99.2%; Pred. No. 7, 1e-21;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gatccgcgtggcagggcgagcgtccggtcctctcgagacacactgcgtccacgtt 60
|||
Db 107 gaccgcgtggcagggcgagcgtccggtcctctcgagacacactgcgtccacgtt 166
|||
QY 61 gaggtggcgtggggtggcgagacgaattgaagcggaaagtctgggaagctttaggtcgc 120
|||
Db 167 gaggtggcgtggggtggcgagacgaattgaagcggaaagtctgggaagctttaggtcgc 226
|||
QY 121 tggag 125
|||
Db 227 tggag 231

RESULT 12

US-09-471-275-3315/c
Sequence 3315, Application US/09471275
GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Contigs Obtained
FILE REFERENCE: 782
CURRENT APPLICATION NUMBER: US/09/471, 275
EARLIER APPLICATION NUMBER: US 09/235, 076
EARLIER FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: US 09/234, 611
EARLIER FILING DATE: 1999-01-22
EARLIER APPLICATION NUMBER: US 09/240, 371
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: US 09/277, 227
EARLIER FILING DATE: 1999-03-25
EARLIER APPLICATION NUMBER: US 09/271, 490
EARLIER FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: US 09/293, 972
EARLIER FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: US 09/274, 861
EARLIER FILING DATE: 1999-03-23
EARLIER APPLICATION NUMBER: US 60/125, 453
EARLIER FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: US 60/126, 605
EARLIER FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: US 09/306, 350
EARLIER FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 09/399, 720
EARLIER FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER: US 09/404, 284
EARLIER FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER:
EARLIER FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 10451
SOFTWARE: pt_ct_genes Version 1.0
SEQ ID NO 3315
LENGTH: 575
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (465)...(578)
OTHER INFORMATION: similar to g1178067 in the genepept database release 114,
OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-471-275-3315

Query Match 98.7%; Score 123.4; DB 18; Length 575;
Best Local Similarity 99.2%; Pred. No. 7, 1e-21;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gatccgcgtggcagggcgagcgtccggtcctctcgagacacactgcgtccacgtt 60
|||
Db 313 GACCCGCTGGGCGAGCGGCGGCGAGCTCCGCGCTCTCTGGAGACCACTGCGCTCCACGTT 254
|||
QY 61 gaggtggcgtggggtggcgagacgaattgaagcggaaagtctgggaagctttaggtcgc 120
|||
Db 253 GAGGTGGCGCTGGGCGGCGGCGAGACGAATTTGAAGCGGAAGCTTGGGAAGCTTGGGCTCCG 194
|||
QY 121 tggag 125
|||
Db 193 TGGAG 189

RESULT 13

US-09-362-510-3927/c
Sequence 3927, Application US/09362510
GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-759CON1
CURRENT APPLICATION NUMBER: US/09/362, 510
EARLIER FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 09/221, 820
NUMBER OF SEQ ID NOS: 62165
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3927
LENGTH: 404
TYPE: DNA
ORGANISM: Homo sapiens
US-09-362-510-3927

Query Match 97.4%; Score 121.8; DB 17; Length 404;
Best Local Similarity 98.4%; Pred. No. 1, 8e-20;
Matches 123; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gatccgcgtggcagggcgagcgtccggtcctctcgagacacactgcgtccacgtt 60
|||
Db 174 GACCCGCTGGGCGAGCGGCGGCGAGCTCCGCGCTCTCTGGAGACCACTGCGCTCCACGTT 115
|||
QY 61 gaggtggcgtggggtggcgagacgaattgaagcggaaagtctgggaagctttaggtcgc 120
|||
Db 114 GAGGTGGCGCTGGGCGGCGGCGAGCAATTTGAAGCGGAAGCTTGGGAAGCTTGGGCTCCG 55
|||
QY 121 tggag 125
|||
Db 54 TGGAG 50

RESULT 14

US-09-362-510A-3927/c
Sequence 3927, Application US/09362510A
GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-759CON1
CURRENT APPLICATION NUMBER: US/09/362, 510A
EARLIER FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 09/221, 820
NUMBER OF SEQ ID NOS: 62165
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3927
LENGTH: 404
TYPE: DNA
ORGANISM: Homo sapiens

EARLIER FILING DATE: 1999-02-16


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? EARLIER APPLICATION NUMBER: 60/106,100
? EARLIER FILING DATE: 1998-10-29
? NUMBER OF SEQ ID NOS: 12
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO: 1
? LENGTH: 50937
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Recombinant DNA
US-09-428-517-1
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; FEATURE:
; OTHER INFORMATION: PLASMID POS3410H57
US-09-017-706-4

Query Match          22.2%; Score 27.8; DB 3; Length 1981;
Best Local Similarity 54.4%; Pred. No. 10;
Matches 56; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

OY 1 gatccgcgtggcagggcgagcgtccgcgtcctcctcgagacccactgctccacgtt 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1451 gatcgagggcgccacgagatgctgtccgcaccccttatgtgcgcgcgatccacgtc 1510

OY 61 gaggtggcgctggggggcgagacgaattgaagcggaagctcg 103
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Db 1511 ggtgcgcgcacgcgcagacgcagcagagtgacagagtgctcag 1553

RESULT 6
US-09-017-706-5
; Sequence 5, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTASE, VECTOR CONTAINING SAID GENE AND
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1981
; TYPE: DNA
; ORGANISM: Pseudomonas sp., Strain KO-8940
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1848)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (85)..(1848)
; OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: E
; FEATURE:
; OTHER INFORMATION: MUTATED GENOMIC DNA
; OTHER INFORMATION: PLASMID POS3410H57
US-09-017-706-5

Query Match          22.2%; Score 27.8; DB 3; Length 1981;
Best Local Similarity 54.4%; Pred. No. 10;
Matches 56; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

OY 1 gatccgcgtggcagggcgagcgtccgcgtcctcctcgagacccactgctccacgtt 60
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Db 1451 gatcgagggcgccacgagatgctgtccgcaccccttatgtgcgcgcgatccacgtc 1510

OY 61 gaggtggcgctggggggcgagacgaattgaagcggaagctcg 103
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Db 1511 ggtgcgcgcacgcgcagacgcagcagagtgacagagtgctcag 1553

RESULT 7
US-09-017-706-6
; Sequence 6, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTASE, VECTOR CONTAINING SAID GENE AND
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1981
; TYPE: DNA
; ORGANISM: Pseudomonas sp., Strain KO-8940
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1848)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (85)..(1848)
; OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: E
; FEATURE:
; OTHER INFORMATION: MUTATED GENOMIC DNA
; OTHER INFORMATION: PLASMID: POS3410H139
US-09-017-706-7

Query Match          22.2%; Score 27.8; DB 3; Length 1981;
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; TITLE OF INVENTION: TRANSFORMANT
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 1981
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; ORGANISM: Pseudomonas sp., Strain KO-8940
; FEATURE:
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; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (85)..(1848)
; FEATURE:
; OTHER INFORMATION: MUTATED GENOMIC DNA
; FEATURE:
; OTHER INFORMATION: PLASMID: POS3410F139
US-09-017-706-6

Query Match          22.2%; Score 27.8; DB 3; Length 1981;
Best Local Similarity 54.4%; Pred. No. 10;
Matches 56; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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OY 61 gaggtggcgctggggggcgagacgaattgaagcggaagctcg 103
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Db 1511 ggtgcgcgcacgcgcagacgcagcagagtgacagagtgctcag 1553

RESULT 8
US-09-017-706-7
; Sequence 7, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTASE, VECTOR CONTAINING SAID GENE AND
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1981
; TYPE: DNA
; ORGANISM: Pseudomonas sp., Strain KO-8940
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1848)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (85)..(1848)
; OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: E
; FEATURE:
; OTHER INFORMATION: MUTATED GENOMIC DNA
; OTHER INFORMATION: PLASMID: POS3410H139
US-09-017-706-7

Query Match          22.2%; Score 27.8; DB 3; Length 1981;
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TELEX: 810-221-8317
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 803 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: exon
LOCATION: 1..803
IDENTIFICATION METHOD: experimental
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OTHER INFORMATION: /standard_name= "Alternate Exon 3: D4.7"
OTHER INFORMATION: /note= "This sequence represents the third exon of
OTHER INFORMATION: allele D4.7 of the human D4 dopamine receptor
OTHER INFORMATION: gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 257..262
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OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "Psi site"
OTHER INFORMATION: /label= Psi
OTHER INFORMATION: /note= "This sequence is a Psi site whereby
OTHER INFORMATION: digestion of human genomic DNA produces a RFLP"
FEATURE:
NAME/KEY: repeat_region
LOCATION: 346..682
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OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /rpt_unit= 346..394
OTHER INFORMATION: /note= "This sequence is a repeat found in 7 known
OTHER INFORMATION: alleles of the human D4 dopamine receptor gene
OTHER INFORMATION: encoding a 16 amino acid sequence repeated 7 times
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NAME/KEY: CDS
LOCATION: 2..803
US-07-928-611-12
Query Match 22.1%; Score 27.6; DB 1; Length 803;
Best Local Similarity 60.8%; Pred. No. 9.7;
Matches 62; Conservative 0; Mismatches 39; Indels 1; Gaps 1;
QY 5 ccgctggcgaagcgagctccgcgcctcctcgagagcacctgcgctccacgttgagg 64
DB 561 CCCCCGGGAAGCGCGGGCGCGGCGGCGCAGTCGGGCGCCGACAGGGGTCTGGGGAGG 502
QY 65 -tggcgctggggcgagcagaattgaagcggaagtcggg 105
DB 501 CCGGGCGGGGGGGCGCACAGTCGGGGCCCGCAGGGGTCCGGG 460
RESULT 12
US-08-487-811A-12/C
Sequence 12, Application US/08487811A
Patent No. 5883226
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Van Tol, Hubert H.M.
TITLE OF INVENTION: A No. 5883226el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,811A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5883226nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 803 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: exon
LOCATION: 1..803
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "Alternate Exon 3: D4.7"
OTHER INFORMATION: /note= "This sequence represents the third exon of
OTHER INFORMATION: allele D4.7 of the human D4 dopamine receptor
OTHER INFORMATION: gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 257..262
IDENTIFICATION METHOD: experimental
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OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "Psi site"
OTHER INFORMATION: /label= Psi
OTHER INFORMATION: /note= "This sequence is a Psi site whereby
OTHER INFORMATION: digestion of human genomic DNA produces a RFLP"
FEATURE:
NAME/KEY: repeat_region
LOCATION: 346..682
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OTHER INFORMATION: /rpt_type= "tandem"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /rpt_unit= 346..394
OTHER INFORMATION: /note= "This sequence is a repeat found in 7 known
OTHER INFORMATION: alleles of the human D4 dopamine receptor gene
OTHER INFORMATION: encoding a 16 amino acid sequence repeated 7 times
FEATURE:
NAME/KEY: CDS
LOCATION: 2..803
US-08-487-811A-12
Query Match 22.1%; Score 27.6; DB 2; Length 803;
Best Local Similarity 60.8%; Pred. No. 9.7;
Matches 62; Conservative 0; Mismatches 39; Indels 1; Gaps 1;
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DB 561 CCCCCGGGAAGCGCGGGCGCGGCGGCGCAGTCGGGCGCCGACAGGGGTCTGGGGAGG 502
QY 65 -tggcgctggggcgagcagaattgaagcggaagtcggg 105
DB 501 CCGGGCGGGGGGGCGCACAGTCGGGGCCCGCAGGGGTCCGGG 460
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1      US-09-060-694-12/c
2      : Sequence 12, Application US/09060694
3      : Patent No. 6203998
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5      : GENERAL INFORMATION:
6      : APPLICANT: Civeilli, Olivier
7      : APPLICANT: Van Tol, Hubert H.M.
8      : TITLE OF INVENTION: A No. 6203998a1 Human Dopamine Receptor and Uses
9      : NUMBER OF SEQUENCES: 24
10     : CORRESPONDENCE ADDRESS:
11     : ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
12     : STREET: 300 South Wacker Drive
13     : CITY: Chicago
14     : STATE: IL
15     : COUNTRY: USA
16     : ZIP: 60606
17
18     : COMPUTER READABLE FORM:
19     : MEDIUM TYPE: Floppy disk
20     : COMPUTER: IBM PC compatible
21     : OPERATING SYSTEM: PC-DOS/MS-DOS
22     : SOFTWARE: Patentin Release #1.0, Version #1.25
23
24     : CURRENT APPLICATION DATA:
25     : APPLICATION NUMBER: US/09/060,694
26     : FILING DATE: 15-APR-1998
27     : CLASSIFICATION: 530
28
29     : ATTORNEY/AGENT INFORMATION:
30     : NAME: No. 6203998a1, Kevin E
31     : REGISTRATION NUMBER: 35,303
32     : REFERENCE/DOCKET NUMBER: 90,1092-MM
33     : TELECOMMUNICATION INFORMATION:
34     : TELEPHONE: 312-913-0001
35     : TELEFAX: 312-913-0002
36
37     : TELEX:
38
39     : INFORMATION FOR SEQ. ID NO. 12:
40
41     : SEQUENCE CHARACTERISTICS:
42     : LENGTH: 803 base pairs
43     : TYPE: nucleic acid
44     : STRANDEDNESS: single
45     : TOPOLOGY: linear
46
47     : MOLECULE TYPE: DNA (genomic)
48
49     : FEATURE:
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51     : NAME/KEY: exon
52     : LOCATION: 1..803
53     : IDENTIFICATION METHOD: experimental
54     : OTHER INFORMATION: /evidence=EXPERIMENTAL
55     : OTHER INFORMATION: /standard.name="Altimate Exon 3: D4.7"
56     : OTHER INFORMATION: /note="This sequence represents the third exon of
57     : OTHER INFORMATION: allele D4.7 of the human D4 dopamine receptor
58     : OTHER INFORMATION: gene"
59
60     : FEATURE:
61     : NAME/KEY: misc-feature
62     : LOCATION: 257..262
63     : IDENTIFICATION METHOD: experimental
64     : OTHER INFORMATION: /function="Psi site"
65     : OTHER INFORMATION: /evidence=EXPERIMENTAL
66     : OTHER INFORMATION: /standard.name="Psi site"
67     : OTHER INFORMATION: /label="Psi
68     : OTHER INFORMATION: /note="This sequence is a Psi site whereby
69     : OTHER INFORMATION: digestion of human genomic DNA produces a RFLP"
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71     : FEATURE:
72     : NAME/KEY: repeat_region
73     : LOCATION: 346..682
74     : IDENTIFICATION METHOD: experimental
75     : OTHER INFORMATION: /rpt_type="candem"
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77     : OTHER INFORMATION: /rpt_unit=346..394
78     : OTHER INFORMATION: /note="This sequence is a repeat found in 7 known
79     : OTHER INFORMATION: alleles of the human D4 dopamine receptor gene
80     : OTHER INFORMATION: encoding a 16 amino acid sequence repeated 7 times
81
82     : NAME/KEY: CDS
83     : LOCATION: 2..803
84
85     : US-09-060-694-12

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Query Match          22.1%; Score 27.6; DB 4; Length 803;
Best Local Similarity 60.8%; Pred. No. 9.7;
Matches 62; Conservative 0; Mismatches 39; Indels 1; Gaps 1;

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Db       561  ccccgagggaagccgcggcgccggggcgacacagtcggggcccgacaggggctgggggag 502
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      65  -tgggcgtgtyggggcgagcagaatggaagcgagtcgtgg 105
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Db       501  ccggcgccggggggcgacagtcggggcccgacaggggctccgg 460

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; Sequence 12, Application PC/TUS9307370
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A Novel Human Dopamine Receptor and Uses
; NUMBER OF SEQUENCES: 22
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07370
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 803 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1..803
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence=EXPERIMENTAL
; OTHER INFORMATION: /standard.name="Alternate Exon 3: D4.7"
; OTHER INFORMATION: /note="This sequence represents the third exon of
; OTHER INFORMATION: allele D4.7 of the human D4 dopamine receptor
; OTHER INFORMATION: gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 257..262
; IDENTIFICATION METHOD: experimental
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; OTHER INFORMATION: /evidence=EXPERIMENTAL
; OTHER INFORMATION: /standard.name="Psi site"
; OTHER INFORMATION: /label=Psi
; OTHER INFORMATION: /note="This sequence is a Psi site whereby
; OTHER INFORMATION: digestion of human genomic DNA produces a RFLP"
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 346..682
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /rpt_type="tandem"
; OTHER INFORMATION: /evidence=EXPERIMENTAL
; OTHER INFORMATION: /rpt_unit=346..394
; OTHER INFORMATION: /note="This sequence is a repeat found in 7 known
; OTHER INFORMATION: alleles of the human D4 dopamine receptor gene
; OTHER INFORMATION: encoding a 16 amino acid sequence repeated 7 times
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..803
; PCT-US93-07370-12

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:40:33 ; Search time 1139.19 Seconds
(without alignments)
188.392 Million cell updates/sec

Title: US-09-834-291-2_COPY_1_125
Perfect score: 125
Sequence: 1 gatccgcctgagcagcgcggg.....aaqctttagggctcgtgag 125

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	36.6	29.3	4743	21	AA291408	Human SHIP-2 nucle
3	32.8	26.2	3768	21	AA281955	Human Meg-3 cDNA.
4	32.8	26.2	3995	22	AA168201	Human osteoclast e
5	32.4	25.9	1110	22	AA529777	Human cytoskeletal
6	32.4	25.9	1110	22	AA101443	Human reproductiv
7	32.2	25.8	1388	21	AA244059	zebra mays DNA fragm
8	32.2	25.6	511	22	AA292251	Human cDNA 5'-end
9	32	25.6	511	22	AA293511	Human cDNA clone r

10	32	25.6	1371	22	AA529822	Human cytoskeletal
11	32	25.6	1371	22	AA105199	Human reproductiv
12	32	25.6	1544	22	AA294547	Human full-length
13	32	25.6	1553	19	AA294361	Human secreted pro
14	31.6	25.3	1485	16	AA287721	Human auxiliary cy
15	31.6	25.3	1485	16	AA287722	Human auxiliary cy
16	31.6	25.3	1485	17	AA283887	Human cytochrome p
17	31.6	25.3	1485	17	AA283888	Human cytochrome p
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22	31.6	25.3	1485	17	AA283893	Human cytochrome p
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25	30.6	24.5	1662	18	AA283896	Human cytochrome p
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ALIGNMENTS

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KW	Cancer chemotherapy; ss.	
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OS	Homo sapiens.	
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PD	03-FEB-2000.	
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PF	16-OCT-1998;	98DE-1047779.
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PR	16-OCT-1998;	98DE-1047779.
XX		
PA	(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.	
XX		
PI	Krammer P, Mueller-Schilling M, Oren M;	
XX		

DR WPI: 2000-162245/15.
 XX Novel receptor DNA useful for identifying apoptosis-modulating
 PT substances potentially useful for cancer chemotherapy
 XX
 PS Claim 2; Fig 4; 12pp; German.
 XX
 CC This invention describes a novel p53-binding region of a human CD95
 CC receptor DNA molecule. The p53-binding region, or a vector containing
 CC it, can be used to screen for apoptosis-modulating substances
 CC potentially useful for cancer chemotherapy. This sequence represents a
 CC fragment of the human CD95 receptor intron 1 which contains a p53 binding
 CC region described in the method of the invention.
 CC
 XX Sequence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;
 SQ

Query Match Best Local Similarity 100.0%; Score 125; DB 21; Length 266;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatccgctggagcagcgagctccgagctctcctcgagacacactgcgtccagctt 60
 Db 1 gatccgctggagcagcgagctccgagctctcctcgagacacactgcgtccagctt 60
 QY 61 gaagtgagcgctggggcgagcaggaattgaagcggaagctctgggaagctttagggctcgc 120
 Db 61 gaagtgagcgctggggcgagcaggaattgaagcggaagctctgggaagctttagggctcgc 120
 QY 121 tggag 125
 Db 121 tggag 125

RESULT 2
 AA291408
 ID AA291408 standard; cDNA; 4743 BP.
 XX
 AC AA291408;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Human Ship-2 nucleotide sequence SEQ ID NO:1.
 XX
 KW Human; Ship-2; antisense oligonucleotide; phosphorothioate; detection;
 KW inhibition; SH2-containing phosphatidylinositol phosphatase-2; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 212..3988
 FT /*tag= a
 FT /product= "Ship-2"
 XX
 PN US6025198-A.
 XX
 PD 15-FEB-2000.
 XX
 PF 25-JUN-1999; 99US-0339964.
 XX
 PR 25-JUN-1999; 99US-0339964.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Cowser LM;
 DR WPI: 2000-181819/16.
 DR P-PSDB; AAT80120.
 XX
 PT Antisense oligonucleotides, useful for inhibiting human Ship-2
 PT expression and for detecting nucleic acids encoding Ship-2
 XX
 PS Example 13; Column 41-52; 34pp; English.

XX
 CC The present invention describes phosphorothioate antisense
 CC oligonucleotides that specifically hybridize with, and inhibit the
 CC expression of, nucleic acids encoding human Ship-2 (also called
 CC SH2-containing phosphatidylinositol phosphatase-2). Also described
 CC is a method of inhibiting the expression of Ship-2 in human cells
 CC or tissues in vitro comprising contacting the cells with the
 CC phosphorothioate antisense oligonucleotides. The phosphorothioate
 CC antisense oligonucleotides can be used to treat animals (especially
 CC humans) suspected of having or being prone to a disease or condition
 CC associated with Ship-2 expression. The present sequence encodes
 CC human Ship-2.
 CC
 XX Sequence 4743 BP; 939 A; 1466 C; 1448 G; 890 T; 0 other;
 SQ

Query Match Best Local Similarity 29.3%; Score 36.6; DB 21; Length 4743;
 Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 3 tccgcgtggagcagcgagctccgagctctcctcgagacacactgcgtccagcttga 62
 Db 4348 ttcaccgggctctgaaccacagcgaggaagctccgcttaagactccaccctggg 4407
 QY 63 ggtgggagctggggcgagcaggaattgaagcggaagcttggaagc 109
 Db 4408 ggtgggagcggtggtgctcccggaatgaaggaatgaccgagagacc 4454

RESULT 3
 AAC81955
 ID AAC81955 standard; cDNA; 3768 BP.
 XX
 AC AAC81955;
 XX
 DT 01-MAR-2001 (first entry)
 XX
 DE Human Meg-3 cDNA.
 XX
 KW Meg-3; human; mesangial kidney cell; treatment; diagnosis; renal;
 KW antidiabetic; vaccine; gene therapy; pathogenesis; kidney disease;
 KW glomerulonephritis; diabetes; proliferation; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 53..2254
 FT /*tag= a
 FT /product= "Meg-3"
 XX
 PN WO200066729-A1.
 XX
 PD 09-NOV-2000.
 XX
 PF 28-APR-2000; 2000WO-JP02831.
 XX
 PR 30-APR-1999; 99JP-0123561.
 XX
 PA (KUROO/) KUROKAWA K.
 PA (MIYA/) MIYATA T.
 XX
 PI Miyata T;
 DR WPI: 2000-687536/67.
 DR P-PSDB; AAB11456.
 XX
 PT Meg-3 protein expressed in mesangial kidney cells for diagnosis and
 PT treatment of kidney disease
 XX
 PS Claim 4; Page 44-53; 65pp; Japanese.
 CC This invention describes a novel protein highly expressed in mesangial
 CC kidney cells which has renal and antidiabetic activity and which can be


```
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234223.
PR 25-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244675.
PR 08-NOV-2000; 2000US-0244676.
PR 08-NOV-2000; 2000US-0244677.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.

PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249248.
PR 17-NOV-2000; 2000US-0249249.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251989.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI: 2001-476182/51.
P-PSDB; AAU18515.

Novel isolated human cytoskeletal element-related polypeptide useful
for diagnosis/treatment of neoplastic disorders, disorders associated
with neural transmission, chromosomal abnormalities, autoimmune
disorders -
XX
PS Claim 1; SEQ ID No 18; 505pp; English.
XX
CC Sequences AAS29770-AAS29813 represent cDNA molecules, which encode the
CC cytoskeletal element-related polypeptides of the invention. Cytoskeletal
CC polypeptides and their associated polynucleotides are useful in the
CC diagnosis, treatment and prevention of various types of disorders in e.g.
CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A
CC pathological condition can be determined by determining the presence or
CC absence of a mutation in a cytoskeletal polynucleotide. The treatable
CC disorders include autoimmune diseases such as rheumatoid arthritis,
CC hyperproliferative disorders such as neoplasms of the breast or liver,
CC cardiovascular disorders such as cardiac arrest, cerebrovascular
CC disorders such as cerebral ischemia, nervous system disorders such as
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi,
CC ocular disorders such as corneal infection, endocrine disorders such as
CC premature labour and infertility, gastrointestinal disorders such as
CC Crohn's disease, renal disorders such as glomerulonephritis and
CC respiratory disorders such as asthma. The polypeptides can also be used
CC to aid wound healing, to prevent skin aging due to sunburn, to maintain
CC organs before transplantation, to regenerate tissues and in chemotaxis.
CC The polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities.
CC Note: The sequence data for this patent did not form part of the printed

Query Match 25.9%; Score 32.4; DB 22; Length 1110;
Best Local Similarity 54.1%; Pred. No. 4;
Matches 66; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
```

Db 656 GCTTGCTACTGCTGGGAGGAGTAACCTCAAGATGGGAGAGTGCAGGTGACCG 597
Oy 123 ga 124
Db 596 CA 595

RESULT 6
AAL01443/c
ID AAL01443 standard; cDNA: 1110 BP.
XX AAL01443;
XX AC
XX 21-NOV-2001 (first entry)
XX Human reproductive system related antigen cDNA SEQ ID NO: 1444.
XX Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ss.
XX Homo sapiens.
XX OS
XX W0200155320-A2.
XX PD 02-AUG-2001.
XX PE 17-JAN-2001; 2001WO-US01339.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225470.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227092.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.

PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
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PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
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PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.

PF 07-JUL-2000; 2000EP-0114089.
 XX
 PR 08-JUL-1999; 99JP-0194486.
 PR 11-JAN-2000; 2000JP-018774.
 PR 02-MAY-2000; 2000JP-0183765.
 XX
 XX (HELI-) HELIX RES INST.
 XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 DR WPI; 2001-524255/58.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 XX
 PS Claim 2; SEQ ID NO 711; 1380bp + sequence listing; English.
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5' - and 3' -ends of the cDNA
 CC molecules have been determined. Primers for synthesizing the full length
 CC cDNA are useful for clarifying the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesised by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence is the nucleotide
 CC sequence of the 5' -end of a cDNA provided in the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from EPO.
 CC
 SQ Sequence 511 BP; 77 A; 173 C; 180 G; 78 T; 3 other;

Query Match 25.6%; Score 32; DB 22; Length 511;
 Best Local Similarity 55.4%; Pred. No. 4.7;
 Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 5 ccgctggcagcagcgagcagctccgcgcctccgcgagaccacatgcgctccacgttagg 64
 DB 309 CCGCGGGGCGACGCGCGGACACGAGTGCAGACCGCGGCGTCCCGACGCGCG 250
 QY 65 tgggcgtggggggcgagcaggaattgaagcggaagctctgggaagcttagg 116
 DB 249 AGGTGGGCGACCGCGGGCGACGCGGTGGCTGGCAGACCGCGGGCGACGAGGG 198

RESULT 9
 AAK93511/C
 ID AAK93511 standard; cDNA; 511 BP.
 XX
 AC AAK93511;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human cDNA clone representative sequence, SEQ ID NO: 1971.
 KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
 KW
 OS Homo sapiens.
 XX
 PN EP1130094-A2.
 PD
 PD 05-SEP-2001.
 PF 07-JUL-2000; 2000EP-0114089.
 XX
 PR 08-JUL-1999; 99JP-0194486.
 PR 11-JAN-2000; 2000JP-018774.
 PR 02-MAY-2000; 2000JP-0183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 DR WPI; 2001-524255/58.
 XX
 XX 830 Primers useful for synthesizing full length cDNA clones and their
 XX use in genetic manipulation -
 XX
 PS Example 11; SEQ ID NO 1971; 1380bp + sequence listing; English.
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5' - and 3' -ends of the cDNA
 CC molecules have been determined. Primers for synthesizing the full length
 CC cDNA are useful for clarifying the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesised by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence was used as the
 CC representative sequence from a human clone which was used in
 CC homology searches to identify the clone.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from EPO.
 CC
 SQ Sequence 511 BP; 77 A; 173 C; 180 G; 78 T; 3 other;

Query Match 25.6%; Score 32; DB 22; Length 511;
 Best Local Similarity 55.4%; Pred. No. 4.7;
 Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 5 ccgctggcagcagcgagcagctccgcgcctccgcgagaccacatgcgctccacgttagg 64
 DB 309 CCGCGGGGCGACGCGCGGACACGAGTGCAGACCGCGGCGTCCCGACGCGCG 250
 QY 65 tgggcgtggggggcgagcaggaattgaagcggaagctctgggaagcttagg 116
 DB 249 AGGTGGGCGACCGCGGGCGACGCGGTGGCTGGCAGACCGCGGGCGACGAGGG 198

RESULT 10
 AAS29822
 ID AAS29822 standard; DNA; 1371 BP.
 XX
 AC AAS29822;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE Human cytoskeletal element-related polypeptide encoding genomic DNA #9.
 XX
 KW Cytoskeletal element-related protein; human; mouse; rabbit; goat; horse;
 KW cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic;
 KW antirheumatic; antiproliferative; cytoskeletal; cardiant; neuroprotective;
 KW cerebroprotective; neurotopic; antibacterial; virucide; fungicide; cancer;
 KW ophtalmological; vulnary; gene therapy; autoimmune disease; neoplasm;
 KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
 KW cerebrovascular disorder; nervous system disorder; bacterial infection;
 KW fungal infection; viral infection; ocular disorder; endocrine disorder;
 KW gastrointestinal disorder; renal disorder; respiratory disorder;
 KW wound healing; skin aging; organ transplantation; food preservative;
 KW tissue regeneration; anti-fertility; food additive;
 XX
 OS Homo sapiens.
 XX
 PN W0200155168-A1.
 PD
 PD 02-AUG-2001.
 PF 17-JAN-2001; 2001WO-US01331.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 XX

PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 23-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229309.
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PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 25-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.

PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239395.
PR 13-OCT-2000; 2000US-0239397.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249219.
PR 17-NOV-2000; 2000US-0249224.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.

PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-476182/51.
XX
XX Novel isolated human cytoskeletal element-related polypeptide useful
PT for diagnosis/treatment of neoplastic disorders, disorders associated
PT with neutral transmission, chromosomal abnormalities, autoimmune
XX disorders -
PS Claim 1; SEQ ID No 107; 505pp; English.

CC Sequences AAS29814-AAS29838 represent genomic DNA molecules, which encode
CC the cytoskeletal element-related polypeptides of the invention.
CC Cytoskeletal polypeptides and their associated polynucleotides are useful
CC in the diagnosis, treatment and prevention of various types of disorders
CC in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or
CC sheep. A pathological condition can be determined by determining the
CC presence or absence of a mutation in a cytoskeletal polynucleotide. The
CC treatable disorders include autoimmune diseases such as rheumatoid
CC arthritis, hyperproliferative disorders such as neoplasms of the breast
CC or liver, cardiovascular disorders such as cardiac arrest,
CC cerebrovascular disorders such as cerebral ischaemia, nervous system
CC disorders such as Alzheimer's disease, infections caused by bacteria,
CC viruses and fungi, ocular disorders such as corneal infection, endocrine
CC disorders such as premature labour and infertility, gastrointestinal
CC disorders such as Crohn's disease, renal disorders such as
CC glomerulonephritis and respiratory disorders such as asthma. The
CC polypeptides can also be used to aid wound healing, to prevent skin aging
CC due to sunburn, to maintain organs before transplantation, to regenerate
CC tissues and in chemotaxis. The polypeptides can also be used as a food
CC additive or preservative to increase or decrease storage capabilities.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO

Query Match 25.6%; Score 32; DB 22; Length 1371;

Best Local Similarity 54.2%; Pred. No. 5.4;

Matches 65; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 5 ccgctggcgaagcgaggcagctccgctctcgtgagaccattgctccacgttagg 64

Db 616 ccgctggcgaagcagcagctgagtgagagctcgtgagctccgctccgacgtgagc 675

QY 65 tgggcgtggggcggaagcgaatgaagcgaagcttggaagcttaggcgcgcgga 124

Db 676 ttggtgactgctgtggcgaggaagtaacctcaagaagtgggacagtgccgagccgca 735

RESULT 11

AL05199/c

XX ID AAL05199 standard; DNA; 1371 BP.

XX AC AAL05199;

XX DT 21-NOV-2001 (first entry)

DE Human reproductive system related antigen DNA SEQ ID NO: 7887.

XX Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.

OS Homo sapiens.

XX PN MO200155320-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001MO-US01339.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

XX PR 19-MAY-2000; 2000US-0205515.

XX PR 07-JUN-2000; 2000US-0209467.

XX PR 28-JUN-2000; 2000US-0214886.

XX PR 30-JUN-2000; 2000US-0215135.

XX PR 07-JUL-2000; 2000US-0216647.

XX PR 07-JUL-2000; 2000US-0216880.

XX PR 11-JUL-2000; 2000US-0217487.

XX PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.

RESULT 13
AAV43618/c
ID AAV43618 standard; DNA; 1553 BP.
XX
AC AAV43618;
XX
DT 24-SEP-1998 (first entry)
XX
DE Human secreted protein 18 encoding DNA.
XX
KW Secreted protein; human; cell proliferation; cytokine activity;
KW tissue growth; cellular differentiation; regeneration; activin;
KW inhibin; chemotactic; haemostatic; thrombolytic; tumour inhibition;
KW anti-inflammatory activity; biomarker; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 65..1495
FT /tag=a
FT /product="human secreted protein"
XX
PN WO9825959-A2.
XX
PD 18-JUN-1998.
XX
PE 11-DEC-1997; 97WO-US22787.
XX
PR 11-DEC-1996; 96US-0032757.
XX
PA (CHIR) CHIRON CORP.
XX
PI Escobedo J, Garcia P, Hu Q, Kothakota S, Williams LT;
XX WPI; 1998-348453/30.
XX DR P-PSDB; AAW63698.
XX
PT Secreted human polypeptides - having cytokine, cell proliferation or
PT differentiation, activin or inhibin, tumour inhibition or
PT anti-inflammatory activities
XX
PS Claim 6; Pages 45-46; 78pp; English.
XX
CC This DNA encodes a human secreted protein. The specification provides
CC secreted protein sequences (AAW63681 to AAW63699) encoded by the nucleic
CC acid sequences shown in AAV43601 to AAV43619. The invention provides a
CC method of identifying a secreted polypeptide which is modified by rough
CC microsomes. The secreted proteins can be used in assays to determine
CC biological activities, such as cytokine, cell proliferation, or cellular
CC differentiation activities, tissue growth or regeneration, activin or
CC inhibin activity, chemotactic or chemokinetic activity, haemostatic or
CC thrombolytic activity, receptor/ligand activity, tumour inhibition, or
CC anti-inflammatory activity. The proteins can also be used as
CC biomarkers, to identify tissues or cell types which express the proteins,
CC or a stage- or disease-specific alteration in protein expression. They
CC can be used in protein interaction assays, to identify ligands or binding
CC proteins. Compounds which affect the biological activities of the
CC secreted proteins or their ability to interact with specific ligands can
CC be identified using the proteins in screening assays. The proteins and
CC antibodies that bind specifically to the protein can also be used to
CC design diagnostic tests and therapeutic compositions for diseases which
CC may be associated with altered expression of these proteins. Fusion
CC proteins comprising, e.g. signal sequences or transmembrane domains of
CC the proteins can be used to target other protein domains to cellular
CC membrane or they can be secreted extracellularly.
XX
SQ Sequence 1553 BP; 348 A; 384 C; 467 G; 354 T; 0 other;

Query Match 25.6%; Score 32; DB 19; Length 1553;
Best Local Similarity 55.4%; Pred. No. 5.4;

Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 5 ccgttgagcagcgaggcagctccgcgcctctcgagaccactgcgtccagttgagg 64
DB 287 ccctggggcagcagccgacacagcgcacagctgcgaacacgcggctggtccacagcgcc 228
QY 65 tgggctggggcgagcaggaattgaagcggagctctgggaactttagg 116
DB 227 agtggcagcagccggggcagccgctggcctggcagaccggcggtcagagagg 176

RESULT 14
AA087721
ID AA087721 standard; cDNA; 1485 BP.
XX
AC AA087721;
XX
DT 14-NOV-1995 (first entry)
XX
DE Human auxillary cytochrome P450 species 2A6 coding region.
XX
KW Human cytochrome P450; amplification; PCR; primer; expression vector;
KW yeast NADPH-P450 reductase; safety; fusion protein; metabolite;
KW carcinogen; mutagen; liver metabolism; ds.
XX
OS Homo sapiens.
XX
FN EP644267-A.
XX
PD 22-MAR-1995.
XX
PE 20-JUL-1994; 94EP-0111298.
XX
PR 21-JUL-1993; 93JP-0180246.
PR 20-JUL-1993; 93JP-0201120.
PR 30-JUL-1993; 93JP-0208279.
XX
PA (HAYASHI) HAYASHI K.
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
PI Hayashi K, Kaneko H, Komai K, Nakatsuka I, Sakaki T;
PI Yabusaki Y;
XX
XX WPI; 1995-116991/16.
XX DR P-PSDB; AAR72367.
XX
PT Evaluation of safety of a chemical cpd. - using recombinant yeast
PT expressing human cytochrome P450 and a yeast NADPH-P450 reductase
XX
PS Examples; Page 49-51; 124pp; English.
XX
CC The nucleotide sequence of the cDNA coding region for the human
CC auxillary cytochrome P450 species 2A6. The gene encodes a protein of 494
CC amino acids. The cDNA was amplified by PCR using the primers AA087751-4.
CC The product was cloned into the yeast expression vectors PAH5N or PAHRH
CC to produce the vectors p2A6 for the expression of the cytochrome P450
CC alone or p2A6R for co-expression with the yeast NADPH-P450 reductase.
CC The vectors are used in a method for evaluating the safety of a chemical
CC compound by reacting the chemical compound with recombinantly produced
CC human cytochrome P450 molecular species 1A2 (AA087714), 2C9 (AA087715),
CC 2E1 (AA087716), or 3A4 (AA087717) or their auxillary species and
CC variants (AA087718-32), and yeast NADPH-P450 reductase, either as a fused
CC protein or in cell extracts, and analysing the resulting metabolite to
CC assess the safety of the chemical compound. The method is useful for
CC determining whether the chemical compound, or its metabolite, will be
CC converted into a carcinogenic or mutagenic form through metabolism in the
CC liver.
XX
SQ Sequence 1485 BP; 327 A; 430 C; 413 G; 315 T; 0 other;

Query Match 25.3%; Score 31.6; DB 16; Length 1485;
Best Local Similarity 58.5%; Pred. No. 7;

us-09-834-291-2_copy_1_125.rng

to assess the safety of the chemical compound. The method is useful for determining whether the chemical compound or its metabolites will be

Db 420 gggaagcagagcatcgaagagcgcatccaggag 453

Search completed: September 7, 2002, 18:40:35
Job time: 29929 sec

